



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 174153

TO: Nita M Minnifield
Location: rem/3C01/3C18
Art Unit: 1645
Monday, December 19, 2005

Case Serial Number: 09/970076

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

*Reviewed
12/05
mm*

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STIC-Biotech/ChemLib

174153

mg

From: Chan, Christina
Sent: Tuesday, December 13, 2005 6:38 PM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush interference sequence search

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, December 13, 2005 1:27 PM
To: Chan, Christina
Subject: rush interference sequence search

Christina, please approve, AF amdt.

STIC

09/970076

Please do an interference sequence search on the following sequences found in the above application.

Please search against both aa and nt databases.

SEQ ID NO: 1
nt 104-1207 of SEQ ID NO: 1
SEQ ID NO: 2
aa 27-321 of SEQ ID NO: 2
aa 28-320 of SEQ ID NO: 2
aa 41-227 of SEQ ID NO: 2
aa 44-216 of SEQ ID NO: 2
aa 42-222 of SEQ ID NO: 2

Please provide a paper copy of all results.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 12/14/05
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search _____
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

reverse to AA
reverse to NA

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; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 2,52e-108 Length: 1609
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-09-620-312D-8 (1-1609)

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Oy 21 TyrPheValGIuGIuLeuAlaHISLyPheIleSerProGIuLeuArgMetSerPheIle 40
Db 498 TACTTGTGGAAACAGTTGGCTCACAATTCATCAGCCACAGTTGAGAAATGCTTTATTT 557
Oy 41 ValPheSerThrArgGIyThrThrLeuMetLySeuThrGIuAsnArgGIuGIuIleArg 60
Db 558 GTTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAAACAATCCGT 617
Oy 61 GInGIyLeuGIuGIuLeuGIuLeuValLeuProGIyGIyAepThrTYrMetHISGIuGIy 80
Db 618 CAAAGCCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTAAGTATGATGAAGA 677
Oy 81 PheGIuArgAlaSerGIuGIuIleTYrTYrGIuAsnArgGIuGIyTYrArgThrAlaSer 100
Db 678 TTGAAAGGGCCAGAGAGAGATTATTTGAAAACAGACAAAGGGTACAGACAGCCAGC 737
Oy 101 ValIleIleAlaLeuThrAspGIyGIuLeuHISGIuAsnPhePheTYrSerGIuArg 120
Db 738 GTCAATCATTTGCTTGAATGATGAGAACTCCAGAAAGCTCTTTTCTATTCAGAGAGG 797
Oy 121 GIuAlaAsnArgSerArgAspLeuGIyAlaIleValTYrCySeValGIyValIyAsnPhe 140
Db 798 GAGGCTATAGCTCTCGAGATCTTGCGCAATGTTTACTGTGGTGTGAAGATTTTC 857
Oy 141 AenGIuThrGIuLeuAlaArgIleAlaAspSerLyAsnPheIleValPheProValAsnAsp 160
Db 858 AATGAGACACAGCTGGCCGAGATTCGGGACAGTAAAGATCATGTGTTCCTCGATGATGAC 917
Oy 161 GIyPheGIuAlaLeuGIuGIyIleIleHISerIleu 173
Db 918 GGCCTTCAGGCTCTGCAGAGCATCATCACTCAATTTTG 956

RESULT 2
US-10-104-047-669
; Sequence 669, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10104,047
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 669
; LENGTH: 2234
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-104-047-669

Alignment Scores:
Pred. No.: 4,49e-58 Length: 2234
Score: 519.00 Matches: 103
Percent Similarity: 79.19% Conservative: 34
Best Local Similarity: 59.54% Mismatches: 34
Query Match: 57.73% Indels: 2
DB: 3 Gaps: 1

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Db 658 GATCTCACTTCGCTCGTGCACAACTGGAGTGTGGCAATTAATCTGATTTGAATTTAT 717
Oy 21 TyrPheValGIuGIuLeuAlaHISLyPheIleSerProGIuLeuArgMetSerPheIle 40
Db 718 AATTCGTACAGAACTTGGAGAGATTGTGAGCTCTGAAATGAGATTATCTTTCAATT 777
Oy 41 ValPheSerThrArgGIyThrThrLeuMetLySeuThrGIuAsnArgGIuGIuIleArg 60
Db 778 GTGTTTCTTCTCAAGCACTATTAATTTGGCATTAATGAGACAGAGCAAAATCAGT 837
Oy 61 GInGIyLeuGIuGIuLeuGIuLeuValLeuProGIyGIyAepThrTYrMetHISGIuGIy 80
Db 838 AAAGCCTTGGAGATTTTAAACGTGTAGTCCAGTGAAGAGACATATATCCATGAAGA 897
Oy 81 PheGIuArgAlaSerGIuGIuIleTYrTYrGIuAsnArgGIuGIyTYrArgThrAlaSer 100
Db 898 CTAAAGCTAGCAATGAACAAATTT-----CAGAAAGCAGAGGCTTAAACCTCCAGT 951
Oy 101 ValIleIleAlaLeuThrAspGIyGIuLeuHISGIuAsnPhePheTYrSerGIuArg 120
Db 952 ATCATTAATTTGCTTGAACAGATGGCAAGTTGACCGCTGTGGCCATCATATGACAGAAA 1011
Oy 121 GIuAlaAsnArgSerArgAspLeuGIyAlaIleValTYrCySeValGIyValIyAsnPhe 140
Db 1012 GAGGCAAGATATCATGAGTCACTTGGGCTAGTGTATTGTGTGGTGTCTTGAATTTT 1071
Oy 141 AenGIuThrGIuLeuAlaArgIleAlaAspSerLyAsnPheIleValPheProValAsnAsp 160
Db 1072 GAAACAAGCAGCTTGAAGAAATGCTGATTCAGAGAGCAAGTTTCCCTCTCAAGCT 1131
Oy 161 GIyPheGIuAlaLeuGIuGIyIleIleHISerIleu 173
Db 1132 GGAATTCAGGCTCTTAAAGAAATATTAATCTATACTA 1170

RESULT 3
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyao
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37, Search time 121.458 Seconds
(without alignments)
3531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_44_216
Perfect score: 899
Sequence: 1 DLYFLDKSGSVLHMHNEIY.....HYFVNDQFALQGIHSIL 173

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Ygapop 10.0, Ygapext 0.5
Pgapop 6.0, Pgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blodum62 -TRANS=human40.cdt
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-DEF TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/65.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/65.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE.COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 899 | 100.0 | 1609 | 3 | US-09-620-312D-8 |
| 2 | 519 | 57.7 | 2234 | 3 | US-10-104-047-669 |
| 3 | 461 | 51.3 | 1492 | 3 | US-09-774-528-297 |
| 4 | 461 | 51.3 | 1492 | 3 | US-10-120-988-297 |
| 5 | 138.5 | 15.4 | 3528 | 2 | US-08-286-889-36 |
| 6 | 138.5 | 15.4 | 3528 | 2 | US-08-485-618-36 |
| 7 | 138.5 | 15.4 | 3528 | 2 | US-08-362-652-36 |
| 8 | 138.5 | 15.4 | 3528 | 2 | US-08-605-672-36 |
| 9 | 138.5 | 15.4 | 3528 | 2 | US-08-482-293A-36 |

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| 10 | 138.5 | 15.4 | 3528 | 2 | US-08-943-363-36 | Sequence 36, Appl |
| 11 | 138.5 | 15.4 | 3528 | 3 | US-09-193-043-36 | Sequence 36, Appl |
| 12 | 138.5 | 15.4 | 3528 | 3 | US-09-688-307A-36 | Sequence 36, Appl |
| 13 | 138.5 | 15.4 | 3528 | 3 | US-09-350-259-36 | Sequence 36, Appl |
| 14 | 138.5 | 15.4 | 3597 | 2 | US-08-485-618-54 | Sequence 54, Appl |
| 15 | 138.5 | 15.4 | 3597 | 2 | US-08-362-652-54 | Sequence 54, Appl |
| 16 | 138.5 | 15.4 | 3597 | 2 | US-08-605-672-54 | Sequence 54, Appl |
| 17 | 138.5 | 15.4 | 3597 | 2 | US-08-482-293A-54 | Sequence 54, Appl |
| 18 | 138.5 | 15.4 | 3597 | 2 | US-08-943-363-54 | Sequence 54, Appl |
| 19 | 138.5 | 15.4 | 3597 | 3 | US-09-193-043-54 | Sequence 54, Appl |
| 20 | 138.5 | 15.4 | 3597 | 3 | US-09-688-307A-54 | Sequence 54, Appl |
| 21 | 138.5 | 15.4 | 3597 | 3 | US-09-350-259-54 | Sequence 54, Appl |
| 22 | 134.5 | 15.0 | 3519 | 2 | US-08-286-889-45 | Sequence 45, Appl |
| 23 | 134.5 | 15.0 | 3519 | 2 | US-08-485-618-45 | Sequence 45, Appl |
| 24 | 134.5 | 15.0 | 3519 | 2 | US-08-362-652-45 | Sequence 45, Appl |
| 25 | 134.5 | 15.0 | 3519 | 2 | US-08-605-672-45 | Sequence 45, Appl |
| 26 | 134.5 | 15.0 | 3519 | 2 | US-08-482-293A-45 | Sequence 45, Appl |
| 27 | 134.5 | 15.0 | 3519 | 2 | US-08-943-363-45 | Sequence 45, Appl |
| 28 | 134.5 | 15.0 | 3519 | 3 | US-09-193-043-45 | Sequence 45, Appl |
| 29 | 134.5 | 15.0 | 3519 | 3 | US-09-688-307A-45 | Sequence 45, Appl |
| 30 | 134.5 | 15.0 | 3519 | 3 | US-09-350-259-45 | Sequence 45, Appl |
| 31 | 134.5 | 15.0 | 3803 | 2 | US-08-485-618-52 | Sequence 52, Appl |
| 32 | 134.5 | 15.0 | 3803 | 2 | US-08-362-652-52 | Sequence 52, Appl |
| 33 | 134.5 | 15.0 | 3803 | 2 | US-08-605-672-52 | Sequence 52, Appl |
| 34 | 134.5 | 15.0 | 3803 | 2 | US-08-482-293A-52 | Sequence 52, Appl |
| 35 | 134.5 | 15.0 | 3803 | 2 | US-08-943-363-52 | Sequence 52, Appl |
| 36 | 134.5 | 15.0 | 3803 | 3 | US-09-193-043-52 | Sequence 52, Appl |
| 37 | 134.5 | 15.0 | 3803 | 3 | US-09-688-307A-52 | Sequence 52, Appl |
| 38 | 134.5 | 15.0 | 3803 | 3 | US-09-350-259-52 | Sequence 52, Appl |
| 39 | 128.5 | 14.3 | 3533 | 2 | US-08-476-062A-40 | Sequence 40, Appl |
| 40 | 128.5 | 14.3 | 3533 | 6 | PCT-US96-01314-40 | Sequence 40, Appl |
| 41 | 128.5 | 14.3 | 3533 | 9 | 5424399-1 | Patent No. 5424399 |
| 42 | 128.5 | 14.3 | 3533 | 3 | US-09-023-655-1147 | Sequence 1147, Ap |
| 43 | 128.5 | 14.3 | 4045 | 3 | US-09-809-517A-37 | Sequence 37, Appl |
| 44 | 128.5 | 14.3 | 4124 | 3 | US-09-023-655-1178 | Sequence 1178, Ap |
| 45 | 128.5 | 14.3 | 4740 | 3 | US-09-902-481B-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1

US-09-620-312D-8

Sequence 8, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Aundt, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yungqun

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghast

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIP2B

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pc_fl_genes Version 1.0

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/ SOFTWARE: pc_Fl_genes Version 2.0
/ SEQ ID NO 297
/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79)..(1434)
US-09-974-528-297

Alignment Scores:
Pred. No.: 1.09e-50 Length: 1492
Score: 461.00 Matches: 92
Percent Similarity: 78.12% Conservative: 33
Best Local Similarity: 57.50% Mismatches: 33
Query Match: 51.28% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_COPY_44_216 (1-173) x US-09-974-528-297 (1-1492)
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D 16 AATPACTGGAATTAATTATTTGTCACAGCACTTGGGAGAGATTGTGAGCCCT 75
QY 34 GlnLeuArgMetSerPHEIleValPHESerThrArgLyThrThrLeuMetLysLeuThr 53
D 76 GAATGAGATTATCTTCATTGTGTTCTTCACAGCACTATTATTGGCCATTAACT 135
QY 54 GluAspArgGluGlnIleArgGlnLyLeuGluGluLeuGlnLysValLeuProGlyGly 73
D 136 GGAGACAGAGCGAAATCAGTAAGCTTGAGAGATTAAACGTTAGTCCAGTAGGA 195
QY 74 AspThrTyRmetHisGluGlyPHEGluArgAlaSerGluGlnIleTyTYRGLuAsnArg 93
D 196 GAGACATATTCATCGATGAGACTAAAGCTGACCAATGACAAAT-----CAGAAACA 249
QY 94 GlnGlyTyRArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHISGluAsp 113
D 250 GGAGGCTTGAAACCTCCAGTATCATTAATGCTCTGACAGTGGCAGTGGACGCTCTG 309
QY 114 LeuPHEPHEtyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyR 133
D 310 GTGCCATCATATGACAGAAAGAGCAAGATATCCAGGTCACTGGGCTAGGTTAT 369
QY 134 CyValGlyValIlyAspPHEAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAsp 153
D 370 TGTGTTGGGCTCTTGAATTTTGAACAAGCAGCTTGAAGAATGCTGATTCAGAGAG 429
QY 154 HIsValPHEProValaAsnAspGlyPHEGlnAlaLeuGlnGlyIleIleHISerIleLeu 173
D 430 CAAGTTTCCCTGTCAGAAAGTGATTCAGGCTCTTAAGAAATTAATTATTTCTATCTA 489

RESULT 4
US-10-120-988-297
/ Sequence 297, Application US/10120988
/ Patent No. 6919193
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Ren, Feiyen
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6919193el Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 802CON
/ CURRENT APPLICATION NUMBER: US/10/120,988
/ PRIOR FILING DATE: 2002-04-11
/ PRIOR APPLICATION NUMBER: 09/774,528
/ PRIOR FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: pc_Fl_genes Version 2.0
/ SEQ ID NO 297
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/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79)..(1434)
US-10-120-988-297

Alignment Scores:
Pred. No.: 1.09e-50 Length: 1492
Score: 461.00 Matches: 92
Percent Similarity: 78.12% Conservative: 33
Best Local Similarity: 57.50% Mismatches: 33
Query Match: 51.28% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_COPY_44_216 (1-173) x US-10-120-988-297 (1-1492)
QY 14 HSHIETPANGIUIETTYRPhEVALGluGluLeuLAlAHISLysPHEIleSerPro 33
D 16 AATPACTGGAATTAATTATTTGTCACAGCACTTGGGAGAGATTGTGAGCCCT 75
QY 34 GlnLeuArgMetSerPHEIleValPHESerThrArgLyThrThrLeuMetLysLeuThr 53
D 76 GAATGAGATTATCTTCATTGTGTTCTTCACAGCACTATTATTGGCCATTAACT 135
QY 54 GluAspArgGluGlnIleArgGlnLyLeuGluGluLeuGlnLysValLeuProGlyGly 73
D 136 GGAGACAGAGCGAAATCAGTAAGCTTGAGAGATTAAACGTTAGTCCAGTAGGA 195
QY 74 AspThrTyRmetHisGluGlyPHEGluArgAlaSerGluGlnIleTyTYRGLuAsnArg 93
D 196 GAGACATATTCATCGATGAGACTAAAGCTGACCAATGACAAAT-----CAGAAACA 249
QY 94 GlnGlyTyRArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHISGluAsp 113
D 250 GGAGGCTTGAAACCTCCAGTATCATTAATGCTCTGACAGTGGCAGTGGACGCTCTG 309
QY 114 LeuPHEPHEtyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyR 133
D 310 GTGCCATCATATGACAGAAAGAGCAAGATATCCAGGTCACTGGGCTAGGTTAT 369
QY 134 CyValGlyValIlyAspPHEAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAsp 153
D 370 TGTGTTGGGCTCTTGAATTTTGAACAAGCAGCTTGAAGAATGCTGATTCAGAGAG 429
QY 154 HIsValPHEProValaAsnAspGlyPHEGlnAlaLeuGlnGlyIleIleHISerIleLeu 173
D 430 CAAGTTTCCCTGTCAGAAAGTGATTCAGGCTCTTAAGAAATTAATTATTTCTATCTA 489

RESULT 5
US-08-286-889-36
/ Sequence 36, Application US/08286889
/ Patent No. 5470953
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Mich
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Marshall, O'Toole, Gerstein, Murray & Bornun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/286,889
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FILING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/173,497
APPLICATION NUMBER: 23-DEC-1993
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-286-889-36

Alignment Scores:
Pred. No.: 1,136-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
DB: 2 Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-08-286-889-36 (1-3528)

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DB 484 AAGCACTTGTCAAGCTTGATGGAGAGTTGGCAGACCAAGCACTTGTCTCTCCCTG 543
QY 40 lleAlpHeSerThaRgLyThyRleuMeLyLeuThRglu----- 54
DB 544 ATGCATATCTCAAACTCTCTGAAGACCTTTACTTCACTGAATTCAGAAATCCCTG 603
QY 55 AaPArGluGlnIleAryGlnleuGluInleuGlnIleValleuProGlyGlyAaP 74
DB 604 GACCCCTCAAGGCTGTGATCCCATTTGCCAGCTGCA-----GGCCCTG 648
QY 75 ThTyRMeChIaGluGlyPheGluAaGlaSerGluGlnIleTyTyTyRgluAaPArgGln 94
DB 649 ACCTACACAGCCACAGACATCCGAGACGATGGAAGAGCTATTTCATAGCAAGAAATGG 708
QY 95 GlTyTyARgThRaIa---ServalIleIleAlaLeuThAaPlyGluIleuNhiGluAaP 113
DB 709 TCCCGTAAAGTCCCAAGAAAGATCTCTCTGTATCAACATGGGCAAGAAATACAGAGAC 768
QY 114 LeuPhePheTySerGlu-----ArgGluAlaAaArySerAryAaPleuGlyAlaIle 131
DB 769 CCCCTGAGTATATGATGTCATTTCCGCGCAGACAAAGCT-----GGCATCATTT 819
QY 132 ValTyTyCyVaIGlyVallyAaP---PheAaGlu---ThRInleuAlaAaGlyle--- 148
DB 820 CGTTATGCTATTGGGGTGGAGATGCCCTTCACAGAGCCCACTGCCCTGAAGAGCTGAAC 879
QY 149 -----AlaAaPserLyAaPPhIleValPheProValAaAaPlyPheGlnAla 164
DB 880 ACCATTGGCTCAAGCTCCCAAGACAGACAGCTGTTCAAGTAAAGCAAC---TTTGAAGCA 936
QY 165 leuGlnIlyle 168
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DB 937 CTTCGACGATC 948

RESULT 6
US-08-485-618-36
Sequence 36, Application US/08485618
Parent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-485-618-36

Alignment Scores:
Pred. No.: 1,136-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
DB: 2 Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-08-485-618-36 (1-3528)

QY 1 AaPLeuTyRPhelileuAaPlySerglyServal---LeuNhiEhItrPaNgluile 19
DB 424 GACATTGGCTTCTCGATTGATGTTCTGGCAGCATTAACCAAGGACCTTGGCCCAAG 483
QY 20 TyTyTyRPhenaIGluInleuAhiLySpheilleSerProGlnleuArygMeSerPhe 39
DB 484 AAGCACTTGTCAAGCTTGATGGAGAGTTGGCAGACCAAGCACTTGTCTCTCCCTG 543
QY 40 lleAlpHeSerThaRgLyThyRleuMeLyLeuThRglu----- 54
DB 544 ATGCATATCTCAAACTCTCTGAAGACCTTTACTTCACTGAATTCAGAAATCCCTG 603
QY 55 AaPArGluGlnIleAryGlnleuGluInleuGlnIleValleuProGlyGlyAaP 74
DB 604 GACCCCTCAAGGCTGTGATCCCATTTGCCAGCTGCA-----GGCCCTG 648
QY 75 ThTyRMeChIaGluGlyPheGluAaGlaSerGluGlnIleTyTyTyRgluAaPArgGln 94
DB 649 ACCTACACAGCCACAGACATCCGAGACGATGGAAGAGCTATTTCATAGCAAGAAATGG 708
QY 95 GlTyTyARgThRaIa---ServalIleIleAlaLeuThAaPlyGluIleuNhiGluAaP 113
DB 709 TCCCGTAAAGTCCCAAGAAAGATCTCTCTGTATCAACATGGGCAAGAAATACAGAGAC 768
QY 114 LeuPhePheTySerGlu-----ArgGluAlaAaArySerAryAaPleuGlyAlaIle 131
DB 769 CCCCTGAGTATATGATGTCATTTCCGCGCAGACAAAGCT-----GGCATCATTT 819
QY 132 ValTyTyCyVaIGlyVallyAaP---PheAaGlu---ThRInleuAlaAaGlyle--- 148
DB 820 CGTTATGCTATTGGGGTGGAGATGCCCTTCACAGAGCCCACTGCCCTGAAGAGCTGAAC 879
QY 149 -----AlaAaPserLyAaPPhIleValPheProValAaAaPlyPheGlnAla 164
DB 880 ACCATTGGCTCAAGCTCCCAAGACAGACAGCTGTTCAAGTAAAGCAAC---TTTGAAGCA 936
QY 165 leuGlnIlyle 168
|||::: |||

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QY 40 ILevalPheSerThrArgGlyThrThreumetySLeuThrGlu----- 54
DB 544 ATGCAATCTGCAACATCTGTAAGACCCATTTTACCTTCAGTAATTCAGAAACATCTGG 603
QY 55 AApArgGluGlnIleArgGlnIleuGluGlnIleValLeuProGlyValAsp 74
DB 604 GACCTTCAGAGCTGTGGATCCCATTTCCAGCTGCACA-----GGCCTG 648
QY 75 ThrTyMetHisGluGlyPheGluArgAlaSerGluGlnIleTyThrGluAsnArgGln 94
DB 649 ACCTACACAGCCACAGGATCCGACAGATGAGAAAGCTTTCATTCAGCAAGATGG 708
QY 95 GlyTyArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 113
DB 709 TCCGCTAAAGTCCAGAAAGATCTCTTCATCAGACAGATGGGACAGAAATACAGAGAC 768
QY 114 LeuPhePheTySerGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 131
DB 769 CCCCTGAGATAGTATGATGTCTATTCGCCGCGCAGACAAAGCT-----GGCATCAT 819
QY 132 ValTyCyValGlyValIleAsp---PheAsnGlu---ThrGlnLeuAlaArgIle--- 148
DB 820 CGTATGCTATTGGGTGGAGATGCTTCCAGAGCCCATCTGCCCTGAGAGAGCTGAAC 879
QY 149 -----AlaAspSerLyAspHisValPheProValAsnAspGlyPheGlnAla 164
DB 880 ACCATTGGCTACGCTCCCCACAGACACCGTTCAGAGTGGACAC---TTTCACACA 936
QY 165 LeuGlnGlyIle 168
DB 937 CTCGACAGCATC 948

RESULT 7
US-08-362-652-36
Sequence 36, Application US/08362652
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
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SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-362-652-36

Alignment Scores:
Pred. No.: 1,13e-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
DB: Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-08-362-652-36 (1-3528)

QY 1 AApLeuTyPhePheIleLeuAspLySerGlySerVal---LeuHisIleThrAsnGluIle 19
DB 424 GACATGCTTTCGATGATGATGCTTCCGACATTAACCAAGGACTTTGCCAGATG 483
QY 20 TyTyArgPheValGluGlnLeuAlaHisLyAspHeIleSerProGlnLeuArgMetSerPhe 39
DB 484 AAGACCTTTCGCAAGCTTGTATGGAGAGATTGGAGACACAGACACTTGTCTCCCTG 543
QY 40 ILevalPheSerThrArgGlyThrThreumetySLeuThrGlu----- 54
DB 544 ATGCAATCTGCAACATCTGTAAGACCCATTTTACCTTCAGTAATTCAGAAACATCTGG 603
QY 55 AApArgGluGlnIleArgGlnIleuGluGlnIleValLeuProGlyValAsp 74
DB 604 GACCTTCAGAGCTGTGGATCCCATTTCCAGCTGCACA-----GGCCTG 648
QY 75 ThrTyMetHisGluGlyPheGluArgAlaSerGluGlnIleTyThrGluAsnArgGln 94
DB 649 ACCTACACAGCCACAGGATCCGACAGATGAGAAAGCTTTCATTCAGCAAGATGG 708
QY 95 GlyTyArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 113
DB 709 TCCGCTAAAGTCCAGAAAGATCTCTTCATCAGACAGATGGGACAGAAATACAGAGAC 768
QY 114 LeuPhePheTySerGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 131
DB 769 CCCCTGAGATAGTATGATGTCTATTCGCCGCGCAGACAAAGCT-----GGCATCAT 819
QY 132 ValTyCyValGlyValIleAsp---PheAsnGlu---ThrGlnLeuAlaArgIle--- 148
DB 820 CGTATGCTATTGGGTGGAGATGCTTCCAGAGCCCATCTGCCCTGAGAGAGCTGAAC 879
QY 149 -----AlaAspSerLyAspHisValPheProValAsnAspGlyPheGlnAla 164
DB 880 ACCATTGGCTACGCTCCCCACAGACACCGTTCAGAGTGGACAC---TTTCACACA 936
QY 165 LeuGlnGlyIle 168
DB 937 CTCGACAGCATC 948

RESULT 8
US-08-605-672-36
Sequence 36, Application US/08605672
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
```

CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-605-672-36
US-08-605-672-36
Alignment Scores:
Pred. No.: 1.13e-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
DB: 2 Gaps: 10
US-09-970-076-2_COPY_44_216 (1-173) x US-08-605-672-36 (1-3528)
QY 1 AspleuTyrrPheleleuAaplySserGlySerVal---LeuHshstPnaengluile 19
DB 424 GACATTGCTTCTTCTGATGATGCTTGCGAGCATTTAACCAAGGACCTTGCCCATG 43
QY 20 TyrrTyrrPheValGluGluLeuAlaHshPheleSserProGluLeuAargMetSerPhe 39
DB 484 AAGGACTTGTCAAGCTTGAAGGAGGAGATTTCGCGACACGACACCTGTTCTCCCTG 543
QY 40 lleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlu----- 54
DB 544 ATGCATTAACGCAACATCCGAGAGACCATTTACTTCACTGAATTCAAGAACATCCTG 603
QY 55 AsparGluGluInleatGngInGlyLeuGluGluLeuGlnValLeuProGlyGlyAsp 74
DB 604 GACCCCTGAGAGCTGCGATGCCATTGTCCAGCTGCA-----GGCTG 648
QY 75 ThrTyrrMetHisGluGlyPheGluArgAlaSerGluGluInleTyrrTyrrGluAenArgGln 94
DB 649 ACCTACACAGCCACAGGACATCCGACAGTGTATGAGAGAGCTATTTCATAGCAAGATGGG 708
QY 95 G1TyrrArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHshGluAsp 113

DB 709 TCCCTTAAGAGTCCCAAGAAATCTCTTGTGCATCAGATGGCGAGAAATACAGAGAC 768
QY 114 LeuPhePheTyrrSerGlu-----ArgGluAlaAenArgSerArgAspLeuGlyAlaIle 131
DB 769 CCCCTGAGATGATGATGATGATCTCCCGCCGAGCAAAAGCT-----GGCATCATTT 819
QY 132 ValTyrrCySerValGlyValLysAsp---PheAenglu---ThrGlnLeuAlaArgIle--- 148
DB 820 CGTATGCTATTGGGGGTGGAGATGCTTCCAGAGAGCCCATGCTGCTGAAGAGCTGAAC 879
QY 149 -----AlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 164
DB 880 ACCATTGGCTCAGCTCCCCCAGAGACACGATGTTCAAGTATGGCAAC---TTTGACGCA 936
QY 165 LeuGngGlyIle 168
DB 937 CTTCGACGATC 948
RESULT 9
US-08-482-293A-36
Sequence 36, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-482-293A-36

Alignment Scores:
 Pred. No.: 1,13e-07 Length: 3528
 Score: 138.50 Matches: 52
 Percent Similarity: 47.83% Conservative: 36
 Best Local Similarity: 28.26% Mismatches: 71
 Query Match: 15.41% Indels: 25
 DB: 2 Gaps: 10

US-09-970-076-2_copy_44_216 (1-173) x US-08-482-293A-36 (1-3528)

QY 1 AspleuYrPheilleuAaplySerglyServal---LeuHshstPaspngluile 19
 DB 424 GACATTCCTTCTGATGATGTTCTGGCAGCATTAACCAAGGAGCTTGTCCAGATG 483
 QY 20 TyrTyrrPheValIgluInleuAlahleYpheiIeserProglInleuAargMetSerPhe 39
 DB 484 AAGGACTTGTCAAGCTTGAAGAGATTGGAGACCTTGGACACAGACCTTGTCTCCCTG 543
 QY 40 IleValPheSerThraArglyThrThleuMetlySleuthrglu----- 54
 DB 544 ATGCATATCTGACATCTGAGATCCCATTTTACTTCACTGATTCAGAAATCTCTG 603
 QY 55 AspargluInleuAargInglyLeuInluInleuInlySvalleuProglyYasp 74
 DB 604 GACCTCAGAGCTGGTGATCCCATTTGTCCAGCTGCA-----GGCCTG 648
 QY 75 ThrTyrrMetIleaglIgluPhegluAarglaserIgluInleuTyrrTyrgluAasnArgln 94
 DB 649 ACCTACACAGCCAGGATCCGAGCATGTGAAGCATTTCAATGACAAATGAGG 708
 QY 95 GlyTyrrArgThraIa---ServalIleleAlaIleuThraSrglygluInleuHsgluAap 113
 DB 709 TCCCGTAAAGTGCAGAAAGATCTCTCTGTCTACAGATGGGCAAAATACAGAGAC 768
 QY 114 LeupheheryrSerglu-----ArggluAlaasnArgserAargleuGlyAlaIle 131
 DB 769 CCCCTGAGTATGATGATGTCATTCGCCGCCAGACAAAGT-----GGCATCTT 819
 QY 132 ValTyrrCyavaIgluVallyAap---Pheasnglu---ThrgInleuAlaArgIle--- 148
 DB 820 CGTTATCTATTTGGGTGGAGATCCCTTCAGAGACCCCATGCCCTGAAGAGACTGAC 879
 QY 149 -----AlaasPserLyasPheIvalPheProvalaasnArgglyPhegluAla 164
 DB 880 ACCATGCTCAGCTCCGCCACAGACACGTTTCAAGTAGGCAAC---TTGCAGCA 936
 QY 165 LeuInglyIle 168
 DB 937 CTTGCGAGCATC 948

RESULT 10

US-08-943-363-36

Sequence 36 Application US/08943363

Patent No. 5837478

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vlieten, Monica

TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Seair Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943.363

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32684

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 3528 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3456

US-08-943-363-36

Alignment Scores:

Pred. No.: 1,13e-07 Length: 3528

Score: 138.50 Matches: 52

Percent Similarity: 47.83% Conservative: 36

Best Local Similarity: 28.26% Mismatches: 71

Query Match: 15.41% Indels: 25

DB: 2 Gaps: 10

US-09-970-076-2_copy_44_216 (1-173) x US-08-943-363-36 (1-3528)

QY 1 AspleuYrPheilleuAaplySerglyServal---LeuHshstPaspngluile 19
 DB 424 GACATTCCTTCTGATGATGTTCTGGCAGCATTAACCAAGGAGCTTGTCCAGATG 483
 QY 20 TyrTyrrPheValIgluInleuAlahleYpheiIeserProglInleuAargMetSerPhe 39
 DB 484 AAGGACTTGTCAAGCTTGAAGAGATTGGAGACCTTGGACACAGACCTTGTCTCCCTG 543
 QY 40 IleValPheSerThraArglyThrThleuMetlySleuthrglu----- 54
 DB 544 ATGCATATCTGACATCTGAGATCCCATTTTACTTCACTGATTCAGAAATCTCTG 603
 QY 55 AspargluInleuAargInglyLeuInluInleuInlySvalleuProglyYasp 74
 DB 604 GACCTCAGAGCTGGTGATCCCATTTGTCCAGCTGCA-----GGCCTG 648
 QY 75 ThrTyrrMetIleaglIgluPhegluAarglaserIgluInleuTyrrTyrgluAasnArgln 94
 DB 649 ACCTACACAGCCAGGATCCGAGCATGTGAAGCATTTCAATGACAAATGAGG 708
 QY 95 GlyTyrrArgThraIa---ServalIleleAlaIleuThraSrglygluInleuHsgluAap 113
 DB 709 TCCCGTAAAGTGCAGAAAGATCTCTCTGTCTACAGATGGGCAAAATACAGAGAC 768
 QY 114 LeupheheryrSerglu-----ArggluAlaasnArgserAargleuGlyAlaIle 131
 DB 769 CCCCTGAGTATGATGATGTCATTCGCCGCCAGACAAAGT-----GGCATCTT 819
 QY 132 ValTyrrCyavaIgluVallyAap---Pheasnglu---ThrgInleuAlaArgIle--- 148
 DB 820 CGTTATCTATTTGGGTGGAGATCCCTTCAGAGACCCCATGCCCTGAAGAGACTGAC 879

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Oy 149 -----AlaAspSerIySaSpHiSaValPheProValIaSaAspGlyPheGlnIla 164
Db 880 ACCATTGGCTGACGCTCCCCACAGACGACGCTTCAAGTAGGCAAC---TTTCACAGA 936
Oy 165 LeuGlnGlyIle 168
Db 937 CTCGCAGCAGATC 948

RESULT 11
US-09-193-043-36
/ Sequence 36, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6251395el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ EARLIER FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 36
/ LENGTH: 3528
/ TYPE: DNA
/ ORGANISM: Rattus rattus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(3453)
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-36

Alignment Scores:
Pred. No.: 1.13e-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83 Conservative: 36
Best Local Similarity: 28.26 Mismatches: 71
Query Match: 15.41 Indels: 25
DB: Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-09-193-043-36 (1-3528)
Oy 1 AAPLeuTyRPhelIleuSaSpHiSaValPheProValIaSaAspGlyPheGlnIle 19
Db 424 GACATTGCTTCTCTGATTGATGCTTGGCAGCATTAACCAAGGACCTTGGCCCGAGATG 483
Oy 20 TyTyTyRPhaValGluInLeuAlaHisIySaPheIleSerProGlnLeuAlaGlyMetSerPhe 39
Db 484 AAGGACTTGTCAAACTTGTGATGGAGAGTTGGCAGACCAAGCACTTGTCTCCG 543
Oy 40 ILeValPheSerThrArgIlyThrIleuMetIyLeuThiGlu----- 54
Db 544 ATGCATTAACCTCGAACTCTGAAAGACCAATTTTACCTTCACTGAATTTCAAGACATCTCG 603
Oy 55 AAPaRgGluGlnIleArgGlnIyLeuGluGlnIleuValLeuProGlyIyAaP 74
Db 604 GACCCCTCAGAGCTGTGTGATCCCATGTCACCTGCA-----GGCTCG 648
Oy 75 ThrTyMetHisGluGlyPheGluArgAlaSerGluGlnIleTyTyRgIuSaArgIn 94
Db 649 ACCTTACAGCCACAGCATCCGACAGCATGATGAAGAGCTATTTCATGCAAGATGGG 708
Oy 95 GIyTyArgThrAla---SerValIleIleAlaLeuThrSaPglGluLeuHisGluAaP 113
Db 709 TCCCGTAAAGTCCCAAGAAATATCTCTTGTGATCATCAGATGGGACAAATACAGAGAC 768
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Oy 114 LeuPhePheTyRgSerGlu-----ArgGluAlaSaSaArgSerArgAspLeuGlyAlaIle 131
Db 769 CCCCTGAGATTAATGATGATCATTCCTCCGCCACAGCAAAAGCT-----GGCATCATTT 819
Oy 132 ValTyRySaValGlyValIySaPhe---PheAenglu---ThrGlnLeuAlaArgIle--- 148
Db 820 CGTTATGCTATTGGAGTGGAGATGCTTCCAGAGAGCCCACTGCGCTTAAGAGACTGAAC 879
Oy 149 -----AlaAspSerIySaSpHiSaValPheProValIaSaAspGlyPheGlnIla 164
Db 880 ACCATTGGCTGACGCTCCCCACAGACGACGCTTCAAGTAGGCAAC---TTTCACAGA 936
Oy 165 LeuGlnGlyIle 168
Db 937 CTCGCAGCAGATC 948

RESULT 12
US-09-688-307A-36
/ Sequence 36, Application US/09688307A
/ Patent No. 6432404
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6432404el Human Beta-2
/ FILE REFERENCE: 27866/36646
/ CURRENT APPLICATION NUMBER: US/09/688,307A
/ EARLIER FILING DATE: 2000-10-13
/ EARLIER APPLICATION NUMBER: 09/193,043
/ EARLIER FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/605,672
/ EARLIER FILING DATE: 1996-02-22
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 36
/ LENGTH: 3528
/ TYPE: DNA
/ ORGANISM: Rattus rattus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(3453)
/ OTHER INFORMATION: Description of Artificial Sequence: primer
/ NAME/KEY: misc_feature
/ LOCATION: 361
/ OTHER INFORMATION: Xaa = any or unknown amino acid
/ NAME/KEY: misc_feature
/ LOCATION: 464
/ OTHER INFORMATION: Xaa = any or unknown amino acid
/ NAME/KEY: misc_feature
/ LOCATION: 486
/ OTHER INFORMATION: Xaa = any or unknown amino acid
/ NAME/KEY: misc_feature
/ LOCATION: 506
/ OTHER INFORMATION: Xaa = any or unknown amino acid
/ NAME/KEY: misc_feature
/ LOCATION: 1117
/ OTHER INFORMATION: Xaa = any or unknown amino acid
/ NAME/KEY: misc_feature
/ LOCATION: 1118
/ OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-688-307A-36

Alignment Scores:
Pred. No.: 1.13e-07 Length: 3528
Score: 138.50 Matches: 52
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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 3597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..3525
US-08-485-618-54

Alignment Scores:
Pred. No.: 1,166-07 Length: 3597
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
Gaps: 2 10

US-09-970-076-2_copy_44_216 (1-173) x US-08-485-618-54 (1-3597)
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Db 493 GACATTCGTTTCTTCTATGATGCTTCTGACACATTAAACCAAGGACCTTCCCAAGATG 552
Oy 20 TyrrTyrrPheValGluGluLeuAhiLySerPheileSerProGluLeuAryMetSerPhe 39
Db 553 AAGGACTTGTCAAGACTTTTGTGAGAGTTTGAGGAGCCAGCAGCACTTGTTCCTCG 612
Oy 40 lIleValPheSerThrArgGlyThrThrLeuMetLySerValLeuProGlyValAap 54
Db 613 ATGCAATACCTCGAATCCTGTAAGACCTTTTACCTTCAGAAATTCAGAAACATCTCG 672
Oy 55 AapAagGluGluIleArgGluIleuGluGluLeuGluValLeuProGlyValAap 74
Db 673 GACCTTCAGAGCTGCTGATCCCATCTGCAAGCTGCA-----GGCTCG 717
Oy 75 ThrTyrrMetHieGluGlyPheGluArgAlaSerGluGluIleTyrrTyrrGluAangluin 94
Db 718 ACCTACAGACGACGAGGATCCGACAGATGAGAAAGACTATTCATGCAAGATGCG 777
Oy 95 GlyTyrrArgThrAla---SerValIleIleAlaLeuThrAapGlyGluLeuHieGluAap 113
Db 778 TCCCGTAAAGTGCAGAAAGATCTCTTGTGATCAGAGATGGGAGAAATACAGAGAC 837
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Oy 114 LeuPheHieTyrrSerGlu-----ArgGluAlaAapArgSerArgAapLeuGlyAlaIle 131
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Oy 132 ValTyrrCyValGlyValIlyAap---PheAanglu---ThrGluLeuAlaArgIle--- 148
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Db 949 ACCTATGCTCAGCTCCCGCAGACGACGATGTTCAAGTAAAGCAAC---TTTGACAGCA 1005
Oy 165 leuGluInGlyIle 168
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RESULT 15
US-08-362-652-54
Sequence 54: Application US/08362652
Patent No. 576850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 576850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 3597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..3525
US-08-362-652-54

Alignment Scores:
Pred. No.: 1,166-07 Length: 3597
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
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US-09-970-076-2_COPY_44_216 (1-173) x US-08-362-652-54 (1-3597)
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QY 20 TyrTyRrPheValGluInLeuAlaHieIySPheIleSerProGInLeuArGmetSerPhe 39
DB 553 AAGACCTTGTTCAAAGCTTTGATGGAGAGATTGGACACACAGACCTGTCTCCCTG 612
QY 40 IleValPheSerThrArGglyThrThrLeuWelIyLeuThrGlu----- 54
DB 613 ATGCAATACTGAACTGAACTGAACTTTTAACTTCACTGAATTCAAGAACATCCTG 672
QY 55 AsparGluGInIleArGInGlyLeuGluGluLeuValIleuProGlyIyAsp 74
DB 673 GACCTCGAGACCTGGTGATCCCATTTCTCCAGCTGCA-----GGCCTG 717
QY 75 ThrTyRmeCHiGluGlyPheGluArGAlaSerGluGInIleTyTyRgluAsnArGIn 94
DB 718 ACCATACACAGCCACAGCATCCGACAGTATGGAAGACTATTTCATAGCAAGATGG 777
QY 95 GlyTyRArGThraIa---SerValIleIleAlaLeuThrAspGlyGluLeuHieGluAsp 113
DB 778 TCCGTAAGAGTGCACAGAGATCTCTCTGTATCACAGATGGCAGAAATACAGAGAC 837
QY 114 LeuPhePheTyRserGlu-----ArgIuAlaAsnArGserArGAspLeuGlyAlaIle 131
DB 838 CCCCTGAGATATGATGATCATTCGCCCGACAGACAAAGCT-----GGCATCATT 888
QY 132 ValTyRCyValGlyValIyAsp---PheAsnGlu---ThrGInLeuAlaArGile--- 148
DB 889 CGTATGCTATTTGGGGTGGAGATGCCCTTCAGAGACCCACTGCCCTGAAGAGCTGAAC 948
QY 149 -----AlaAspSerIyAspPheHieValPheProValAsnAspGlyPheGInAla 164
DB 949 ACCATTGGCTACGCTCCCCACAGAGACCGTTCAGGTAGGCAAC---TTTGCAGCA 1005
QY 165 leuGInGlyIle 168
DB 1006 CTCGACAGATC 1017

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Job time : 133.458 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37 ; Search time 127.075 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Perfect score: 943

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: Issued Patents NA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 542 | 57.5 | 2234 | 3 | US-10-104-047-669 |
| 3 | 478 | 50.7 | 1492 | 3 | US-09-774-528-297 |
| 4 | 478 | 50.7 | 1492 | 3 | US-10-120-988-297 |
| 5 | 158 | 16.8 | 3981 | 3 | US-09-799-451-250 |
| 6 | 141.5 | 15.0 | 3528 | 2 | US-08-286-889-36 |
| 7 | 141.5 | 15.0 | 3528 | 2 | US-08-485-618-54 |
| 8 | 141.5 | 15.0 | 3528 | 2 | US-08-362-652-36 |
| 9 | 141.5 | 15.0 | 3528 | 2 | US-08-605-672-36 |



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|----|-------|------|------|---|--------------------|--------------------|
| 10 | 141.5 | 15.0 | 3528 | 2 | US-08-482-293A-36 | Sequence 36, Appl |
| 11 | 141.5 | 15.0 | 3528 | 2 | US-08-943-363-36 | Sequence 36, Appl |
| 12 | 141.5 | 15.0 | 3528 | 3 | US-09-193-043-36 | Sequence 36, Appl |
| 13 | 141.5 | 15.0 | 3528 | 3 | US-09-688-307A-36 | Sequence 36, Appl |
| 14 | 141.5 | 15.0 | 3528 | 2 | US-09-350-259-36 | Sequence 36, Appl |
| 15 | 141.5 | 15.0 | 3597 | 2 | US-08-485-618-54 | Sequence 54, Appl |
| 16 | 141.5 | 15.0 | 3597 | 2 | US-08-362-652-54 | Sequence 54, Appl |
| 17 | 141.5 | 15.0 | 3597 | 2 | US-08-605-672-54 | Sequence 54, Appl |
| 18 | 141.5 | 15.0 | 3597 | 2 | US-08-482-293A-36 | Sequence 54, Appl |
| 19 | 141.5 | 15.0 | 3597 | 2 | US-08-943-363-54 | Sequence 54, Appl |
| 20 | 141.5 | 15.0 | 3597 | 3 | US-09-193-043-54 | Sequence 54, Appl |
| 21 | 141.5 | 15.0 | 3597 | 3 | US-09-688-307A-54 | Sequence 54, Appl |
| 22 | 141.5 | 15.0 | 3597 | 3 | US-09-350-259-54 | Sequence 54, Appl |
| 23 | 138.5 | 14.7 | 3519 | 2 | US-08-286-889-45 | Sequence 45, Appl |
| 24 | 138.5 | 14.7 | 3519 | 2 | US-08-485-618-45 | Sequence 45, Appl |
| 25 | 138.5 | 14.7 | 3519 | 2 | US-08-362-652-45 | Sequence 45, Appl |
| 26 | 138.5 | 14.7 | 3519 | 2 | US-08-605-672-45 | Sequence 45, Appl |
| 27 | 138.5 | 14.7 | 3519 | 2 | US-08-482-293A-45 | Sequence 45, Appl |
| 28 | 138.5 | 14.7 | 3519 | 2 | US-08-943-363-45 | Sequence 45, Appl |
| 29 | 138.5 | 14.7 | 3519 | 3 | US-09-193-043-45 | Sequence 45, Appl |
| 30 | 138.5 | 14.7 | 3519 | 3 | US-09-688-307A-45 | Sequence 45, Appl |
| 31 | 138.5 | 14.7 | 3519 | 3 | US-09-350-259-45 | Sequence 45, Appl |
| 32 | 138.5 | 14.7 | 3803 | 2 | US-08-485-618-52 | Sequence 52, Appl |
| 33 | 138.5 | 14.7 | 3803 | 2 | US-08-362-652-52 | Sequence 52, Appl |
| 34 | 138.5 | 14.7 | 3803 | 2 | US-08-605-672-52 | Sequence 52, Appl |
| 35 | 138.5 | 14.7 | 3803 | 2 | US-08-482-293A-52 | Sequence 52, Appl |
| 36 | 138.5 | 14.7 | 3803 | 2 | US-08-943-363-52 | Sequence 52, Appl |
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| 38 | 138.5 | 14.7 | 3803 | 3 | US-09-688-307A-52 | Sequence 52, Appl |
| 39 | 138.5 | 14.7 | 3803 | 3 | US-09-350-259-52 | Sequence 52, Appl |
| 40 | 132.5 | 14.1 | 3533 | 2 | US-08-476-062A-40 | Sequence 40, Appl |
| 41 | 132.5 | 14.1 | 3533 | 6 | PCT-US96-01314-40 | Sequence 40, Appl |
| 42 | 132.5 | 14.1 | 3533 | 9 | 5424399-1 | Patent No. 5424399 |
| 43 | 132.5 | 14.1 | 3595 | 3 | US-09-023-655-1147 | Sequence 1147, Ap |
| 44 | 132.5 | 14.1 | 4045 | 3 | US-09-809-517A-37 | Sequence 37, Appl |
| 45 | 132.5 | 14.1 | 4124 | 3 | US-09-023-655-1178 | Sequence 1178, Ap |

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dimaec, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 3 05e-113 Length: 1609
Score: 943.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

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DB 432 GGAATTGACCTGACTTCACTTTGGCAATCAGAAAGTGTCTGCACCACTGGAATGAA 491
QY 21 ILeTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSer 40
DB 492 ATCTATTACTTGTGGACACAGTTGGCTCCAAATTCACTGCCACCAAGTTGAGAAATGTC 551
QY 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGln 60
DB 552 TTTATGTTTCTCCACCCAGGAAACCTTAACTGACAGAGACAGAGACAA 611
QY 61 ILeArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHis 80
DB 612 ATCCGCAAGGCTAGAGAAATCCAGAAAGTCTGCCAGAGAGACACTTACATGCAAT 671
QY 81 GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
DB 672 GAAAGATTGGAAAGGGCCAGTGGACAGATTATTAAGAAAACAGACAAAGGATCAGACA 731
QY 101 AlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
DB 732 GCCAGGCTCATCTTCTGCTTGAATGATGAGAACTCCATGAATCTCTTTCTATTC 791
QY 121 GluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLys 140
DB 792 GAAGAGGAGGCTAATAGTCTCCAGATCTTGTCATCTTTAATGTTGATGAGAAA 851
QY 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
DB 852 GATTTCATGACACACAGCTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCGTG 911
QY 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
DB 912 AATGACGCGCTTTCAGGCTCTGCAAGCATCATCTCAATTTTGAAGAAAGTCTGATC 971
QY 181 Glu 181
DB 972 GAA 974

RESULT 2
US-10-104-047-669
/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. 6943241el Full length cDNA
/ FILE REFERENCE: HI-A0105
/ CURRENT APPLICATION NUMBER: US/10/104, 047
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
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/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 1 34e-60 Length: 2234
Score: 542.00 Matches: 107
Percent Similarity: 78.89% Conservative: 35
Best Local Similarity: 59.44% Mismatches: 36
Query Match: 57.48% Indels: 2
Gaps: 1

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QY 22 TyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPhe 41
DB 715 TATTAATTCGTACACCACTTCCGAGAGAAATTTGGAGCCCTGAATGAGATTAATCTTTC 774
QY 42 ILeValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIle 61
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QY 62 ArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAspThrTyrArgThrAla 81
DB 835 AGTAAAGGCTTGGAGGATTTAAACGTGTAGTCCAGTAGAGAGACATATATCCATGAA 894
QY 82 GlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAla 101
DB 895 GGACTAAAGCTGACGAAATGAACTT-----CAAGAAACAGAGAGCTTGAACCTCC 948
QY 102 SerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu 121
DB 949 AGTATATATATGCTCTGACATGAGCAAGTGGACCGCTGTCATCATATGACAGAG 1008
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DB 1009 AAAGAGCAAGATATCCAGTCACTTGGGGCTAAGTATATGTTGTTGCTCTGAT 1068
QY 142 PheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsn 161
DB 1069 TTTGAACCAAGCACAGCTTGAAGAAATGCTGATTCAGAGAGCAAGTTTCCCTGCAAA 1128
QY 162 AspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIleGlu 181
DB 1129 GGTGGATTCAGGCTCTTAAAGGAATATTAATCTATACCTACGTCATGATCTGAA 1188

RESULT 3
US-09-774-528-297
/ Sequence 297, Application US/09774528
/ Patent No. 6743619
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Ren, Felyan
/ APPLICANT: Zhang, Jie
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Xue, Aiding J.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Dmanac, Radolje T.
/ TITLE OF INVENTION: No. 6743619el Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
```



```
/ FILE REFERENCE: 802
/ CURRENT APPLICATION NUMBER: US/09/774.528
/ CURRENT FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: PL_FL_genes Version 2.0
/ SEQ ID NO 297
/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79)..(1434)
US-09-774-528-297

Alignment Scores:
Pred. No.: 1,75e-52 Length: 1492
Score: 478.00 Matches: 95
Percent Similarity: 77.71% Conservative: 34
Best Local Similarity: 57.23% Mismatches: 35
Query Match: 50.69% Indels: 2
Gaps: 1

US-09-970-076-2_COPY_42_222 (1-181) x US-09-774-528-297 (1-1492)

QY 16 HieHieTTPanGluileTyTyTyPheValGluGluLeuAlaHisLysPheHisSerPro 35
Db 16 AATACTGATGATGAATTTATTAATTCCTACAGCAACTTCGAGAGATTTGTAGCCCT 75
QY 36 GluLeuArgMetSerPheHisLeuAlaPheSerThrArgGlyThrThrLeuMetLysLeuThr 55
Db 36 GAATGAGATTAATTCATATGTTCTTCTTCAAGCAACTATTAATTTGCCATTAAT 135
QY 56 GluAspArgGluGlnIleArgGlnIleuGluGluGluGlnLysValLeuProGlyGly 75
Db 56 GAGACAGAGGCAAAATCAATAAGCTTGAGAGATTTAAACGTTAGTCCAGTGA 195
QY 136 GAGACAGAGGCAAAATCAATAAGCTTGAGAGATTTAAACGTTAGTCCAGTGA 195
Db 136 GAGACAGAGGCAAAATCAATAAGCTTGAGAGATTTAAACGTTAGTCCAGTGA 195
QY 76 AspThrTyMetHisGluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsnArg 95
Db 76 GAGACATATATCCATGAAAGCACTAAGCTAGCAATGAAATTT-----CAGAAAGCA 249
QY 96 GluGlyTyArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 115
Db 96 GAGAGCTTGAAACCTCCAGTATCATATATGCTTGACAGTGGCAAGTTGGACGCTGTG 309
QY 116 LeuPhePheTySerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyx 135
Db 116 GTGCCATCATATGACAGAAAGGCAAAAGTATCCAGTCACTTGGGCGTATGTTAT 369
QY 310 GTGCCATCATATGACAGAAAGGCAAAAGTATCCAGTCACTTGGGCGTATGTTAT 369
Db 310 GTGCCATCATATGACAGAAAGGCAAAAGTATCCAGTCACTTGGGCGTATGTTAT 369
QY 136 CyValAlGlyValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAsp 155
Db 136 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGAAATGCTGATTTCAAGAG 429
QY 370 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGAAATGCTGATTTCAAGAG 429
Db 370 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGAAATGCTGATTTCAAGAG 429
QY 156 HisValPheProValaAsnArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 175
Db 156 CAAATTTTCCCTGCAAGGTGATTTCAAGGCTTTAAAGAAATTAATTAATTTCTATCTA 489
QY 430 CAAATTTTCCCTGCAAGGTGATTTCAAGGCTTTAAAGAAATTAATTAATTTCTATCTA 489
Db 430 CAAATTTTCCCTGCAAGGTGATTTCAAGGCTTTAAAGAAATTAATTAATTTCTATCTA 489
QY 176 LysLysSerCysIleGlu 181
Db 176 LysLysSerCysIleGlu 181
QY 490 GCTCAGTCACTGACTGA 507
Db 490 GCTCAGTCACTGACTGA 507

RESULT 4
US-10-120-988-297
/ Sequence 297, Application US/10120988
/ Patent No. 6919193
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Ren, Feiyun
/ APPLICANT: Wang, Duntui
/ APPLICANT: Demanc, Radoje T.
/ TITLE OF INVENTION: No. 6919193el Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
```

```
/ FILE REFERENCE: 802CON
/ CURRENT APPLICATION NUMBER: US/10/120.988
/ CURRENT FILING DATE: 2002-04-11
/ PRIOR APPLICATION NUMBER: 09/774,528
/ PRIOR FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: PL_FL_genes Version 2.0
/ SEQ ID NO 297
/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79)..(1434)
US-10-120-988-297

Alignment Scores:
Pred. No.: 1,75e-52 Length: 1492
Score: 478.00 Matches: 95
Percent Similarity: 77.71% Conservative: 34
Best Local Similarity: 57.23% Mismatches: 35
Query Match: 50.69% Indels: 2
Gaps: 1

US-09-970-076-2_COPY_42_222 (1-181) x US-10-120-988-297 (1-1492)

QY 16 HieHieTTPanGluileTyTyTyPheValGluGluLeuAlaHisLysPheHisSerPro 35
Db 16 AATACTGATGATGAATTTATTAATTCCTACAGCAACTTCGAGAGATTTGTAGCCCT 75
QY 36 GluLeuArgMetSerPheHisLeuAlaPheSerThrArgGlyThrThrLeuMetLysLeuThr 55
Db 36 GAATGAGATTAATTCATATGTTCTTCTTCAAGCAACTATTAATTTGCCATTAAT 135
QY 56 GluAspArgGluGlnIleArgGlnIleuGluGluGluGlnLysValLeuProGlyGly 75
Db 56 GAGACAGAGGCAAAATCAATAAGCTTGAGAGATTTAAACGTTAGTCCAGTGA 195
QY 136 GAGACAGAGGCAAAATCAATAAGCTTGAGAGATTTAAACGTTAGTCCAGTGA 195
Db 136 GAGACAGAGGCAAAATCAATAAGCTTGAGAGATTTAAACGTTAGTCCAGTGA 195
QY 76 AspThrTyMetHisGluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsnArg 95
Db 76 GAGACATATATCCATGAAAGCACTAAGCTAGCAATGAAATTT-----CAGAAAGCA 249
QY 96 GluGlyTyArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 115
Db 96 GAGAGCTTGAAACCTCCAGTATCATATATGCTTGACAGTGGCAAGTTGGACGCTGTG 309
QY 116 LeuPhePheTySerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyx 135
Db 116 GTGCCATCATATGACAGAAAGGCAAAAGTATCCAGTCACTTGGGCGTATGTTAT 369
QY 310 GTGCCATCATATGACAGAAAGGCAAAAGTATCCAGTCACTTGGGCGTATGTTAT 369
Db 310 GTGCCATCATATGACAGAAAGGCAAAAGTATCCAGTCACTTGGGCGTATGTTAT 369
QY 136 CyValAlGlyValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAsp 155
Db 136 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGAAATGCTGATTTCAAGAG 429
QY 370 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGAAATGCTGATTTCAAGAG 429
Db 370 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGAAATGCTGATTTCAAGAG 429
QY 156 HisValPheProValaAsnArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 175
Db 156 CAAATTTTCCCTGCAAGGTGATTTCAAGGCTTTAAAGAAATTAATTAATTTCTATCTA 489
QY 430 CAAATTTTCCCTGCAAGGTGATTTCAAGGCTTTAAAGAAATTAATTAATTTCTATCTA 489
Db 430 CAAATTTTCCCTGCAAGGTGATTTCAAGGCTTTAAAGAAATTAATTAATTTCTATCTA 489
QY 176 LysLysSerCysIleGlu 181
Db 176 LysLysSerCysIleGlu 181
QY 490 GCTCAGTCACTGACTGA 507
Db 490 GCTCAGTCACTGACTGA 507

RESULT 5
US-09-799-451-250
/ Sequence 250, Application US/09799451
/ Patent No. 6783969
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Aundt, Vinod
/ APPLICANT: Ren, Feiyun
/ APPLICANT: Zhang, Jie
```

APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yunging
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Weinman, Tom
APPLICANT: Ghosh, Keena
APPLICANT: Dimanac, Radoje T.
TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 250
LENGTH: 3981
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)..(1118)
US-09-799-451-250

Alignment Scores:
Pred. No.: 5,07e-10 Length: 3981
Score: 158.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.76% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-09-799-451-250 (1-3981)

QY 152 AppSerLyAspHisValPheProValAspArgLyPheGlnAlaLeuGlnGlyIle 171
DB 3 GACAGTAAAGATCATGTGTTCCCGTAATGACGCGCTTCAGGCTCTGCAAGCATCATC 62
QY 172 HisSerIleLeuLyAspSerCysIleGlu 181
DB 63 CACTCAATTTGAGAGAGTCCTTCATCGAA 92
RESULT 6
US-08-286-889-36
Sequence 36, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5470953e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-286-889-36

Alignment Scores:
Pred. No.: 6.12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-08-286-889-36 (1-3528)

QY 3 AppLeuTyRPhelIleLeuAspLySergLyServal---LeuHisIstRphenGluIle 21
DB 424 GACATGCTTCTCCATGATGATGATGCTTGGCAGCATTAACCAAGGACATTGCCCGCAGATG 483
QY 22 TyTyTyRphenValGluGlnLeuAlaHisLySphenIleSergProGlnLeuArgMetSerphe 41
DB 484 AAGGACTTGTCTCAAGCTTTGATGGAGAGTTGGAGAGCCAGACGACCTTGTTCTCCCTG 543
QY 42 ILeValPheSergThrArgGlyThrThrLeuMetLySLeuThrGlu----- 56
DB 544 ATGCATATCTCAACATCTCTGAAGCCCATTTTACCTTCATCGAATTAAGAACATCTG 603
QY 57 AParArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnValLeuProGlyGlyAsp 76
DB 604 GACCTCAGAGCGCTGTGATGCCATTTGCCAGCTGCA-----GGCCTG 648
QY 77 ThrTyTmetHisGluGlyPheGluArgAlaSerGluGlnIleTyTyGlnLeuAspArgGln 96
DB 649 ACCTACACAGCAGCAGGCGATCCGACAGTGAAGAGCTTTTATATAGCAAGATGGG 708
QY 97 GlyTyArgThrAla---ServalIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 115
DB 709 TCCCGTAAAGTCCCAAGAGATCTCTCTGTGCATCAGAGAGGGCAAGATACAGAGAC 768
QY 116 LeuPhePheTySergLuu-----ArgGluAlaAspArgSerpArgSerpGlyAlaIle 133
DB 769 CCCCGAAGTAAAGATGATGATCTCCCGCGAGCAAGACT-----GGCATCATT 819
QY 134 ValTyTyCysValGlyValLyAsp---PheAsnGlu---ThcGlnLeuAlaArgIle--- 150
DB 820 CGTATGCTATTGGGATGGAGATGCTTCAGAGAGCCCATGCTTGAAGAGCTGAGAC 879
QY 151 -----AlaAspSerLyAspHisValPheProValAspArgLyPheGlnAla 166
DB 880 ACCATTGGCTCAGCTCCCGACAGACCAAGCTTTCAAGATGAGCAAC---TTTGAAGCA 926
QY 167 LeuGlnGlyIleIleHisSerIleLeuLyS 177
DB 937 CTTGCGAGCATCGAAGGCACTTCAGAGAAA 969
RESULT 7
US-08-485-618-36

Sequence 36, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 5728533 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-485-618-36
Alignment Scores:
Pred. No.: 6.12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: 2 Gaps: 10
US-09-970-076-2_COPY_42_222 (1-181) x US-08-485-618-36 (1-3528)
Qy 3 AspleuYrPheileuAplyserglYserVal--LeuHSHstPAsngluile 21
Db 424 GACATTGCTTCCGATGATGCTTGGCAGCATTAACCAAGGACTTGGCCAGATG 483
Qy 22 TyrTyRpheValgluInLeuAlaHlelYsPheileSerProglInLeuAlygMetSerPhe 41
Db 484 AAGGACTTGTCAAGCTTGTGATGGAGAGATTGGCAGCAGACACCTGTCTCCCTG 543
Qy 42 lLeValPheSerThrAryglYThrThreunetYsLeuThrglu----- 56
Db 544 ATGCATTAATCTGAACATCTGAGAGCCATTTCCTTCACTGAATTCAAGACATCTG 603

Qy 57 AspArggluInleAryglInglYleuIngluInleuInlySValLeuProglYcYAsp 76
Db 604 GACCTTCAGAGCTCGGAGATCCCATTTGTCAGCTGCA-----GGCTG 648
Qy 77 ThrTyRmetHleaglInglYpHeuAlaAlyserglInleYrTyRgluAAsnArgIn 96
Db 649 ACCTACAGCAGCAGACGATCCGAGATGAGAGCTATTTCATTCAGCAAGATGG 708
Qy 97 glYTyRArgThraAla---SerValleleleAlaLeuThrAAspglYgluLeuHsgluAsp 115
Db 709 TCCGTAAGAGCTCCAGAGATATCTCTTGTATCAGATGGCAGAAATACAGAGAC 768
Qy 116 LeuPhePheTyRserglu-----ArggluAlaAsnArgSerAryAspLeuGlYAlaile 133
Db 769 CCCCTGAGATATGATGATGATTCCTCCGCGCAGACAAAGCT-----GGCATCAT 819
Qy 134 ValTyRcySValglYValYAsp---PheAsnlu---ThrgInleuAlaArgile--- 150
Db 820 CGTATGCTATGAGGAGGAGATGCTCCAGAGCCCACTGCTGAGAGAGCTGAAAC 879
Qy 151 -----AlaAspserLyAAspHleValPheProValAAspglYpHeuAla 166
Db 880 ACATGCTCAGCTCCCGCAGAGACAGCTGTTCAAGTAAAGCAAC---TTTGCAGCA 936
Qy 167 LeuInglYlleleHleSerleLeuYlyls 177
Db 937 CTTCGAGCATTCAGAGCAACTTCAGAGAA 969
RESULT 8
US-08-362-652-36
Sequence 36, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 5766850 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```

/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3456
US-08-362-652-36

Alignment Scores:
Pred. No.: 6,12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-08-362-652-36 (1-3528)
QY 3 AarLeuTyrrPheIleuAarLySerGlySerVal---LeuNiHiStrPraengluile 21
DB 424 GACATTGCTTCTCGATGATGATGCTTGGCAGCATTAACCAAGGACCTTGGCCCGAGATG 483
QY 22 TyrrTyrrPheValGluInleuAhiLysrPheIleSerProGluInleuArygMetSerPhe 41
DB 484 AAGGACTTTGTCAAGCTTTGATGGAGAGTTGGCAGACCAAGCAACCTTGTCTCTCCG 543
QY 42 ILevalPheSerThrArgGlyThrThyLeuMetLysLeuThyGlu----- 56
DB 544 ATGCAATATCTCAACATCTCGAAGACCTTTTACCTTCATCGAATTCAGAAACATCTCG 603
QY 57 AarAargGluGlnIleArgGlnInleuGluGluLeuGlnLysValLeuProGlyGlyAar 76
DB 604 GACCTTCAGAGCTGTGGATCCCATTTGTCAGCTGCA-----GGCCCTG 648
QY 77 ThrTyrrMetHiGluGluIlyrPheGluAargAlaSerGluGlnIleTyrrTyrrGluAenAargGln 96
DB 649 ACCTTACACAGCCACAGACCTCCGAGACGTAGTGAAGAGTATTTCATAGCAAGATGGG 708
QY 97 GlyTyrrArgThrAla---SerValIleIleAlaLeuThrAarGlyGluLeuNiHiGluAar 115
DB 709 TCCCGTAAAGTCCCAAGAAATCTCTGTGATCAGAGATGGGCAAAATACAGAGAC 768
QY 116 LeuPhePheTyrrSerGlu-----ArgGluAlaAarArgSerArgAarLeuGlyAlaIle 133
DB 769 CCCCTGAGTATAGTATGATCATTTCCCGCCGACAGACAAAGCT-----GGCATCATT 819
QY 134 ValTyrrCysValGlyValLysAar---PheAenGlu---ThrGluInleuAargIle---- 150
DB 820 CGTTATGCTATTTGGGTGGAGATGCTTCCAGAGACCCCACTGCCCTGAAGAGCTGAAC 879
QY 151 -----AlaAarSerLysAarPheIleValPheProValAaAarGlyPheGlnAla 166
DB 880 ACCATTGGCTCAAGTCCCCCAAGACGACGATGTTCAAGGTATGAGCAAC---TTTGCAGCA 936
QY 167 LeuGlnGlyIleIleHisSerIleLeuLysLys 177
DB 937 CTTGCGAGATCCAGAGGCACTTCAGAGGAAA 969

RESULT 9
US-08-605-672-36
/ Sequence 36, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerslein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402

```

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/605,672
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3528 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3456
US-08-605-672-36

Alignment Scores:
Pred. No.: 6,12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-08-605-672-36 (1-3528)
QY 3 AarLeuTyrrPheIleuAarLySerGlySerVal---LeuNiHiStrPraengluile 21
DB 424 GACATTGCTTCTCGATGATGATGCTTGGCAGCATTAACCAAGGACCTTGGCCCGAGATG 483
QY 22 TyrrTyrrPheValGluInleuAhiLysrPheIleSerProGluInleuArygMetSerPhe 41
DB 484 AAGGACTTTGTCAAGCTTTGATGGAGAGTTGGCAGACCAAGCAACCTTGTCTCTCCG 543
QY 42 ILevalPheSerThrArgGlyThrThyLeuMetLysLeuThyGlu----- 56
DB 544 ATGCAATATCTCAACATCTCGAAGACCTTTTACCTTCATCGAATTCAGAAACATCTCG 603
QY 57 AarAargGluGlnIleArgGlnInleuGluGluLeuGlnLysValLeuProGlyGlyAar 76
DB 604 GACCTTCAGAGCTGTGGATCCCATTTGTCAGCTGCA-----GGCCCTG 648
QY 77 ThrTyrrMetHiGluGluIlyrPheGluAargAlaSerGluGlnIleTyrrTyrrGluAenAargGln 96
DB 649 ACCTTACACAGCCACAGACCTCCGAGACGTAGTGAAGAGTATTTCATAGCAAGATGGG 708
QY 97 GlyTyrrArgThrAla---SerValIleIleAlaLeuThrAarGlyGluLeuNiHiGluAar 115
DB 709 TCCCGTAAAGTCCCAAGAAATCTCTGTGATCAGAGATGGGCAAAATACAGAGAC 768
QY 116 LeuPhePheTyrrSerGlu-----ArgGluAlaAarArgSerArgAarLeuGlyAlaIle 133

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DB 769 CCCCTGGAGTATGATGTCATTCCTCCCGCCGAGCAAAAGCT-----GGCATTCATT 819
QY 134 ValTYrCyValGIyValIyAsP---PheAnglu---ThrGlnLeuAlaArgIle--- 150
DB 820 CGTTATGCTATTGGGTGGGAGATGCTTCCAGAGCCACCTGCCCTGAAGAGCTGAAC 879
QY 151 -----AlaAspSerIyAspHisValPheProValAsnAspGlyPheGlnAla 166
DB 880 ACCATTGGCTCAGCTCCCCACAGACCACTGTTCAGGTAGGCAAC---TTTCAGACA 936
QY 167 LeuGlnGlyIleIleHisSerIleLeuIyAs 177
DB 937 CTTCGACGATCCAGAGCAACTTCAGAGAAA 969

RESULT 10
US-08-482-293A-36
; Sequence 36, Application US/08482293A
; Patent No.5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,293A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3528 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3456
; US-08-482-293A-36

Alignment Scores:
Pred. No.: 6.12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
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Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: 2 Gaps: 10

US-09-970-076-2_copy_42_222 (1-181) x US-08-482-293A-36 (1-3528)
QY 3 AspleuTYrPheIleLeuAspIySergIySerVal---LeuHisIeTrpAsnGluIle 21
DB 424 GACATGGCTTTCCTGATGATGATGTTCTGGCAGCATTAACCAAGGCACTTGGCCCAAGT 483
QY 22 TYrTYrPheValGlnGlnLeuAlaHisIyAsPheIleSergProGlnLeuArgMetSerphe 41
DB 484 AAGACCTTGTCAAAAGCTTTATGAGAGAGTTGGACAGCAAGCACTTGTTCCTCG 543
QY 42 ILevalPheSerThrArgIyThrIleuMetIySergIyIleu--- 56
DB 544 ATGCAATACCTGAACATCTCGAAGCCCATTTTACCTTCATGATTCAGAACATCTCG 603
QY 57 AspArgGlnGlnIleArgGlnIyLeuGlnGlnIySValLeuProGlyGlyAsp 76
DB 604 GACCTTCAGAGCCTGGTGATCCCATTTGTCAGCTGCA--- 648
QY 77 ThrTYrMetHisGlnGlyPheGlnAlaSerGlnGlnIleTYrTYrGlnAlaAsnArgGln 96
DB 649 ACCTACACGCCACAGGATCCGACAGTGAAGAGCTATTTCATAGCAAGAAATGG 708
QY 97 GLYrArgThrAla---SerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnAsp 115
DB 709 TCCGTAAGATGTCAGAAAGATCTCTGTCATCACAGATGGCAGAAATACAGAGAC 768
QY 116 LeuPhePheTYrSergIle---ArgGlnAlaAsnArgSeraArgAspLeuGlyAlaIle 133
DB 769 CCCCTGGAGTATGATGTCATTCCTCCCGCCGAGCAAAAGCT-----GGCATTCATT 819
QY 134 ValTYrCyValGIyValIyAsP---PheAnglu---ThrGlnLeuAlaArgIle--- 150
DB 820 CGTTATGCTATTGGGTGGGAGATGCTTCCAGAGCCACCTGCCCTGAAGAGCTGAAC 879
QY 151 -----AlaAspSerIyAspHisValPheProValAsnAspGlyPheGlnAla 166
DB 880 ACCATTGGCTCAGCTCCCCACAGACCACTGTTCAGGTAGGCAAC---TTTCAGACA 936
QY 167 LeuGlnGlyIleIleHisSerIleLeuIyAs 177
DB 937 CTTCGACGATCCAGAGCAACTTCAGAGAAA 969

RESULT 11
US-08-943-363-36
; Sequence 36, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
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QY      134 ValTYrCyValGIyValIlyeAsp---PheAsnGlu---ThrGlnLeuAlaArgIle--- 150
      820 CGTTATGCTATTGGGGTGGGAGATGCTTCAGAGAGCCCTGAGAGAGAGCTGAAC 879
QY      151 -----AlaAspSerIlyeAspHisValPheProValAsnAspGlyPheGlnAla 166
      880 ACCATTGGCTCAGCTCCCAACAGACACGCTGTTCAAGTAGGCAAC---TTTGACGCA 936
QY      167 LeuGlnGlyIleIleHisSerIleLeuIlyeLys 177
      937 CTTGCGAGCATCCAGAGCAACTTCAGAGAAA 969

RESULT 13
US-09-688-307A-36
; Sequence 36, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3528
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3453)
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: misc_feature
; LOCATION: 361
; OTHER INFORMATION: Xaa = any or unknown amino acid
; NAME/KEY: misc_feature
; LOCATION: 464
; OTHER INFORMATION: Xaa = any or unknown amino acid
; NAME/KEY: misc_feature
; LOCATION: 466
; OTHER INFORMATION: Xaa = any or unknown amino acid
; NAME/KEY: misc_feature
; LOCATION: 506
; OTHER INFORMATION: Xaa = any or unknown amino acid
; NAME/KEY: misc_feature
; LOCATION: 1117
; OTHER INFORMATION: Xaa = any or unknown amino acid
; NAME/KEY: misc_feature
; LOCATION: 1118
; OTHER INFORMATION: Xaa = any or unknown amino acid
; OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-688-307A-36

Alignment Scores:
Pred. No.: 6,12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: 3 Gaps: 10
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US-09-970-076-2_copy_42_222 (1-181) x US-09-688-307A-36 (1-3528)
QY      3 AspLeuTYrPheIleLeuAspIlySerGlySerVal---LeuHisThrPAsnGluIle 21
      424 GACATTGCTTTCTTGATTTGATGTTCTGGAGACATTAACCAAGGACCTTGCCCAATG 483
QY      22 TYrTYrPheValGlnIleuAlaHisIlyePheIleSerProGlnLeuArgMetSerPhe 41
      484 AACGACTTGTCTCAAGCTTTGATGGAGAGTTGGAGGACCAAGACCTTGTTCTCCCTG 543
QY      42 IleValPheSerThrArgGlyThrThrLeuMetIlyeLeuThrGlu----- 56
      544 ATGCAATACTCGAACATCTCGAAGCCATTTCCTTCACTGAATTCAGAAATCCTCTG 603
QY      57 AspArgGlnGlnIleArgGlnIlyeGlnIlyeGlnIlyeValIleuPheProGlyGlyAsp 76
      604 GACCTCAGAGCTGGTGGATGCCATTTGTCAGCTGCA-----GGCCTG 648
QY      77 ThrTYrMetHisGlnIlyePheGluArgAlaSerGlnIleTYrTYrGlnAsnArgGln 96
      649 ACCTACACAGCCACAGCAGCATCCGACAGTGAAGAGCTATTTCATACAGAAATGGG 708
QY      97 GlyTYrArgThrAla---SerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAsp 115
      709 TCCCGTAAAGTGCAGAAAGATCCCTGTCATCAGATGGGAGCAAAATCAGAGAC 768
QY      116 LeuPhePheTYrSerGlu-----ArgGlnAlaAsnArgSerArgAspLeuGlyAlaIle 133
      769 CCCCTGAGTATATGATATGATTCATTCGCCGCCGAGACAAAGCT-----GCCATCAT 819
QY      134 ValTYrCyValGIyValIlyeAsp---PheAsnGlu---ThrGlnLeuAlaArgIle--- 150
      820 CGTTATGCTATTGGGGTGGGAGATGCTTCAGAGAGCCCACTGCTGAAAGAGAGCTGAAC 879
QY      151 -----AlaAspSerIlyeAspHisValPheProValAsnAspGlyPheGlnAla 166
      880 ACCATTGGCTCAGCTCCCAACAGACACGCTGTTCAAGTAGGCAAC---TTTGACGCA 936
QY      167 LeuGlnGlyIleIleHisSerIleLeuIlyeLys 177
      937 CTTGCGAGCATCCAGAGCAACTTCAGAGAAA 969

RESULT 14
US-09-350-259-36
; Sequence 36, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3528
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3453)
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-36

Alignment Scores:
Pred. No.: 6,126-08      Length: 3528
Score: 141.50           Matches: 53
Percent Similarity: 47.64%  Conservative: 38
Best Local Similarity: 27.75%  Mismatches: 75
Query Match: 15.01%      Indels: 25
DB: 3                    Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-09-350-259-36 (1-3528)

QY 3 AepLeuTYrPheHleLeuAaPrySergIySerVal---LeuNHleTPrAnGluIle 21
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Db 424 GACATGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
QY 22 TyTYrPheValGluGlnLeuAlaNHlyuPheHleSerProGlnLeuAryMetSerPhe 41
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 AAGGACTTGTTCAGAGCTTTGATGGAGAGGTTTGGAGACACAGACACCTGTCTCCCTG 543
QY 42 ILevalPheSerThrArgGlyThrThreuMetLyLeuThrGlu----- 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 544 ATGCAATACCTGACATCCTGAAAGACCCATTTTACCTTCATGAAATTCAGAAACATCCTG 603
QY 57 AepAryGluGlnIleArgGlnIleuGlnIleuGlnIleValLeuProGlyIyAer 76
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 604 GACCTCAGAGCTGTGATGATCCCATGCTTCAGCTGCA-----GGCTCG 648
QY 77 ThrTYrMetNHleGluGlyPheGluAryAserGluGlnIleTyTYrGluAaAryGln 96
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 649 ACCTACACAGCCACAGGATCCGACAGATGAGAGAGCTATTCATGCAAGATGGG 708
QY 97 GlyTYrArgThraA---SerValIleIleAlaLeuThraPryGluLeuNHleGluAer 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 709 TCCCGTAAAGTCCAGAAAGATCCCTCTGTCATCAGATGGGCAAAATACAGAGAC 768
QY 116 LeuPhePheTySerGlu-----ArgGluAlaAaArySerAryAerPryGluAlaIle 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 769 CCCCTGAGATATGATGATCATTCCTCCCGCCGACAGAAAGCT-----GGCATCATT 819
QY 134 ValTYrCyValGlyValIyAaP---PheAnGlu---ThrGlnLeuAlaAryGle--- 150
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 820 CCTTATGCTATGGGTGGAGATGCTTCACAGAGCCACCTGCTGAAGAGCTGAAAC 879
QY 151 -----AlaAerSerLyAaPryNHleValPheProValAaAryGlyPheGlnAla 166
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 880 ACCATTGGCTCAGCTCCCGACAGACACAGCTGTTCAGAGTGGCAAC---TTTGCAGCA 936
QY 167 LeuGlnGlyIleIleHleSerIleLeuLyAer 177
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Db 937 CTTCGACATCCAGAGCAATTTCAGAGAGAA 969

RESULT 15
US-08-485-618-54
Sequence 54, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vaeren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Bear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 3597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..3525
US-08-485-618-54
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Alignment Scores:
Pred. No.: 6,296-08      Length: 3597
Score: 141.50           Matches: 53
Percent Similarity: 47.64%  Conservative: 38
Best Local Similarity: 27.75%  Mismatches: 75
Query Match: 15.01%      Indels: 25
DB: 2                    Gaps: 10
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US-09-970-076-2_COPY_42_222 (1-181) x US-08-485-618-54 (1-3597)

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   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 493 GACATGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 552
QY 22 TyTYrPheValGluGlnLeuAlaNHlyuPheHleSerProGlnLeuAryMetSerPhe 41
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 553 AAGGACTTGTTCAGAGCTTTGATGGAGAGGTTTGGAGACACAGACACCTGTCTCCCTG 612
QY 42 ILevalPheSerThrArgGlyThrThreuMetLyLeuThrGlu----- 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 613 ATGCAATACCTGACATCCTGAAAGACCCATTTTACCTTCATGAAATTCAGAAACATCCTG 672
QY 57 AepAryGluGlnIleArgGlnIleuGlnIleuGlnIleValLeuProGlyIyAer 76
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 673 GACCTCAGAGCTGTGATGATCCCATGCTTCAGCTGCA-----GGCTCG 717
QY 77 ThrTYrMetNHleGluGlyPheGluAryAserGluGlnIleTyTYrGluAaAryGln 96
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 718 ACCTACACAGCCACAGGATCCGACAGATGAGAGAGCTATTCATGCAAGATGGG 777
QY 97 GlyTYrArgThraA---SerValIleIleAlaLeuThraPryGluLeuNHleGluAer 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 778 TCCCGTAAAGTCCAGAAAGATCCCTCTGTCATCAGATGGGCAAAATACAGAGAC 837
QY 116 LeuPhePheTySerGlu-----ArgGluAlaAaArySerAryAerPryGluAlaIle 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 838 CCCCTGAGATATGATGATCATTCCTCCCGCCGACAGAAAGCT-----GGCATCATT 888
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| | | | | | |
|----|------|--------------------------------|-----------------------------|------------------------|------|
| QY | 134 | ValTyrGlyValIleValIleAsp---- | Pheanglu---- | ThrGluLeuAlaArgIle---- | 150 |
| | | | | | |
| Db | 889 | CgTtATGCTATTGGGAGTGGAGATCC | TTTCCAGAGGCCACTGGCCCTTAA | GAGAGCTGAAC | 948 |
| | | | | | |
| QY | 151 | -----AlaAspSerIleAspHisVal | PheProValIleAspGlyPheGluAla | | 166 |
| | | | | | |
| Db | 949 | ACCATTGGCTAGCTCCCCACAGGACCA | CGGTTCACAGTAGGCAAC-- | TTTGACAGA | 1005 |
| | | | | | |
| QY | 167 | LeuGlnGlyIleIleHisSerIleLeuIle | Valys | | 177 |
| | | | | | |
| Db | 1006 | CTTCGACAGATCCAGAGCAACTTGA | GAGAGAAA | | 1038 |

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GenCore version 5.1.6
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(without alignments)
2531.884 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 970 | 100.0 | 1609 | 3 | US-10-620-312D-8 | Sequence 8, Appl |
| 2 | 550 | 56.7 | 2234 | 3 | US-10-104-047-665 | Sequence 699, App |
| 3 | 486 | 50.1 | 1492 | 3 | US-09-774-528-297 | Sequence 297, App |
| 4 | 486 | 50.1 | 1492 | 3 | US-10-120-988-297 | Sequence 297, App |
| 5 | 179 | 18.5 | 3981 | 3 | US-09-799-451-250 | Sequence 36, Appl |
| 6 | 141.5 | 14.6 | 3528 | 2 | US-08-286-889-36 | Sequence 36, Appl |
| 7 | 141.5 | 14.6 | 3528 | 2 | US-08-485-618-36 | Sequence 36, Appl |
| 8 | 141.5 | 14.6 | 3528 | 2 | US-08-362-652-36 | Sequence 36, Appl |
| 9 | 141.5 | 14.6 | 3528 | 2 | US-08-605-672-36 | Sequence 36, Appl |

| | | | | | | |
|----|-------|------|------|---|--------------------|-------------------|
| 10 | 141.5 | 14.6 | 3528 | 2 | US-08-482-293A-36 | Sequence 36, Appl |
| 11 | 141.5 | 14.6 | 3528 | 2 | US-08-943-363-36 | Sequence 36, Appl |
| 12 | 141.5 | 14.6 | 3528 | 3 | US-09-193-043-36 | Sequence 36, Appl |
| 13 | 141.5 | 14.6 | 3528 | 3 | US-09-688-307A-36 | Sequence 36, Appl |
| 14 | 141.5 | 14.6 | 3528 | 3 | US-09-350-259-36 | Sequence 36, Appl |
| 15 | 141.5 | 14.6 | 3528 | 2 | US-08-485-618-54 | Sequence 54, Appl |
| 16 | 141.5 | 14.6 | 3528 | 2 | US-08-362-652-54 | Sequence 54, Appl |
| 17 | 141.5 | 14.6 | 3528 | 2 | US-08-605-672-54 | Sequence 54, Appl |
| 18 | 141.5 | 14.6 | 3528 | 2 | US-08-482-293A-54 | Sequence 54, Appl |
| 19 | 141.5 | 14.6 | 3528 | 3 | US-08-943-363-54 | Sequence 54, Appl |
| 20 | 141.5 | 14.6 | 3528 | 2 | US-09-193-043-54 | Sequence 54, Appl |
| 21 | 141.5 | 14.6 | 3528 | 3 | US-09-688-307A-54 | Sequence 54, Appl |
| 22 | 141.5 | 14.6 | 3528 | 3 | US-09-350-259-54 | Sequence 54, Appl |
| 23 | 138.5 | 14.3 | 3519 | 2 | US-08-286-889-45 | Sequence 45, Appl |
| 24 | 138.5 | 14.3 | 3519 | 2 | US-08-485-618-45 | Sequence 45, Appl |
| 25 | 138.5 | 14.3 | 3519 | 2 | US-08-362-652-45 | Sequence 45, Appl |
| 26 | 138.5 | 14.3 | 3519 | 2 | US-08-605-672-45 | Sequence 45, Appl |
| 27 | 138.5 | 14.3 | 3519 | 2 | US-08-482-293A-45 | Sequence 45, Appl |
| 28 | 138.5 | 14.3 | 3519 | 2 | US-08-943-363-45 | Sequence 45, Appl |
| 29 | 138.5 | 14.3 | 3519 | 3 | US-09-193-043-45 | Sequence 45, Appl |
| 30 | 138.5 | 14.3 | 3519 | 3 | US-09-688-307A-45 | Sequence 45, Appl |
| 31 | 138.5 | 14.3 | 3519 | 3 | US-09-350-259-45 | Sequence 45, Appl |
| 32 | 138.5 | 14.3 | 3803 | 2 | US-08-485-618-52 | Sequence 52, Appl |
| 33 | 138.5 | 14.3 | 3803 | 2 | US-08-362-652-52 | Sequence 52, Appl |
| 34 | 138.5 | 14.3 | 3803 | 2 | US-08-605-672-52 | Sequence 52, Appl |
| 35 | 138.5 | 14.3 | 3803 | 2 | US-08-482-293A-52 | Sequence 52, Appl |
| 36 | 138.5 | 14.3 | 3803 | 2 | US-08-943-363-52 | Sequence 52, Appl |
| 37 | 138.5 | 14.3 | 3803 | 3 | US-09-193-043-52 | Sequence 52, Appl |
| 38 | 138.5 | 14.3 | 3803 | 3 | US-09-688-307A-52 | Sequence 52, Appl |
| 39 | 138.5 | 14.3 | 3803 | 3 | US-09-350-259-52 | Sequence 52, Appl |
| 40 | 132.5 | 13.7 | 3533 | 2 | US-08-476-062A-40 | Sequence 40, Appl |
| 41 | 132.5 | 13.7 | 3533 | 6 | PCT-US96-01314-40 | Sequence 40, Appl |
| 42 | 132.5 | 13.7 | 3533 | 3 | 5424399-1 | Sequence 40, Appl |
| 43 | 132.5 | 13.7 | 3595 | 3 | US-09-023-655-1147 | Sequence 1147, Ap |
| 44 | 132.5 | 13.7 | 4045 | 3 | US-09-809-517A-37 | Sequence 37, Appl |
| 45 | 132.5 | 13.7 | 4124 | 3 | US-09-023-655-1178 | Sequence 1178, Ap |

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Tonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Danni
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 6,46e-116      Length: 1609
Score: 970.00           Matches: 187
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 3                      Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-09-620-312D-8 (1-1609)

QY 1 G1YGYPhaApLeuTYrPhe1LeuApLySserG1SeVa1LeuH1eH1eTTPaSn 20
    |||
DB 429 GGGGATTGACCTGCTTCTTATTTGGACAAATCAGGAAGTGTGTCACACCTGGAAT 488
QY 21 G1u1eTYrTYrPheVa1G1uG1nLeuA1aH1eLyPhe1LeSserProG1nLeuA1gMeC 40
    |||
DB 489 GAAATCTAATTACTTGTGGAAcAGTTGGCTCAAAATTCATCAGCCCAcAGTTGAAGATG 548
QY 41 SerPhe1LeVa1PheSerThArG1YThrThrLeuMe1LySLeuThrG1uAaPaRg1u 60
    |||
DB 549 TCTTTATTTGTTTCTTCCACCCGAGAAcAACTTAACTGAACAGAGACAGAA 608
QY 61 G1n1eArG1nG1YLeuG1uG1nLeuG1nLyVa1LeuProG1YGYaSPThrTYrMeC 80
    |||
DB 609 CAATTCGCTCAAGGCTGAGAGAACTCCAGAAAGTTCTGcAGAGAGAGACATTACATG 668
QY 81 H1eG1uG1YPhEG1uA1gA1SeRg1uG1n1eTYrTYrG1uAaPaRg1uTYrA1g 100
    |||
DB 669 CATAGAGATTGAAAGGCGCAGAGAGAGATTATTTAGAAACAGACAGAGGATCACGG 728
QY 101 Thr1aSeRva11e1e1a1eUThraSPG1Yg1uH1eG1uAaSPLeuPhePheTYr 120
    |||
DB 729 ACACCGACGCTCATCTATTCCTTGACTATGAGAACTCCATGAAGATCTCTTTTCTAT 788
QY 121 SerG1uArG1uA1aAaPaRgSerArG1aSPLeuG1YAla1eVa1TYrCYaVa1GYa1 140
    |||
DB 789 TCAAGAGGAGGAGCTTAATAGCTCGAGATCTTGCTCAATTGTTTACTGTGTGTGTG 848
QY 141 LyAaSPheAaNG1uThrG1nLeuA1aRg1LeA1aSPSerLyAaSPH1eVa1PhePr 160
    |||
DB 849 AAAAGATTTCATGAGACACAGCTGCGCGAGTGGGACAGTAAAGATCATGTGTCTCC 908
QY 161 ValaNaSPG1YPhEG1a1aLeuG1nG1Y1e1eH1eSser1eLeuLyS1eSerCYs 180
    |||
DB 909 GTGAATGACGGCTTTCAGGCTCTGAAAGCATCACTCATTTTAAAGAGTCTGTC 968
QY 181 11eG1u1eLeuA1a1aG1u 187
    |||
DB 969 ATCGAAATTCAGAGCTGAA 989

RESULT 2
US-10-104-047-669
/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. 6943241el Full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
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/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 3,64e-61      Length: 2234
Score: 550.00           Matches: 109
Percent Similarity: 79.12%      Conservative: 35
Best Local Similarity: 59.89%    Mismatches: 36
Query Match: 56.70%           Indels: 2
DB: 3                      Gaps: 1

US-09-970-076-2_COPY_41_227 (1-187) x US-10-104-047-669 (1-2234)

QY 3 PheaSPLeuTYrPhe1LeuApLySserG1SeVa1LeuH1eH1eSTTPaNG1u1e 22
    |||
DB 655 TTTGATCTCTACTTCCTGCTGACCAAGTCTGGAGTGTGGCAATTAACCTGATTGAAT 714
QY 23 TYrTYrPheVa1G1uG1nLeuA1aH1eLyPhe1LeSserProG1nLeuA1gMeCSeR 42
    |||
DB 715 TATTAATTCGTAACGCAACTTGGCGAGAGATTGTGAGCCCTGAAGATGAATTATCTTTC 774
QY 43 11eVa1PheSerThArG1YThrThrLeuMe1LySLeuThrG1uAaPaRg1uG1n1e 62
    |||
DB 775 ATTGTGTTTCTTCTCAAGCACTTATTTTGGCATTTACTGAGACAGAGCAAAATC 834
QY 63 ArG1nG1YLeuG1uG1nLeuG1nLyVa1LeuProG1YGYaSPThrTYrMeC1eG1u 82
    |||
DB 835 AGTAAGGCTTGGAGGATTTAAAGCGTTAGTCCAGTAAGAGACATATATCATGAA 894
QY 83 G1YPhEG1uArG1a1aSeRg1uG1n1eTYrTYrG1uAaPaRg1uTYrA1gThrA1a 102
    |||
DB 895 GGACTAAAGCTAGGAATGAACAAAT-----CAGAAAGAGAGAGCTTAAGAACTCC 948
QY 103 SerVa11e1e1a1eUThraSPG1Yg1uH1eG1uAaSPLeuPhePheTYrSeRg1u 122
    |||
DB 949 AGTATCAATTAATGCTTTCGACAGATGGCAAGTTGACGGCTGTGTCCTCATATGCAAG 1008
QY 123 ArG1uA1aAaPaRgSerArG1aSPLeuG1YAla1eVa1TYrCYaVa1GYa1YaAaP 142
    |||
DB 1009 AAAAGGCAAAAGATCAAGCTCACTTGGGCTAGTGTATTGTTGTTGTTGCTCTGAT 1068
QY 143 PheaNG1uThrG1nLeuA1aRg1LeA1aSPSerLyAaSPH1eVa1PheProVa1Sn 162
    |||
DB 1069 TTTGAACAGCACGCTTGAAAGAAATGCTGATTCAGAGGACAAAGTTTCCCTGTCAA 1128
QY 163 AaPG1YPhEG1a1aLeuG1nG1Y1e1eH1eSser1eLeuLyS1eSerCYs11eG1u 182
    |||
DB 1129 GGTGAATTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCT 1188
QY 183 11eLeu 184
    |||
DB 1189 ATCCTA 1194

RESULT 3
US-09-774-528-297
/ Sequence 297, Application US/09774528
/ Patent No. 6743619
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Ren, Peiyao
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Wang, Jian-Rui
```


Db 937 CTTGCGACATCCAGAGCACTTCAGAGAAA 969

RESULT 7

US-08-485-618-36

Sequence 36, Application US/08485618

Patent No. 5728531

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5728531el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borum

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 3528 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3456

US-08-485-618-36

Alignment Scores:

Pred. No.: 7.93e-08 Length: 3528

Score: 141.50 Matches: 53

Percent Similarity: 47.64 Conservative: 38

Best Local Similarity: 27.75 Mismatches: 75

Query Match: 14.59 Indels: 25

2 Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-08-485-618-36 (1-3528)

Qy 4 AspleuTyRheleuaplysergylserVal--LeuHieHieTtpaenglulie 22

Db 424 GACATTGCTTCTCTGATGATGCTTGCAGCATTAACCAAGGACTTGCACAGATG 483

Qy 23 TyTyTyRheValGluGluLeuAlaHsblyRheHieSerProGluLeuAlaRgmetserPhe 42

Db 484 AAGGACTTGTCAAGACTTGTATGGAGATTGGCGAGACACAGACCTGTGTCTCCCTG 543

Qy 43 IleValPheSerThrArgGlyThrThreuetlySleuThrglu----- 57

Db 544 ATGCATATCTCGAATCATCTCGAATCCATTTTACCTTCATGAAATTCAGAAATCTCTG 603

Qy 58 AsparGluGluIleuArgGlnGlyLeuGluGluGluGlnValLeuProGlyGlyAsp 77

Db 604 GACCTCTGAGCTGTGTGATCCATGTCTCCAGCTGCA-----GCCCTG 648

Qy 78 ThrTyMetHieGluGlyPheGluAlaArgAlaSerGluGlnIleTyTyRgluAsnArgGln 97

Db 649 ACCTACAGACGCAGCATCCGACAGATGAGAGGCTATTCATGCAAGATGAG 708

Qy 98 GlyTyArgThrAla--SerValIleIleAlaLeuThrArgGlyGluLeuHieGluAsp 116

Db 709 TCCCGTAAAGTCCAGAGATCTCTTGTCTGATCAGAGATGAGGCAAAATACAGAGAC 768

Qy 117 LeuPhePheTyRserGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 134

Db 769 CCCCTGAGTATAGATGTCTATCCGCCGCGACAAAGCT-----GCCATCAT 819

Qy 135 ValTyCyValGlyValIleAsp--PheAsnGlu--ThrgluLeuAlaArgGlyle-- 151

Db 820 CGTTATGTCTATGGGTGGAGATGCTTCCAGAGCCCACTGCCCTGAGAGCTGAAC 879

Qy 152 -----AlaAspSerIleAspHieValPheProValAsnAspGlyPheGluAla 167

Db 880 ACCATTGGCTGCTCCCGCCAGAGCCAGCGTTCAGATGAGCAAC---TTTCAGCA 936

Qy 168 LeuGlnGlyIleIleHieSerIleLeuAla 178

Db 937 CTTGCGACATCCAGAGCACTTCAGAGAAA 969

RESULT 8

US-08-362-652-36

Sequence 36, Application US/08362652

Patent No. 576850

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 576850el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borum

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,652

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32391

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-362-652-36

Alignment Scores:
Pred. No.: 7,93e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-08-362-652-36 (1-3528)

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QY 4 AapLeuTyRPhelIleuAapLySerGlySerVal---LeuHihIstrPaengluIle 22
DB 424 GACATTGCTTCTCTGATGATGGTTCTGGAGCATTAACCAAGGACTTGGCCGAGATG 483
QY 23 TyTyRPhaValGluInleuAahIshLySPhelIseRProGlnleuAghMetSerPhe 42
DB 484 AAGGACTTGTCTCAAACTTGAATGGAGATTGGAGACCCGACGACTTGTCTCCCTG 543
QY 43 IlevAlPheSerThrArgGlyThrThrLeuMetLyLeuThrglu----- 57
DB 544 ATGCAATACCTCGAATCCTGGAAGACCTTTACCTTCAGTAATTCAGAAACATCTG 603
QY 58 AapAagGluGlnIleArgGlnGlyLeuGluGluLeuGlnValLeuProGlyGlyAap 77
DB 604 GACCTTCAGAGCCTGGTGGATCCCATTTGCCAGCTGCA-----GGCCTG 648
QY 78 ThrTyRMeChIseGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAenArgGln 97
DB 649 ACCTACACAGCCCAAGCATCCGAGACGATGAGATGATTCATGACCAAGATGG 708
QY 98 GlyTyArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHihIshGluAap 116
DB 709 TCCCGTAAAGTCCCAAGAAATCTCTGTCTACACAGATGGGCAAAATACAGAGAC 768
QY 117 LeuPhePheTySerGlu-----ArgGluAlaAapSerArgAapLeuGlyAlaIle 134
DB 769 CCCCCTGAGATAGTATGATGATTCATCCCGCCGACGACAAAGCT-----GGCATCAT 819
QY 135 ValTyCyseValGlyValLyAap---PheAenglu---ThrgInleuAlaArgIle--- 151
DB 820 CGTTATGCTATGGGTGGGATGCTTCAGAGAGCCCATCCCTGGAAGAGAGTGAAC 879
QY 152 -----AlaapSerLyAapPhIshValPheProValAenAapGlyPheGlnAla 167
DB 880 ACCATTGGCTCAGCTCCCGACGAGACACAGTGTTCAGAGTAGGCAAC---TTTGACGCA 936
QY 168 LeuGlnGlyIleIleHihSerIleLeuLyLe 178
DB 937 CTTCGAGCATTCAGAGGCACTTCAGAGGAA 969
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RESULT 9
US-08-605-672-36

/ Sequence 36, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vliet, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Seear Tower

CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652

ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456

US-08-605-672-36

Alignment Scores:
Pred. No.: 7,93e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-08-605-672-36 (1-3528)

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QY 4 AapLeuTyRPhelIleuAapLySerGlySerVal---LeuHihIstrPaengluIle 22
DB 424 GACATTGCTTCTCTGATGATGGTTCTGGAGCATTAACCAAGGACTTGGCCGAGATG 483
QY 23 TyTyRPhaValGluInleuAahIshLySPhelIseRProGlnleuAghMetSerPhe 42
DB 484 AAGGACTTGTCTCAAACTTGAATGGAGATTGGAGACCCGACGACCTTGTCTCCCTG 543
QY 43 IlevAlPheSerThrArgGlyThrThrLeuMetLyLeuThrglu----- 57
DB 544 ATGCAATACCTCGAATCCTGGAAGACCTTTTACCTTCAGTAATTCAGAAACATCTG 603
QY 58 AapAagGluGlnIleArgGlnGlyLeuGluGluLeuGlnValLeuProGlyGlyAap 77
DB 604 GACCTTCAGAGCCTGGTGGATCCCATTTGCCAGCTGCA-----GGCCTG 648
QY 78 ThrTyRMeChIseGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAenArgGln 97
DB 649 ACCTACACAGCCCAAGCATCCGAGACGATGAGATGAGACTTATTCATCAAGAAATGG 708
QY 98 GlyTyArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHihIshGluAap 116
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Db      709 TCCCGTAAAGTGCAGAGAGATCTCTTGTATCAGATGGGCAAAATACAGAGAC 768
      117 LeuphetherYserGlu-----ArgGluAaenAgsSerAgsAerLeuGlyAlaIle 134
      769 CCCCTGGAGTATGATGATGATCTCCCGCCCAAGCAAGCT-----GGCATCAT 819
      135 ValTYrCyvAlGlyValIyAAsP--PheAenGlu---ThrGlnLeuAlaArgIle--- 151
      820 CGTATGCTATTGGGGTGGAGATGCTTCCAGAGGCCACTGCCCTGAAAGAGCTGAAAC 879
      152 -----AlaAerSerIyAAsPHisValPheProValAenAerGlyPheGlnAla 167
      880 ACCATTGGCTCAGCTCCCGCCACAGAGCACGTTTCAAGTAGGCAAC---TTTGCAGCA 936
      168 LeuGlnGlyIleIleHisSerIleLeuIyAAs 178
      937 CTTCGACGATCCAGAGCAACTTCAGAGAAA 969

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RESULT 10
US-08-482-293A-36
Sequence 36, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-482-293A-36

```

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Alignment Scores:
Pred. No.: 7.93e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
DB: 2 Gaps: 10

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US-09-970-076-2_copy_41_227 (1-187) x US-08-482-293A-36 (1-3528)

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      4 AsrLeuTYrPheIleLeuAerIySerGlySerVal---LeuHisIAsTrPAenGluIle 22
      424 GACATTCCTTCCGATGATGATGCTTTCGACAGCATTAACCAAGAGACTTCCCAAGATG 483
      23 TYrTYrPheValGlyGlnLeuAlaHisIyAAsPheIleSerProGlnLeuAgsMerSerPhe 42
      484 AAGGACTTTCGAAAGCTTGATGGAGAGTTTGCGAGCACCAGACACTTGTCTCCCTG 543
      43 IleValPheSerThrAAsGlyThrThrLeuMetIyLeuThrGlu----- 57
      544 ATGCATATCTGAAACATCTGAAAGCCCATTTTACCTTCACTGAATTCAAGACATCTCG 603
      58 AsrAerGluGlnIleAerGlnGlyLeuGluGluIyValIyAAsProGlyGlyAAsP 77
      604 GACCTCAGAGCCCTGGAGATCCCATTTGTCAGCTGCA-----GGCCTG 648
      78 ThrTYrMetHisGlnGlyPheGluAAsSerGluGlnIleTYrTYrGluAAsPArgIle 97
      649 ACCTACACAGCAGCAGGATCCGAGAGATGAGAGATTTTCAATTCAGCAAGATGGG 708
      98 GLYrTYrGlyThrAla---SerValIleIleAlaLeuThrAerGlyGluIleHisGluAAsP 116
      709 TCCCGTAAAGTGCAGAGAGATCTCTTGTATCAGATGGGCAAAATACAGAGAC 768
      117 LeuphetherYserGlu-----ArgGluAaenAgsSerAgsAerLeuGlyAlaIle 134
      769 CCCCTGGAGTATGATGATGATCTCCCGCCCAAGCAAGCT-----GGCATCAT 819
      135 ValTYrCyvAlGlyValIyAAsP--PheAenGlu---ThrGlnLeuAlaArgIle--- 151
      820 CGTATGCTATTGGGGTGGAGATGCTTCCAGAGGCCACTGCCCTGAAAGAGACTGAAAC 879
      152 -----AlaAerSerIyAAsPHisValPheProValAenAerGlyPheGlnAla 167
      880 ACCATTGGCTCAGCTCCCGCCACAGAGCACGTTTCAAGTAGGCAAC---TTTGCAGCA 936
      168 LeuGlnGlyIleIleHisSerIleLeuIyAAs 178
      937 CTTCGACGATCCAGAGCAACTTCAGAGAAA 969

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RESULT 11

US-08-943-363-36

Sequence 36, Application US/08943363

Patent No. 5837478

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vlieten, Monica

TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,363

FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-943-363-36

Alignment Scores:
Pred. No.: 7 93e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
DB: 2 Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-08-943-363-36 (1-3528)

QY 4 AappLeuTyRPhelLeuAapLySergLyServal--LeuHiShiSTrPaBngJuIle 22
DB 424 GACATTGCTTCTGATGATGCTTCTGCGACGATTAACCAAGGACCTTGCCCGCATG 483
QY 23 TyTyRPhenaGlInLeuAaHsiSvPheIleSerpProInLeuArMgMetSerPhe 42
DB 484 AAGACTTTGTCAAGCTTGTGATGGAGATTGGACGACCAACGACTTGTCTCCCTG 543
QY 43 IleValPheSerThrArgLyThrThrLeuMetLyLeuThrgInu----- 57
DB 544 ATGCATTACTCGAACATCTCTGAAGACCCATTATTCCTCACTGAATTCAAGAACATCTG 603
QY 58 AaPaRgGlInLeuAaHsiSvPheIleSerpProInLeuArMgMetSerPhe 77
DB 604 GACCTCAAGCTGTGATGCCATGTGCCACTGCA-----GGCCTG 648
QY 78 ThrTyRMeChIeGlInLyPheGlAaRgAlaSerGlInLeTyTyRgIuAaRgIn 97
DB 649 ACCTACACAGCCACAGCATCCGACAGTGAAGAGCTATTTCATAGCAAGAAATGGG 708
QY 98 GLyTyRArgThraA---seValIleIleAlaLeuThraSpGlyGluLeuHiSglAaP 116
DB 709 TCCCGTAAAGTCCAGAAAGATCTCTCTTGTCAATCAGATGGGCAAAATACAGAGAC 768
QY 117 LeuPhePheTyRserGlu-----ArgGluAlaAaRgSerArRgApleuGlyAlaIle 134
DB 769 CCCCTGAGATATGATATGATCATTCGCGCGCAGACAAAGCT-----GGCATCAT 819
QY 135 ValTyRCyAvalGlyVallyAaP---PheAaMgInu---ThrgInLeuAaHsiSglAaP 151
DB 820 CGTTATGCGATATGGGGTGGGAGATGCTTCCAGAGAGCCACTGCGCTGAAGAGCTGAC 879

QY 152 -----AlaAaPserLyAaAaHsiSvAlPheRcovaAlaAaAaSpGlyPheGlIna 167
DB 880 ACCATTGGCTCAGCTCCCGACAGGACCAAGGTCATAGTGGACAC---TTTGACGCA 936
QY 168 LeuGInGlyIleIleHsiSvPheIleSerpProInLeuArMgMetSerPhe 178
DB 937 CTTCGACATCTCAGAGGCACTTCAGAGAAA 969

RESULT 12
US-09-193-043-36
Sequence 36, Application US/09193043
Patent No. 6251395

GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 36
LENGTH: 3528

TYPE: DNA
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3453)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-36

Alignment Scores:
Pred. No.: 7 93e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
DB: 3 Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-09-193-043-36 (1-3528)

QY 4 AappLeuTyRPhelLeuAapLySergLyServal--LeuHiShiSTrPaBngJuIle 22
DB 424 GACATTGCTTCTGATGATGCTTCTGCGACGATTAACCAAGGACCTTGCCCGCATG 483
QY 23 TyTyRPhenaGlInLeuAaHsiSvPheIleSerpProInLeuArMgMetSerPhe 42
DB 484 AAGACTTTGTCAAGCTTGTGATGGAGATTGGACGACCAACGACTTGTCTCCCTG 543
QY 43 IleValPheSerThrArgLyThrThrLeuMetLyLeuThrgInu----- 57
DB 544 ATGCATTACTCGAACATCTCTGAAGACCCATTATTCCTCACTGAATTCAAGAACATCTG 603
QY 58 AaPaRgGlInLeuAaHsiSvPheIleSerpProInLeuArMgMetSerPhe 77
DB 604 GACCTCAAGCTGTGATGCCATGTGCCACTGCA-----GGCCTG 648
QY 78 ThrTyRMeChIeGlInLyPheGlAaRgAlaSerGlInLeTyTyRgIuAaRgIn 97
DB 649 ACCTACACAGCCACAGCATCCGACAGTGAAGAGCTATTTCATAGCAAGAAATGGG 708
QY 98 GLyTyRArgThraA---seValIleIleAlaLeuThraSpGlyGluLeuHiSglAaP 116
DB 709 TCCCGTAAAGTCCAGAAAGATCTCTTGTCAATCAGATGGGCAAAATACAGAGAC 768

| Qy | Db | Sequence | Length | Matches |
|-------------------|----------|--|--------|---------|
| Qy | 117 | LeupPhePheTySerLeu-----ArGluAlaAsnArgSerLeuGlyAlaIle | 134 | |
| Db | 769 | CCCCGAGAGTATNGTATGATCTGATTCGCCGCCGACAGCAAACT-----GGCATCATTT | 819 | |
| Qy | 135 | ValTYCyGvaIGlyValIysaP---PheaSngLu--ThrGlnLeuAlaArgIle-- | 151 | |
| Db | 820 | CCTTATGCTATTAGGGGTGGGAGATGCTTCACAGAGCCCACTGCCCTCCATGAGAGAGCTGAAAC | 879 | |
| Qy | 152 | -----AlaAspSerIysaAPhisValPheProValaIshAsnSgLyPheGlnAla | 167 | |
| Db | 880 | ACCATTTGGCTCAGCTCTCCCCACAGGAGCCACAGTGTTCAGAGTAAAGTAAAGCAAC--TTTGACGACA | 936 | |
| Qy | 168 | LeuGlnGlyIleIleHisSerIleLeuLYLys | 178 | |
| Db | 937 | CTTCCGACGATCCAGAGGCCAACTTCAGAGAA | 969 | |
| RESULT | 13 | US-09-688-307A-36 | | |
| | | Sequence 36, Application US/09688307A | | |
| | | Patent No. 6432404 | | |
| | | GENERAL INFORMATION: | | |
| | | APPLICANT: Gallatin, Michael W. | | |
| | | APPLICANT: Van der Vieren, Monica | | |
| | | TITLE OF INVENTION: No. 6432404el Human Beta-2 | | |
| | | FILE REFERENCE: 27866/36646 | | |
| | | CURRENT APPLICATION NUMBER: US/09/688,307A | | |
| | | CURRENT FILING DATE: 2000-10-13 | | |
| | | PRIOR APPLICATION NUMBER: 09/193,043 | | |
| | | PRIOR FILING DATE: 1998-11-16 | | |
| | | PRIOR APPLICATION NUMBER: 08/605,672 | | |
| | | PRIOR FILING DATE: 1996-02-22 | | |
| | | PRIOR APPLICATION NUMBER: 08/173,497 | | |
| | | PRIOR FILING DATE: 1993-12-23 | | |
| | | PRIOR APPLICATION NUMBER: 08/286,889 | | |
| | | PRIOR FILING DATE: 1994-08-05 | | |
| | | PRIOR APPLICATION NUMBER: 08/362,652 | | |
| | | PRIOR FILING DATE: 1994-12-21 | | |
| | | PRIOR APPLICATION NUMBER: 08/943,363 | | |
| | | PRIOR FILING DATE: 1997-10-03 | | |
| | | NUMBER OF SEQ ID NOS: 114 | | |
| | | SOFTWARE: PatentIn Ver. 2.0 | | |
| | | SEQ ID NO 36 | | |
| | | LENGTH: 3528 | | |
| | | TYPE: DNA | | |
| | | ORGANISM: Rattus rattus | | |
| | | FEATURE: | | |
| | | NAME/KEY: CDS | | |
| | | LOCATION: (1)..(3453) | | |
| | | OTHER INFORMATION: Description of Artificial Sequence: primer | | |
| | | NAME/KEY: misc_feature | | |
| | | LOCATION: 361 | | |
| | | OTHER INFORMATION: Xaa = any or unknown amino acid | | |
| | | NAME/KEY: misc_feature | | |
| | | LOCATION: 464 | | |
| | | OTHER INFORMATION: Xaa = any or unknown amino acid | | |
| | | NAME/KEY: misc_feature | | |
| | | LOCATION: 486 | | |
| | | OTHER INFORMATION: Xaa = any or unknown amino acid | | |
| | | NAME/KEY: misc_feature | | |
| | | LOCATION: 506 | | |
| | | OTHER INFORMATION: Xaa = any or unknown amino acid | | |
| | | NAME/KEY: misc_feature | | |
| | | LOCATION: 1117 | | |
| | | OTHER INFORMATION: Xaa = any or unknown amino acid | | |
| | | NAME/KEY: misc_feature | | |
| | | LOCATION: 1118 | | |
| | | OTHER INFORMATION: Xaa = any or unknown amino acid | | |
| | | US-09-688-307A-36 | | |
| Alignment Scores: | | | | |
| Qy | 7.93e-08 | Length: | 3528 | |
| Db | 141.50 | Matches: | 53 | |

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Percent Similarity: 47.64% Conservative: 38%
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
DB: 3 Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-09-688-307A-36 (1-3528)

QY 4 AepLeuTYrPheIleuAAspLySerGlySerVal---LeuHhIhISrPraEngIuIle 22
|||:::|||||
DB 424 GACATGGTCTTCATATGATGATGGTCTGGACACATTAACCAAGGACCTTGGCCCAAGT 483
23 TYrTYrPheValAGluGlnLeuAlaIhIshYsPheIleSerProGlnLeuAArgMeSerPhe 42
|||:::|||||
DB 484 AAGACCTTGTCCAAAGCTTTGATGGGAAGAATTGGAGAGACCAAGACACCTGTCTCCG 543
43 ILevalPheSerThrArgGlyThrThrLeuMetLybLeuThrGlu-----57
:::|||||
DB 544 ATGCATATCTGCACATCTCGTCAAGACCATTTTACCTTCACATGAATTCAAGAACATCTG 603
58 AepAArgGluGlnIleAArgGlnGlyLeuGluGluGlnIleValLeuProGlyIAsp 77
|||:::|||||
DB 604 GACCTCGAGCGCTGTGATGCCATCTTCACAGTCCA-----GGCCTG 648
78 ThrTYrMetChIsgLugLyPheGluAArgAlaSerGluGlnIleTYrTYrGluAAspAArgI 97
|||:::|||||
DB 649 ACCTTCAACAGCCACAGGATCCGACAGTGAAGAAGACTTTTCATGACCAAGATGG 708
98 GLyTYrAArgThraIa---SerValIleIalaLeuThraSPGlyGluLeuHISgluAAsp 116
|||:::|||||
DB 709 TCCCGTAAAGTGCACAAAGATCTCTCTTCATCACAAGATGGCGAGAAATACAGAGAC 768
117 LeuPhePheTYrSerGlu-----AArgIuAlaAAspSerAArgAAspLeuGlyAlaIle 134
|||:::|||||
DB 769 CCCCTGAGATATGATGATCATCTCCGCCGACCAAGACT-----GCCATCAT 819
135 ValTYrCybValAGlyValIyAsp---PheAEngIu---ThrGlnLeuAlaArgIle--- 151
|||:::|||||
DB 820 CGTATGCTATTTGGGTGGAGATCCCTTCACAGAACCCACCTGCCCTGAAGAGCTGAAC 879
152 -----AlaAspSerLybAAspIhIValPheProValAspAAspGlyPheGlnAla 167
|||:::|||||
DB 880 ACCATGTGCTGACGCTCCCCACAGGACCAACGCTTCAAGGTAGGCAAC---TTTGCAGCA 936
168 LeuGlnGlyIleIleHISerIleLeuLybys 178
|||:::|||||
DB 937 CTTCGACGATCCAGAGGCAACTTCAGAGGAA 969

RESULT 14
US-09-350-259-36
/ Sequence 36, Application US/09350259
/ Patent No. 6620915
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: No. 6620915el Human 2
/ FILE REFERENCE: 2786/35004
/ CURRENT APPLICATION NUMBER: US/09/350,259
/ CURRENT FILING DATE: 1999-07-08
/ EARLIER APPLICATION NUMBER: 09/193,043
/ EARLIER FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 36
/ LENGTH: 3528
/ TYPE: DNA

```

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ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (3453)
FEATURE: (1) .. (3453)
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-36

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Alignment Scores:

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Pred. No.: 7,93e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
Gaps: 10

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US-09-970-076-2_COPY_41_227 (1-187) x US-09-350-259-36 (1-3528)

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QY 4 AapLeuTyrrPheileLeuAapLySerGlySerVal---LeuNH1H1eTrrPaenGluile 22
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 424 GACATGCTTCTCTGATGATGTTCTGGCAGCATTAACCAAGGAGCTTGTCCAGATG 483
QY 23 TyrrTyrrPheValGluGlnLeuA1H1sYrPheileSerProGlnLeuH1gMetSerPhe 42
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 AAGGACTTGTCAAGCTTGTATGGAGAGTTGGAGAGCGAGCAGCAGCCTGTGTCTCCCTG 543
QY 43 ILeValPheSerThrArgGlyThrThrLeuMetLySerThrglu----- 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 544 ATGCATACCTCAACAATCTCTGAAGCCCTTTACTCTCACTGAATTCAGAAACATCTCTG 603
QY 58 AapArgGluGlnIleArgGlnIleuGlnIleuGlnIleValLeuProGlyGlyAap 77
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 604 GACCTCAGAGCTGTGGATCCCATTTGCCAGCTGCAA-----GGCTTG 648
QY 78 ThrTyrrMetH1sGluGlyPheGluArgAlaSerGluGlnIleTyrrTyrrGluAapArgin 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 649 ACCTACAGACGACGAGGATCCGAGACAGTATGAGAGAGCTTTTCATATGCAAGAAATGGG 708
QY 98 GlyTyrrArgThrAla---SerValIleIleAlaLeuThraSerGlyGluLeuH1sGluAap 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 709 TCCCTTAAAGTCCCAAGAAAGATCTCTCTTCATCAGATGAGGAGAAATACAGAAAGC 768
QY 117 LeuPhePheTyrrSerGlu---ArgGluAlaAapA1SerArgAapLeuGlyAlaIle 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 769 CCCCTGAGATATGATGATCATCTCCCGCCGACAGCAAGCT-----GGCATCATTT 819
QY 135 ValTyrrCyseValGlyValLyAap---PheAenGlu---ThrglnLeuAlaArgIle--- 151
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 820 CGTATGCTATGGGGGTGGAGATGCTTCCAGAGAGCCCACTGCTCGAAGAGCTGAAC 879
QY 152 -----AlaAapSerLyAapH1sValPheProValAapAapGlyPheGlnAla 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 880 ACCATGCTCAGCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
QY 168 LeuGlnGlyIleIleH1sSerIleLeuLyLyS 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 937 CTTCCAGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 969

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RESULT 15
US-08-485-618-54
Sequence 54, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Bear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

```

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: William Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 3597 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 40..3525

US-08-485-618-54

Alignment Scores:

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Pred. No.: 8.16e-08 Length: 3597
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
Gaps: 10

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US-09-970-076-2_COPY_41_227 (1-187) x US-08-485-618-54 (1-3597)

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QY 4 AapLeuTyrrPheileLeuAapLySerGlySerVal---LeuNH1H1eTrrPaenGluile 22
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 493 GACATGCTTCTCTGATGATGTTCTGGCAGCATTAACCAAGGAGCTTGTCCAGATG 552
QY 23 TyrrTyrrPheValGluGlnLeuA1H1sYrPheileSerProGlnLeuH1gMetSerPhe 42
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 553 AAGGACTTGTCAAGCTTGTATGGAGAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
QY 43 ILeValPheSerThrArgGlyThrThrLeuMetLySerThrglu----- 57
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Oy      117 LeuPhePheTyrrSerGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 134
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Search completed: December 18, 2005, 07:34:31
 Job time : 144.287 secs

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| Qy | 181 | CGGGCAAGGGGGACGACGAGAGAGATGGGGGTCCAGCCCTGCTACGGCGATTGACTGTGA | 240 |
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| Qy | 541 | TGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTCTAATTCAGAGAGGAGGCTAA | 600 |
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| Qy | 661 | ACAGCTGGCCCGGATTTGCGGACAGTGAAGATCATGTGTTCCCGGATGAGCGGCTTCA | 720 |
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| D _b | 1381 | CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | 1414 |

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| ACCESSION | AF421380 | | | |
| VERSION | AF421380.1 | GI:16566412 | | |
| KEYWORDS | | | | |
| SOURCE | Homo sapiens (human) | | | |

REFERENCE
1 (Pages 1 to 1414)
Bradley, K.A., Mogridge, J., Mounes, M., Collier, R.J. and Young, J.A.
TITLE
Identification of the cellular receptor for anthrax toxin
JOURNAL
Nature 414 (1986), 225-229 (2001)

AUTHORS Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Department of Oncology, University of Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA
FEATURES Location/Qualifiers

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CDS

3' UTR

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VERSION AX393246.1 GI:19701296
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Homnidae; Homo.
REFERENCE
1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
Endothelial cell expression patterns
Patent: WO 0210217-A 176 07-FEB-2002;
JOURNAL The Johns Hopkins University (US)
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 Homnidae; Homo.

REFERENCE
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AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
 TITLE Endothelial cell expression patterns
 JOURNAL Patent: WO 0210217-A 231 07-FEB-2002;
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Homnidae; Homo.
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REFERENCE
AUTHORS Young, J.A., Bradley, K.A., Collier, R.J. and Mogridge, J.S.
TITLE Receptor for b. Anthracis toxin
JOURNAL Patent: WO 0246228-A 5 13 JUN-2002;
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Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 1.7e-286;
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LOCUS Homo sapiens tumor endothelial marker 8 precursor (TEM8) mRNA,
DEFINITION complete cds.
ACCESSION AF279145
VERSION AF279145.2 GI:14017380
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ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
REFERENCE 1 (bases 1 to 5540)
AUTHORS St. Croix,B., Rago,C., Velculescu,V., Traverso,G., Romans,K.E.,
Montgomery,E., Lal,A., Riggin,G.J., Lengauer,C., Vogelstein,B. and
Kinzler,K.W.
Genes expressed in human tumor endothelium
JOURNAL Science 289 (5482), 1197-1202 (2000)
PUBMED 10947988
REFERENCE 2 (bases 1 to 5540)
AUTHORS St. Croix,B., Vogelstein,B. and Kinzler,K.W.
Direct Submission
JOURNAL Submitted (16-JUN-2000) Johns Hopkins Oncology Center, Johns
Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
3 (bases 1 to 5540)
AUTHORS St. Croix,B., Vogelstein,B. and Kinzler,K.W.
Direct Submission
JOURNAL Submitted (09-MAY-2001) Johns Hopkins Oncology Center, Johns
Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
Sequence update by submitter
REMARK On May 9, 2001 this sequence version replaced gi:9857405.
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Best Local Similarity 99.8%; Pred. No. 1.7e-288;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGAACCCGAGAGAGGGCCCGGATGCGCGTCCCTGAGGCTGTGGCGAGTTCCGCG 60
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RESULT 7
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LOCUS
DEFINITION Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
transcript variant 2 (ANTXR1/NGI fusion) mRNA, complete cds.
ACCESSION AY928975
VERSION AY928975.1 GI:62870686
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1576)
Oberthuer, A., Kahle, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
2 (bases 1 to 1576)
Oberthuer, A., Kahle, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
Direct Submission
Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
9, Cologne, NRW D-50924, Germany
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Best Local Similarity 99.5%; Pred. No. 1,6e-288;
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LOCUS Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
DEFINITION transcript variant 4 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY928977.1 GI:62870690
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo;
1 (bases 1 to 1658)
Oberthuer, A., Kahle, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
2 (bases 1 to 1658)
Oberthuer, A., Kahle, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
Direct Submission
Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
9, Cologne, NRW D-50924, Germany
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Best Local Similarity 99.5%; Pred. No. 1.6e-288;
Matches 1197; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 AGGACCCGCGAGGAAAGGCGCGCGGATGCGCGTCCCTGAGGGTGTGCGAGTTCGGCG 60
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RESULT 9
AY928974 1496 bp mRNA linear PRI 10-MAY-2005
LOCUS Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
DEFINITION transcribed variant 1 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY928974
VERSION AY928974.1 GI:62870684
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1496)
Oberthur, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
JOURNAL 2 (bases 1 to 1496)
Oberthur, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
9, Cologne, NRW D-50924, Germany
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RESULT 10
LOCUS AY928976 1578 bp mRNA linear PRI 10-MAY-2005
DEFINITION Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
transcript variant 3 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY928976
VERSION AY928976.1 GI:62870688
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1578)
Oberthuer, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
TITLE 2 (bases 1 to 1578)
Oberthuer, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
Direct Submision
JOURNAL Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Steitzmann-Strasse
9, Cologne, NRW D-50924, Germany
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Best Local Similarity 99.9%; Pred. No. 2,9e-288;
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RESULT 11
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LOCUS AX458372
DEFINITION Sequence 7 from Patent WO0246228.
ACCESSION AX458372
VERSION AX458372.1 GI:21725042
KEYWORDS
SOURCE
ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Young, J. A., Bradley, K. A., Collier, R. J. and Mogridge, J. S.
TITLE Receptor for b. Anthracis toxin
JOURNAL Patent: WO 0246228-A 7 13-JUN-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
LOCATION/Qualifiers

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| LOCUS | | | |
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| SOURCE | | MGC: | |
| ORGANISM | | Homo sapiens (human) | |
| REFERENCE | | Homo sapiens | |
| AUTHORS | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. | |
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| | | Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhac,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stepleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheet,T.E., Brownstein,M.J., Uebelin,T.S., Toshitsuki,S., Carancini,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulys-S.M., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Foley,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schnur,J., Myers,R.M., Butterfield,Y.S., Krzywicki,M.I., Skalka,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marré,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 2112) Strausberg,R. Direct Submission Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing By: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@cgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Maeson, Mike R. Mayo, Josh Moran, Ryan Morin, Tejka Olson, Diana Palomquist, Anca Petrescu, Anna Liisa Pirabdu, Parvanah Saeedi, JR Santos, Angelique Schmerch, Ursula Skalka, Duane Small, Jeff Stott, Miranda Tsai, George Yang, Jaquie Schein, Aaim Siddiqui, Rob Holt, Marco Marra. | |
| REMARK | | Clone distribution: MGC clone distribution information can be found | |
| COMMENT | | | |

through the I.M.A.G.E. Consortium/INTL at: <http://image.llnl.gov>
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 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 16933552.
 location/Qualifiers
 1..2112

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| QY | 181 | CGGCGAAGGGGAGCGCAGGAGAGATGGGGGTCCAGCTTGCTTCCGCGGATTTGACCTGT | 240 | | |
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| QY | 301 | GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGTCTTTATTTTCTC | 360 | | |
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| QY | 361 | CACCCGAGGAACAACCTTAATGAAACTGACAGAGACAGAGAACAAATCCGTCAAGGCT | 420 | | |
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ACCESSION AK23273
VERSION AK23273.1 GI:62898106
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS 1 Maruyama, K. and Sugano, S.
TITLE Oligo-capping: a simple method to replace the cap structure of
eukaryotic mRNAs with oligoribonucleotides
JOURNAL Gene 138 (1-2), 171-174 (1994)
PUBMED 8125298
REFERENCE
AUTHORS 2 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S.
TITLE Construction and characterization of a full length-enriched and a
5'-end-enriched cDNA library
JOURNAL Gene 200 (1-2), 149-156 (1997)
PUBMED 9373149
REFERENCE
AUTHORS 3 (bases 1 to 2052)
Suzuki, Y., Sugano, S., Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y.,
Tanaka, A. and Yokoyama, S.
TITLE Direct Submision
Submited (22-APR-2005) Akiho Tanaka, RIKEN Yokohama Institute,
Protein Research Group, 1-7-22 Suehiro, Tsukumi, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: aktenaka@riken.jp,
URL: http://protein.gsc.riken.jp/, Tel: 81-45-503-9452,

COMMENT
Fax: 81-45-503-9450
This work was supported in part by the National Project on Protein
Structural and Functional Analysis, Ministry of Education, Culture,
Sports, Science and Technology of Japan.
Sumio Sugano, Yutaka Suzuki
Laboratory of Functional Genomics Department of Medical Genome
Sciences Graduate School of Frontier Sciences The University of
Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639 Japan email:
sugano@k.u-tokyo.ac.jp
URL: http://www.k.u-tokyo.ac.jp/index.html.en.
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ACCESSION AR338517.1 GI:33725374
VERSION AR338517.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1609)
AUTHORS Tang, Y.T., Zhou, P. and Drmanac, R.T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: US 6569662-A 8 27-MAY-2003;
Hyeq, Inc.; Sunnyvale, CA
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Matches 908; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Hominoidea; Homo.
REFERENCE
1 Schlegel, R., Endege, W.O. and Monahan, J.E.
AUTHORS
TITLE Genes differentially expressed in human prostate cancer and their use

JOURNAL Patent: WO 0160860-A 30300 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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ORIGIN

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Best Local Similarity 99.7%; Pred. No. 4,4e-216;
Matches 907; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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14: geneseqn2005bs:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| No. | Score | Query Match | Length | DB | ID | Description |
|-----|--------|-------------|--------|----|----------|--------------------|
| 1 | 1414 | 100.0 | 1414 | 6 | ABV73861 | Abv73861 Human ant |
| 2 | 1193.8 | 84.4 | 5540 | 6 | AB192078 | Ab192078 Human Tum |
| 3 | 1193.8 | 84.4 | 5540 | 6 | AB192104 | Ab192104 Human Tum |
| 4 | 1193.8 | 84.4 | 5540 | 6 | ABV73882 | Abv73882 Human ant |
| 5 | 1193.8 | 84.4 | 5540 | 10 | ABV72029 | Abv72029 DNA encod |
| 6 | 1193.8 | 84.4 | 5540 | 10 | ABV72003 | Abv72003 DNA encod |
| 7 | 1193.8 | 84.4 | 5540 | 13 | ADx48215 | Adx48215 Human tum |
| 8 | 1193.8 | 84.4 | 5540 | 14 | ADx70742 | Adx70742 Tumor end |
| 9 | 1193.8 | 84.4 | 5540 | 14 | AEa29804 | AEa29804 DNA encod |
| 10 | 1193.6 | 84.4 | 2447 | 4 | AA005303 | AA005303 Human sec |
| 11 | 1192.4 | 84.3 | 2102 | 6 | ABV73883 | Abv73883 Human ant |
| 12 | 1052.4 | 74.4 | 2112 | 3 | AAAv7455 | AAAv7455 Human TAN |
| 13 | 1052.4 | 74.4 | 2272 | 3 | AD100533 | Ad100533 Human TAN |
| 14 | 1052.4 | 74.4 | 2272 | 11 | ACNm4567 | ACNm4567 Human can |
| 15 | 1052.4 | 74.4 | 2351 | 11 | ACN88807 | ACN88807 Breast ca |
| 16 | 1052.4 | 74.4 | 1674 | 10 | AD100549 | Ad100549 Human TAN |
| 17 | 962.8 | 68.1 | 1674 | 10 | ADm64575 | Adm64575 Mouse TAN |
| 18 | 962.8 | 68.1 | 1674 | 11 | AD100545 | Ad100545 Human TAN |
| 19 | 952.4 | 67.4 | 1650 | 10 | AD100545 | Ad100545 Human TAN |

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| 20 | 953.4 | 67.4 | 1650 | 10 | AD100547 | Human | TAN |
| 21 | 953.4 | 67.4 | 1650 | 11 | AD100548 | Human | TAN |
| 22 | 952.4 | 67.4 | 1650 | 11 | ADMG4589 | TANCO197 | |
| 23 | 951.4 | 67.3 | 1056 | 10 | ADMG4581 | TANCO197 | |
| 24 | 951.4 | 67.3 | 1056 | 11 | AD100555 | Human | TAN |
| 25 | 951.4 | 67.3 | 1056 | 11 | ADMG4581 | Human | TAN |
| 26 | 951.4 | 67.3 | 1056 | 11 | AD100551 | Human | TAN |
| 27 | 951 | 67.3 | 1008 | 11 | ADMG4577 | Human | TAN |
| 28 | 951 | 67.3 | 1008 | 11 | AD100557 | Human | TAN |
| 29 | 950.8 | 67.2 | 1650 | 10 | AD100557 | Human | TAN |
| 30 | 950.8 | 67.2 | 1650 | 11 | ADMG4583 | Human | TAN |
| 31 | 914.4 | 64.7 | 1047 | 10 | AD100541 | Human | TAN |
| 32 | 914.4 | 64.7 | 1047 | 11 | ADMG4585 | Human | TAN |
| 33 | 906.8 | 64.1 | 1402 | 4 | AD100553 | Human | TAN |
| 34 | 906.8 | 64.1 | 1402 | 4 | ADMG4579 | Human | TAN |
| 35 | 906.8 | 64.1 | 1609 | 5 | AA155918 | Human | pol |
| 36 | 906.8 | 64.1 | 1609 | 5 | AA156132 | Human | pol |
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| 38 | 894.6 | 63.3 | 1718 | 5 | ADb48098 | Novel | hum |
| 39 | 890 | 62.9 | 1436 | 6 | ABV30282 | Human | pro |
| 40 | 890 | 62.9 | 1436 | 6 | AD100567 | Human | TAN |
| 41 | 867.6 | 61.4 | 1623 | 10 | AAH14331 | Human | cdn |
| 42 | 867.6 | 61.4 | 1623 | 11 | ABV73884 | Human | ant |
| 43 | 853.4 | 60.4 | 5220 | 6 | AD100543 | Human | TAN |
| 44 | 853.4 | 60.4 | 5220 | 6 | ADMG4587 | TANCO197 | |
| 45 | 853.4 | 60.4 | 5220 | 10 | ABL97085 | Mouse | Tum |
| | | | | | ABL97138 | Mouse | Tum |
| | | | | | ABL92138 | Mouse | Tum |
| | | | | | ABX72010 | DNA | encod |

ALIGNMENTS

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XX RESULT 1
XX ID ABV73881 standard; cDNA; 1414 BP.
XX AC ABV73881;
XX DT 08-JAN-2003 (first entry)
XX DE Human anthrax toxin receptor cDNA.
XX KH Anthrax; toxin; receptor; human; antibacterial; gene; ss.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 104..1210
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FT /*product= "anthrax toxin receptor"
FT sig_peptide 104..182
FT mat_peptide /*tag= b
FT 183..1207
FT /*tag= c
XX MO000246228-A2.
XX PD 13-JUN-2002.
XX PF 03-OCT-2001; 2001WC-US030941.
XX PR 05-DEC-2000; 2000US-0251481P.
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX PA
XX PI Young JAT, Bradley KA, Collier RJ, Mogridge JS;
XX DR WPI; 2002-713235/77.
XX P-PSDB; ABP54903.
XX Novel isolated polypeptide useful for identifying agent that prevents or
XX reduces effect of anthrax toxin on host cell, for treating human or non-
XX human animal suffering from anthrax.
XX

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PS Claim 7; Page 27-29; 45bp; English.
 XX The present sequence is that of cDNA encoding a human surface-bound
 CC anthrax toxin receptor (ATR). The cDNA is a PCR amplification product
 CC from HeLa cells and human placenta cDNA libraries. Anthrax toxin
 CC protective antigen (PA) binds to the ATR at a von Willebrand factor A
 CC domain located in the extracellular domain of ATR. The invention provides
 CC ATR polypeptides and polynucleotides, vectors, host cells, and transgenic
 CC and knock-out animals. The invention also provides methods for
 CC identifying molecules that bind the ATR and which reduce the toxicity of
 CC anthrax toxin. A claimed method for treating anthrax in a human or animal
 CC involves administering an agent that inhibits binding between PA and ATR
 CC at a level effective to reduce the severity of anthrax. Suitable agents
 CC include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at
 CC least 80% identical to these, a fusion protein, a monoclonal or
 CC polyclonal antibody, a polysaccharide, a lipid or a nucleic acid. ATR
 CC polynucleotides can also be used in the recombinant production of ATR
 CC polypeptides, and as molecular probes
 XX
 SQ Sequence 1414 BP; 394 A; 344 C; 344 G; 332 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1414; DB 6; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 AGGACCCGCGAGGAGGCGCGGATGCGCGTCCCTGAGAGTCTGGCGAGTTGCGCG 60
 QY 61 AGCGTGGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGGGGAGCG 120
 DB 61 AGCGTGGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGGGGAGCG 120
 QY 121 GAGAGCCCTGGGCACTCGGCTTCCAGTGCGTCTTTGGCCACTGTGGTCTCATCTGCGC 180
 DB 121 GAGAGCCCTGGGCACTCGGCTTCCAGTGCGTCTTTGGCCACTGTGGTCTCATCTGCGC 180
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 DB 361 CACCCGAGGAACAACCTTAATGAACTGACAGAAAGACAGAGAACAAATCCGTCAGGCCT 420
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 DB 661 ACAGCTGGCCCGGATTTGGGACAGTAAAGATCATGTGTTCCCGTGAATGACGGCTTCA 720

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 DB 721 GGCTTCGCAAGGATCATCTCAATTTTGAAGAGTCTCGCATGGAATTTCCAGACG 780
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 DB 781 TGAACCATCCACCATATGTCAGAGAGAGTCAATTTCAAGTTGTCGTGAGAGAAACGGCTT 840
 QY 841 CGGACATGCCCGGACGTTGACAGAGTCTCTGCAAGTTCAAGATCAATGACTGCTGCTAC 900
 DB 841 CGGACATGCCCGGACGTTGACAGAGTCTCTGCAAGTTCAAGATCAATGACTGCTGCTAC 900
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 QY 961 AAAAGAAAGTTGGATGAGAAAGTCACTCACTCAGAGTCAAGATGAAGAGGCTCTTTAT 1020
 DB 961 AAAAGAAAGTTGGATGAGAAAGTCACTCACTCAGAGTCAAGATGAAGAGGCTCTTTAT 1020
 QY 1021 CTCGAGTTCTGTATCATCAACACACACACTGTTCTGACGTTCCATCTGCGCATCGC 1080
 DB 1021 CTCGAGTTCTGTATCATCAACACACACACTGTTCTGACGTTCCATCTGCGCATCGC 1080
 QY 1081 CTTGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 1081 CTTGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1141 CTGCACTGATTTATCAAGAGGTCCTCCACCCCTGCGAGAGAGTGAAGAAATTA 1200
 DB 1141 CTGCACTGATTTATCAAGAGGTCCTCCACCCCTGCGAGAGAGTGAAGAAATTA 1200
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 DB 1381 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
 RESULT 2
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 XX ABL92078;
 AC ABL92078;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 176.
 XX Human; mouse; rat; TBW; tumour endothelial marker; NEM; PEM; cytostratic;
 KW normal endothelial marker; pan-endothelial marker; immunosuppressant;
 KW antiangiogenic; tumour; neovascularisation; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200210217-A2.
 XX
 XX 07-FEB-2002.
 XX
 XX PD
 XX 01-AUG-2001; 2001MO-US024031.
 XX
 XX

PR 02-AUG-2000; 2000US-0222599P.
PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
XX
XX (UJJO) UNIV JOHNS HOPKINS.
PI St Croix B, Kinzler KM, Vogelstein B;
DR WPI; 2002-29186/33.
XX
XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Disclosure; Page 121-123; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191, normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
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Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 2.4e-285;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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XX
XX ABL92104;
AC
XX 30-MAY-2002 (first entry)
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XX Human Tumour Endothelial Marker polynucleotide SEQ ID NO 231.
DE
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; gene; ss.
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PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
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XX (UJJO) UNIV JOHNS HOPKINS.
PA

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XX St Croix B, Kinzler KM, Vogelstein B;
XX
XX MPI: 2002-291856/33.
XX P-PSDB; ABB90750.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Claim 30; Page 207-209; 33pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumor growth, neoangiogenesis in subjects
XX bearing a vascularized tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences; tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX CC (PEM) ABL91903-ABL91995
XX
XX Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
XX
XX Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
XX Best Local Similarity 99.8%; Pred. No. 2.4e-285;
XX Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 AAGAACCCGAGAGAGAGGCGCGGATGGCGCTCCCTGAGGGGTGCTGGAGTTGGCGG 60
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RESULT 4
ABV73882
ID ABV73882 standard; cDNA; 5540 BP.
XX
AC ABV73882;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human anthrax toxin receptor cDNA.
XX
KW Anthrax; toxin; receptor; human; TEM8; antibacterial; gene; ss.
XX
OS Homo sapiens.
XX
XX
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FT FT /*tag= b
FT FT mat_peptide 225..1838
FT FT /*tag= c
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XX
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PD 13-JUN-2002.
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PF 03-OCT-2001; 2001WO-US030941.
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PR 05-DEC-2000; 2000US-0251481P.
XX
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX

PA (UYJO) UNIV JOHNS HOPKINS.
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 XX WPI, 2003-093016/08.
 DR P-PSDB; ABUS4457.
 XX
 XX New purified human transmembrane protein, designated as tumor endothelial
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
 PT psoriasis.
 XX
 XX Disclosure; Page 223-225; 374pp; English.

The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumor ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neovascularization or tumour angiogenesis, for
 CC inducing an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. The present
 CC sequence represents a human TEM or NEM gene of the invention

Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

Query Match 84.4%; Score 1193.8; DB 10; Length 5540;
 Best Local Similarity 99.8%; Pred. No. 2.4e-285;
 Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCCGGAGAAAGGCGCCGCGATGGCGCTCCCTGAGGTGCTGGCGAGTTCGCGG 60
 DB 41 AGGACCCCGGAGAAAGGCGCCGCGATGGCGCTCCCTGAGGTGCTGGCGAGTTCGCGG 100
 QY 61 AGCGTGGGAAGAGCGGACCTGCTCTCCCGGGCTCGCGGCGCATGGCCAGCGGAGG 120
 DB 101 AGCGTGGGAAGAGCGGACCTGCTCTCCCGGGCTCGCGGCGCATGGCCAGCGGAGG 160
 QY 121 GAGAGCCCTCGGCATCGCTTCAGTGCTCTTTGGCCACTCTGGTCTCATCTGCGC 180
 DB 161 GAGAGCCCTCGGCATCGCTTCAGTGCTCTTTGGCCACTCTGGTCTCATCTGCGC 220
 QY 181 CGGCGAAGGGGAGCGAGGAGGATGGGGGTCCAGCTGCTCGGGGATTGAGACTGTA 240
 DB 221 CGGCGAAGGGGAGCGAGGAGGATGGGGGTCCAGCTGCTCGGGGATTGAGACTGTA 280
 QY 241 CTTCAATTTTGGACAAATCAGAAAGTGTGCTGCACCACTGGAATGAATCTAATCTTGT 300
 DB 281 CTTCAATTTTGGACAAATCAGAAAGTGTGCTGCACCACTGGAATGAATCTAATCTTGT 340
 QY 301 GGAACAGTTGGCTCACAATATCATGCCCAAGTTGAGAGTCTTTATTTGTTTCTC 360
 DB 341 GGAACAGTTGGCTCACAATATCATGCCCAAGTTGAGAGTCTTTATTTGTTTCTC 400
 QY 361 CACCCGAGGAACAACCTTAATGAAGTGAACAAGACAGAAACAAATCCGTCAAGGCT 420
 DB 401 CACCCGAGGAACAACCTTAATGAAGTGAACAAGACAGAAACAAATCCGTCAAGGCT 460
 QY 421 AGAAGAACTCCAGAAAGTCTGCGAGGAGAGACCTTACATGATGAAGATTTGAAAG 480
 DB 461 AGAAGAACTCCAGAAAGTCTGCGAGGAGAGACCTTACATGATGAAGATTTGAAAG 520
 QY 481 GGCCAGTAGAGCAGATTTATATGAAAAACAGACAAAGGTAACAGACACCAAGCTCATCAT 540
 DB 521 GGCCAGTAGAGCAGATTTATATGAAAAACAGACAAAGGTAACAGACACCAAGCTCATCAT 580
 QY 541 TGGTTGACTGATGAGAACTCATGAAGTCTTTTCTTATTCAGAGAGGAGCTTAA 600
 DB 581 TGGTTGACTGATGAGAACTCATGAAGTCTTTTCTTATTCAGAGAGGAGCTTAA 640

QY 601 TAGGTCTGAGATCTTGTCGAATGTTTACTGTGTGTGTGTAAGATTTCAATGAGAC 660
 DB 641 TAGGTCTGAGATCTTGTCGAATGTTTACTGTGTGTGTGTAAGATTTCAATGAGAC 700
 QY 661 ACAGCTGGCCCGGATTTGGGACAGATGAATATGTGTTTCCCGTGAATGAGCGCTTCA 720
 DB 701 ACAGCTGGCCCGGATTTGGGACAGATGAATATGTGTTTCCCGTGAATGAGCGCTTCA 760
 QY 721 GGCCTGCAAGGACATCATCTCAATTTTGAAGAGTCCGTCATGCAATTTCTAGCAGC 780
 DB 761 GGCCTGCAAGGACATCATCTCAATTTTGAAGAGTCCGTCATGCAATTTCTAGCAGC 820
 QY 781 TGAACCATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAACGGCTT 840
 DB 821 TGAACCATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAACGGCTT 880
 QY 841 CCGAATGCCCCGCAACGTGAGACAGGATCCTCTGCAAGCTTCAAGTCAATGATCCGGTCA 900
 DB 881 CCGAATGCCCCGCAACGTGAGACAGGATCCTCTGCAAGCTTCAAGTCAATGATCCGGTCA 940
 QY 901 ACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTGTGTCCAGCGCTATCTT 960
 DB 941 ACTCAATGAGAAGCCCTTTTCTGTGGAAGATCTTATTTACTGTGTCCAGCGCTATCTT 1000
 QY 961 AAAAGAAATTGGCATGAAGAGCTGCACTCCAGGTCAAGATGAAGATGSCCTCTTTTAT 1020
 DB 1001 AAAAGAAATTGGCATGAAGAGCTGCACTCCAGGTCAAGATGAAGATGSCCTCTTTTAT 1060
 QY 1021 CTCGATTTGTGCATCATATACCAACACACACTGTTCTGACGGTTCCATCTGGCCATCCG 1080
 DB 1061 CTCGATTTGTGCATCATATACCAACACACACTGTTCTGACGGTTCCATCTGGCCATCCG 1120
 QY 1081 CCTGTGATCTCTGTTCTCTGCTCTGAGCCCTGAGCTCTCTGTGGTGTGCGCCCTCTG 1140
 DB 1121 CCTGTGATCTCTGTTCTCTGCTCTGAGCCCTGAGCTCTCTGTGGTGTGCGCCCTCTG 1180
 QY 1141 CTGCATGTGATTAATCAAGAGGTCCTCCACCCCTCCGAGAGATGAGGAAAA 1197
 DB 1181 CTGCATGTGATTAATCAAGAGGTCCTCCACCCCTCCGAGAGATGAGGAAAA 1237

RESULT 6
 ABX72003
 ID ABX72003 standard; DNA; 5540 BP.
 XX
 AC ABX72003;
 XX
 DT 12-MAR-2003 (first entry)
 XX
 DE DNA encoding human tumour endothelial marker TEM 8.
 XX
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 KW Tumour endothelial marker; normal endothelial marker; PEM;
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 KW neovascularization; immune response; cytotoxic; antidiabetic; gene;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; de.
 XX
 OS Homo sapiens.
 XX
 PN WO200283874-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US008253.
 XX
 XX 11-APR-2001; 2001US-0282850P.
 PR 06-FEB-2002; 2002US-0354262P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 PI
 XX

DR WPI; 2003-093016/08.
DR P-PSDB; ABU54430.

P-PSDB; ABU54430.

PT New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

PS Disclosure; Page 117-120; 374pp; English.

CC The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neovascularogenesis or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate TEMs for treating tumours. The present
CC sequence represents a human TEM or NEM gene of the invention

Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

| Query Match | 84.48; | Score 1193.8; | DB 10; | Length 5540; |
|-------------|--------|---------------|--------|--------------|
|-------------|--------|---------------|--------|--------------|

Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | I | AGGACCCCGCAGAGAAAGGGCCCGCGGATGGCGCTGCTCTGAGGGGTGCTGGCAGATTCCGGG | 60 |
| Db | 41 | AGGACCCCGCAGAGAAAGGGCCCGCGGATGGCGCTGCTGAGGGGTGCTGGCAGATTCCGGG | 100 |
| Qy | 61 | AGCGTGGGAAGGAGCGGACCTGCTCTCCCGGGCTGGCGGCGCATAGGCCACGGCGGAGCG | 120 |
| Db | 101 | AGCGTGGGAAGGAGCGGACCTGCTCTCCCGGGCTGGCGGCGCATAGGCCACGGCGGAGCG | 160 |
| Qy | 121 | GAGAGCCCTCGGCATTCGGCTTCAGTGGCTCTCTTTGGCCACTCTGGTGTCTCATCTCGGC | 180 |
| Db | 161 | GAGAGCCCTCGGCATTCGGCTTCAGTGGCTCTCTTTGGCCACTCTGGTGTCTCATCTGGGC | 220 |
| Qy | 181 | CGGGGAAAGGGGGAACCCAGGGAGATGGGGGTCAAGCTGTCAAGCGGGAATTTGACCTGTA | 240 |
| Db | 221 | CGGGGAAAGGGGGAACCCAGGGAGATGGGGGTCAAGCTGTCAAGCGGGAATTTGACCTGTA | 280 |
| Qy | 241 | CTTCACTTTTGGACAAATCAGAACTGTGCTGTGACCACTGGATGGAATCTATTACTTTGT | 300 |
| Db | 281 | CTTCACTTTTGGACAAATCAGAACTGTGCTGTGACCACTGGATGGAATCTATTACTTTGT | 340 |
| Qy | 301 | GGACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAGATGTCTTATTGTTTCTC | 360 |
| Db | 341 | GGACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAGATGTCTTATTGTTTCTC | 400 |
| Qy | 361 | CACCCGAGGAAACCTTATGAAACTGACAGAAACAGAGAAACAAATCCGTCAGGCGCT | 420 |
| Db | 401 | CACCCGAGGAAACCTTATGAAACTGACAGAAACAGAGAAACAAATCCGTCAGGCGCT | 460 |
| Qy | 421 | AGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTATCATGCTGAGAGATTTGAAG | 480 |
| Db | 461 | AGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTATCATGCTGAGAGATTTGAAG | 520 |
| Qy | 481 | GGCCAGTGGCAGATTTATTATGAAAACGACAAAGGTTACAGACAGCCAGGTCATCAT | 540 |
| Db | 521 | GGCCAGTGGCAGATTTATTATGAAAACGACAAAGGTTACAGACAGCCAGGTCATCAT | 580 |
| Qy | 541 | TGCTTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTTCAGAGAGGAGCTTAA | 600 |
| Db | 581 | TGCTTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTTCAGAGAGGAGCTTAA | 640 |
| Qy | 601 | TAGGTCTGAGATCTTGGTGCATTTGTTACTGTGTGGTGTGAAAAGATTTCAATGAGAC | 660 |
| Db | 641 | TAGGTCTGAGATCTTGGTGCATTTGTTACTGTGTGGTGTGAAAAGATTTCAATGAGAC | 700 |

| | | | |
|----------|--|--|------|
| Oy | 661 | ACAGCTGGCCCGGATTTGGCGACAGTAAGATCATGTGTTTCCGTGAATGACGGCTTTCA | 720 |
| Db | 701 | ACAGCTGGCCCGGATTTGGCGACAGTAAGATCATGTGTTTCCGTGAATGACGGCTTTCA | 760 |
| Oy | 721 | GGCTCTGCAAGGGCATCATCCACTGAATTTTGAAGAAGCCCTGCATCGAAATTTTCAGCAGC | 780 |
| Db | 761 | GGCTCTGCAAGGGCATCATCCACTGAATTTTGAAGAAGCTCTGCATTCGAAATTTTCAGCAGC | 820 |
| Oy | 781 | TGAACCATCCACCATATGTGACAGAGATCATTTTCAAGTTGTCTGTGAAGAGAAACGGCTT | 840 |
| Db | 821 | TGAACCATCCACCATATGTGACAGAGATCATTTTCAAGTTGTCTGTGAAGAGAAACGGCTT | 880 |
| Oy | 841 | CCGACATGCCCGCAACGTGGAACAGGGTCTCTGCAGCTTCAAGATTCATATGCTGGTTCAC | 900 |
| Db | 881 | CCGACATGCCCGCAACGTGGAACAGGGTCTCTGCAGCTTCAAGATTCATATGCTGGTTCAC | 940 |
| Oy | 901 | ACTCAATGAGAGGCCCTTTTCTGTGGAAGACACTTATTTACTGTGTCCAGGCGCTATCTT | 960 |
| Db | 941 | ACTCAATGAGAGGCCCTTTTCTGTGGAAGACTTATTTACTGTGTCCAGGCGCTATCTT | 1000 |
| Oy | 961 | AAAAGAGTTGGCATGAAAGCTGCACTCCAGCTGACATGAACGATGGCCCTCTCTTTTAT | 1020 |
| Db | 1001 | AAAAGAGTTGGCATGAAAGCTGCACTCCAGCTGACATGAACGATGGCCCTCTCTTTTAT | 1060 |
| Oy | 1021 | CTCCAGTTCTGTCAATCATCACCAACAACACTTTTTCAGCGTTTCATCTGGCCATGCG | 1080 |
| Db | 1061 | CTCCAGTTCTGTCAATCATCACCAACAACACTTTTTCAGCGTTTCATCTGGCCATGCG | 1120 |
| Oy | 1081 | CCGTGTGATCTGTGTTCCCTGCTCCAGCCCTGCTCTCTCTGAGTTCCTGGCCCTCTG | 1140 |
| Db | 1121 | CCGTGTGATCTGTGTTCCCTGCTCCAGCCCTGCTCTCTCTGAGTTCCTGGCCCTCTG | 1180 |
| Oy | 1141 | CTGCACCTGTATTATCAAGAGAGTCCCTCCACCCCTGCGCAGAGAGATGAGAGAAA | 1197 |
| Db | 1181 | CTGCACCTGTATTATCAAGAGAGTCCCTCCACCCCTGCGCAGAGAGATGAGAGAAA | 1237 |
| RESULT 7 | | | |
| ADR48215 | | | |
| ID | ADR48215 | standard; cDNA; 5540 BP. | |
| XX | AC | ADR48215; | |
| XX | DT | 18-NOV-2004 (first entry) | |
| XX | DE | Human tumour endothelial marker 8 precursor encoding cDNA SEQ:3. | |
| XX | XX | | |
| KW | pancreatic cancer-associated transcript; pancreatic cancer; human; cytosolic; gene therapy; protein therapy; | | |
| KW | tumour endothelial marker 8 precursor; TEM8; gene; ss. | | |
| OS | Homo sapiens. | | |
| XX | XX | | |
| FH | Key | Location/Qualifiers | |
| FT | FT | 144..1838 | |
| FT | CDS | /*tag= a | |
| FT | | /product= "tumour endothelial marker 8 precursor (TEM8) " | |
| XX | FN | WO2004074510-A1. | |
| PD | XX | 02-SEP-2004. | |
| XX | XX | | |
| PF | 18-FEB-2004; | 2004MO-AU000194. | |
| XX | XX | | |
| FR | 18-FEB-2003; | 2003AU-00900747. | |
| XX | XX | | |
| PA | (GARV-) GARVAN INST MEDICAL RES. | | |
| XX | XX | | |
| PI | Blankin A, Segara D, Henshall S, Sutherland R; | | |
| XX | XX | | |
| WI | WPI; 2004-635591/61. | | |
| DR | P-PSDB; ADR48216. | | |
| XX | XX | | |

PT Detecting pancreatic cancer-associated transcript in a biological sample,
PT useful for diagnosing or treating the disease, comprises contacting the
PT sample with a polynucleotide that selectively hybridizes to a specific
sequence.

PS Claim 70; SEQ ID NO 3; 263bp; English.

XX The present invention describes a method for detecting a pancreatic
XX cancer-associated transcript in a biological sample. The method comprises
XX contacting the biological sample with a polynucleotide that selectively
XX hybridizes to a sequence at least 80% identical to a sequence as shown in
XX any one of Tables 3 to 25 in the specification or having the Genbank
XX Accession Number AF279145. Also described: (1) diagnosing pancreatic
XX cancer in a human or animal subject being tested, determining the
XX likelihood that a subject having a pancreatic cancer will survive, or
XX determining the suitability of a subject having a pancreatic cancer for
XX surgical resection therapy; (2) detecting a pancreatic cancer-associated
XX polypeptide in a biological sample; (3) determining the likelihood that a
XX subject having a pancreatic cancer will survive; and (4) monitoring the
XX efficacy of a therapeutic treatment of pancreatic cancer. A pancreatic
XX cancer-associated transcript has cytosolic activity, and can be used in
XX gene and protein therapy. A pancreatic cancer-associated transcript
XX polynucleotide, a vector comprising the polynucleotide, an isolated
XX polypeptide or an antibody that binds to the isolated polypeptide can be
XX used for diagnosing or prognosing pancreatic cancer or for preparing a
XX diagnostic method for the treatment of pancreatic cancer. The prognostic or
XX diagnostic methods are useful for the early detection of pancreatic
XX cancer or its metastases, and for monitoring the progress of disease such
XX as during remission or following surgery or chemotherapy. The present
XX sequence encodes human tumour endothelial marker 8 precursor (Tem8),
XX which is used in the exemplification of the present invention.

SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

Query Match 84.4%; Score 1193.8; DB 13; Length 5540;

Best Local Similarity 99.8%; Pred. No. 2.4e-285;

Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGGAGGCGCGGATGGCGCGTCCCTGAGGGTCGTGGGAGTTGGCGG 60
DB 41 AGGACCCGCGAGGAGGCGCGGATGGCGCGTCCCTGAGGGTCGTGGGAGTTGGCGG 100
QY 61 AGCGTGGAGAGAGCGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGSCCAACGCGGAGCG 120
DB 101 AGCGTGGAGAGAGCGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGSCCAACGCGGAGCG 160
QY 121 GAGAGCCCTCGGATGGCTTCCAGTGGCTCTTTGGCCACTCTGTCTATCTGCGC 180
DB 161 GAGAGCCCTCGGATGGCTTCCAGTGGCTCTTTGGCCACTCTGTCTATCTGCGC 220
QY 181 CGGGCAAGGGGGAGCGAGGAGAGTGGGGTCCAGGCTGTAAGGGGATTTGACCTGTA 240
DB 221 CGGGCAAGGGGGAGCGAGGAGAGTGGGGTCCAGGCTGTAAGGGGATTTGACCTGTA 280
QY 241 CTTTCATTTTGAACAATTCAGAAAGTGTGTCACCACTGGAATGAATCTATTACTTTGT 300
DB 281 CTTTCATTTTGAACAATTCAGAAAGTGTGTCACCACTGGAATGAATCTATTACTTTGT 340
QY 301 GGAACGTTGGCTCACAATTCATCAGCCCAAGTTGAAGTCTCTTATTGTTTTTC 360
DB 341 GGAACGTTGGCTCACAATTCATCAGCCCAAGTTGAAGTCTCTTATTGTTTTTC 400
QY 361 CACCCGAGGAACAACCTTAATGAAGTGAAGAGAGAGCAAGAAACAATCCGTAAGGCT 420
DB 401 CACCCGAGGAACAACCTTAATGAAGTGAAGAGAGAGCAAGAAACAATCCGTAAGGCT 460
QY 421 AGAAGAACTCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAG 480
DB 461 AGAAGAACTCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAG 520
QY 481 GGCAGTGAAGCATTTATTATGAAAACAGACAGAGGTACAGACAGCCAGGCTCATCAT 540
DB 521 GGCAGTGAAGCATTTATTATGAAAACAGACAGAGGTACAGACAGCCAGGCTCATCAT 580

QY 541 TCGTTGACTGTAGAGAACTCCATGAAATCTTTTCTATTTCAGAGGAGGCTTA 600
DB 581 TCGTTGACTGTAGAGAACTCCATGAAATCTTTTCTATTTCAGAGGAGGCTTA 640
QY 601 TGGGTCTGAGATCTTTGTGCAATTTGTACTGTGTGTGTGAAAGATTTCAATAGAC 660
DB 641 TGGGTCTGAGATCTTTGTGCAATTTGTACTGTGTGTGAAAGATTTCAATAGAC 700
QY 661 ACAGCTGGCCGGATTTGGGAGAGTAAAGATCATGTTTCCCGTAATGACGGCTTTCA 720
DB 701 ACAGCTGGCCGGATTTGGGAGAGTAAAGATCATGTTTCCCGTAATGACGGCTTTCA 760
QY 721 GCGCTGCAAGGATCATCTCAATTTTGAAGAAGTCCGATGAATTTCTAGACAG 780
DB 761 GCGCTGCAAGGATCATCTCAATTTTGAAGAAGTCCGATGAATTTCTAGACAG 820
QY 781 TGAACCATCCACATATGTGCGAGAGATCATTTCAAGTTGTCGTAGAGAAACGGCTT 840
DB 821 TGAACCATCCACATATGTGCGAGAGATCATTTCAAGTTGTCGTAGAGAAACGGCTT 880
QY 841 CCGACATGCCGCAACGTGAGACAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTCAC 900
DB 881 CCGACATGCCGCAACGTGAGACAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTCAC 940
QY 901 ACTCAATGAAAGCCCTTTTCTGTGAGAGACATTATTACTGTGTCCAGCGCTTATTT 960
DB 941 ACTCAATGAAAGCCCTTTTCTGTGAGAGATCTTATTACTGTGTCCAGCGCTTATTT 1000
QY 961 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGTCAAGATGAGTGGCTCTTTTAT 1020
DB 1001 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGTCAAGATGAGTGGCTCTTTTAT 1060
QY 1021 CTCGAGTTCTGATCATCATCAGCACACACACTGTTCTGACGGTTCATCTGGCCATGCG 1080
DB 1061 CTCGAGTTCTGATCATCATCAGCACACACACTGTTCTGACGGTTCATCTGGCCATGCG 1120
QY 1081 CCGTGTGATCTGTTCTCTGCTCTGACCCCTGCTCTCTGTGTGTTCTGGCCCTCTG 1140
DB 1121 CCGTGTGATCTGTTCTCTGCTCTGACCCCTGCTCTCTGTGTGTTCTGGCCCTCTG 1180
QY 1141 CTGCACTGATTTATCAAGAGAGTCCCTCCACCCCTGCGGAGAGAGTGAAGAAA 1197
DB 1181 CTGCACTGATTTATCAAGAGAGTCCCTCCACCCCTGCGGAGAGAGTGAAGAAA 1237

RESULT 8
AD270742
ID AD270742 standard; cDNA; 5540 BP.
XX
AC AD270742;
XX
DT 14-JUL-2005 (first entry)
XX
DE Tumor endothelial marker 8 precursor (Tem8) cDNA.
XX
XX osteopathic; antiarthritic; gene expression; differentiation;
XX osteopathic; bone disease; osteoarthritis; antiarthritic; osteopathic;
XX musculoskeletal disease; tumor endothelial marker 8 precursor; Tem8; gene;
XX ss.
XX
XX Homo sapiens.
XX OS
XX PN MO2005038022-A1.
XX
XX 28-APR-2005.
XX
XX 20-OCT-2004; 2004MO-JP015879.
XX PF
XX 20-OCT-2003; 2003JP-00359172.
XX PR
XX (TEIJ-) TEIJIN PHARMA LTD.
XX PA (KOMORI) KOMORI T.
PA

XX Komori T, Kanatani N, Yoshida CA, Zama A, Kobayashi S, Yamana K,
 PI MPI; 2005-322866/33.
 DR P-PSDB; AD270743.
 XX
 PT Acquiring chondrogenic differentiation control related gene Runx2/Cbfa1,
 PT by forcibly expressing transcriptional factor related to pathological
 PT condition in cell strain lacking transcriptional factor and screening for
 PT gene.
 XX
 PS Claim 15; SEQ ID NO 27; 357bp; Japanese.
 XX
 CC The invention describes acquiring (M1) a pathological condition related
 CC gene, preferably chondrogenic differentiation control related gene
 CC Runx2/Cbfa1, comprising forcibly expressing a transcriptional factor
 CC related to pathological condition, preferably Runx2/Cbfa1 in a cell
 CC strain or a primary culture cell lacking the transcriptional factor, and
 CC screening for the gene whose expression is induced or suppressed. (M1) is
 CC useful for acquiring a pathological condition related gene, preferably
 CC chondrogenic differentiation control related gene Runx2/Cbfa1.
 CC Polynucleotides detailed in the invention are useful for screening a
 CC preventive and/or therapeutic agent of bone and/or articular disease such
 CC as osteoarthritis. This sequence encodes tumor endothelial marker 8
 CC precursor (Temb) associated with isolation of a pathological condition
 CC related gene.
 CC
 SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
 XX
 Query Match 84.4%; Score 1193.8; DB 14; Length 5540;
 Best Local Similarity 99.8%; Pred. No. 2.4e-285;
 Matches 1199; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGAGAGGCGCGGATGCGCGTCCCTGAGGGTCTGCGGAGTTCCGG 60
 DB 41 AGGACCCGCGAGAGAGGCGCGGATGCGCGTCCCTGAGGGTCTGCGGAGTTCCGG 100
 QY 61 AGCGTGGAGAGAGAGCGGACCTCTCTCCCGGGCTCGGGCCATGCGCGAGCGGAGCG 120
 DB 101 AGCGTGGAGAGAGAGCGGACCTCTCTCCCGGGCTCGGGCCATGCGCGAGCGGAGCG 160
 QY 121 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGGTGCATCTCGC 180
 DB 161 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGGTGCATCTCGC 220
 QY 181 CGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGCTACGCGGATTTGAACCTGA 240
 DB 221 CGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGCTACGCGGATTTGAACCTGA 280
 QY 241 CTTCAATTTGGACAATTCAGAGAGTGTCTGCACCACTGGAATTAATCTTTCTTGT 300
 DB 281 CTTCAATTTGGACAATTCAGAGAGTGTCTGCACCACTGGAATTAATCTTTCTTGT 340
 QY 301 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGGAATGTCCTTATTTGTTTCTC 360
 DB 341 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGGAATGTCCTTATTTGTTTCTC 400
 QY 361 CACCCGAGAACCACTTAATGAATGACAGAGAACAGAACAAATCCGCTCAAGGCT 420
 DB 401 CACCCGAGAACCACTTAATGAATGACAGAGAACAGAACAAATCCGCTCAAGGCT 460
 QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGGAAG 480
 DB 461 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGGAAG 520
 QY 481 GGCCAGTGAAGAGATTTATTATGAAGAACAGAGAGGATCAAGACAGCGCATCAT 540
 DB 521 GGCCAGTGAAGAGATTTATTATGAAGAACAGAGAGGATCAAGACAGCGCATCAT 580
 QY 541 TGCTTTGACTGATGAGAACTCATGAAGATCTCTTTTCTATTCAAGAGAGAGCTAA 600
 DB 581 TGCTTTGACTGATGAGAACTCATGAAGATCTCTTTTCTATTCAAGAGAGAGCTAA 640

QY 601 TAGGTCTGAGATCTTGTCATATGTTTACTGTGTGTGTAAGATTCAATGAGAC 660
 DB 641 TAGGTCTGAGATCTTGTCATATGTTTACTGTGTGTGTAAGATTCAATGAGAC 700
 QY 661 ACAAGTGGCCCGGATTCGGAGACATGATGATGTTTCCGATGAATGACGGCTTTCA 720
 DB 701 ACAAGTGGCCCGGATTCGGAGACATGATGATGTTTCCGATGAATGACGGCTTTCA 760
 QY 721 GGCTCTGCAAGGATCATCATCAATTTGGAAGAGTCTCGATGCAATTTCTAGAGC 780
 DB 761 GGCTCTGCAAGGATCATCATCAATTTGGAAGAGTCTCGATGCAATTTCTAGAGC 820
 QY 781 TGAACCATCCACCATATGTCAGAGAGATGATTTCAAGTTGTGTGAGAGAAACGGCTT 840
 DB 821 TGAACCATCCACCATATGTCAGAGAGATGATTTCAAGTTGTGTGAGAGAAACGGCTT 880
 QY 841 CCGACATGCCCGGACGTCGACAGAGGTCCTTCGACGTTCAAGATCAATGATCTGCTAC 900
 DB 881 CCGACATGCCCGGACGTCGACAGAGGTCCTTCGACGTTCAAGATCAATGATCTGCTAC 940
 QY 901 ACTCAATGAGAGAGCCCTTTTCTGTGGAAGACATTAATTTCTGTGTCAGCGCTATCTT 960
 DB 941 ACTCAATGAGAGAGCCCTTTTCTGTGGAAGATTAATTTCTGTGTCAGCGCTATCTT 1000
 QY 961 AAAAGAAAGTGGGATGAAAGCTGCACTCCAGATCAGATGAACGATGGCTCTTTTAT 1020
 DB 1001 AAAAGAAAGTGGGATGAAAGCTGCACTCCAGATCAGATGAACGATGGCTCTTTTAT 1060
 QY 1021 CTCGAGTTCTGTATCATATCACACACACACTGTTCTGACGTTTCATCTGCGCATGCG 1080
 DB 1061 CTCGAGTTCTGTATCATATCACACACACTGTTCTGACGTTTCATCTGCGCATGCG 1120
 QY 1081 CTGCTATATCTGTTCTGCTCTCTTAAGCCCTGCTCTCTCTGTTGTTTGGCCCTCTG 1140
 DB 1121 CTGCTATATCTGTTCTGCTCTCTTAAGCCCTGCTCTCTCTGTTGTTTGGCCCTCTG 1180
 QY 1141 CTGCACTGTATATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1197
 DB 1181 CTGCACTGTATATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1237

RESULT 9
 ID AEA29804
 AEA29804 standard; DNA; 5540 BP.
 XX
 AC AEA29804;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DB DNA encoding a human tumor endothelial marker 8 protein.
 XX
 KW synergistic induction; tumor-associated antigen; vaccine;
 KW tumor endothelial marker 8; immune stimulation; cytostatic; gene; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 144..1838
 FT /*tag= a
 FT /product= "Human tumor endothelial marker 8 protein"
 XX
 PN W02005048943-A2.
 XX
 PD 02-JUN-2005.
 XX
 PF 15-NOV-2004; 2004WO-US038022.
 XX
 PR 13-NOV-2003; 2003US-0519498P.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Gregor P, Houghton A, Concetti A, Venzani FM;
 XX

DR WPI; 2005-395941/40.
DR P-PSDB; AEA29805.
XX
PT New composition useful as a vaccine for inducing anti-tumor immune
PT response and having a vector with a nucleic acid sequence encoding a
PT tumor-associated antigen and/or encoding a tumor endothelial marker 8.
XX
XX
PS Claim 6; SEQ ID NO 4; 54bp; English.
XX
CC The invention relates to novel compositions and methods for the
CC synergistic induction of antitumor immunity. The invention discloses a
CC synergistic effect between vaccines encoding a tumor-associated antigen
CC and vaccines encoding a tumor endothelial marker 8 (TEM8). The invention
CC further includes a method of inducing anti-tumor immune responses in an
CC individual, comprising administering to the individual a composition
CC cited above or dendritic cells comprising a nucleic acid or protein
CC selected from the composition cited above and proteins encoded by the
CC vectors of the composition. The methods and compositions of the present
CC invention are useful in the field of anti-tumor immunity, in particular
CC for inducing an anti-tumor immune response by targeting both tumor-
CC associated antigens and tumor endothelia, hence have cytostatic activity.
CC This polynucleotide sequence represents the DNA encoding a human tumor
CC endothelial marker 8 protein of the invention.
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
XX
Query Match 84.4%; Score 1193.8; DB 14; Length 5540;
Best Local Similarity 99.8%; Pred. No. 2.4e-285;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGACCCCGGAGGAGGCGCGGATGCGCGCTCCCTGAGAGGTCGTGCGAGTTGCGG 60
DB 41 AGGACCCCGGAGGAGGCGCGGATGCGCGCTCCCTGAGAGGTCGTGCGAGTTGCGG 100
QY 61 AGCGTGGGAGGAGCGGACCTCTCTCCCGGGCTCGGGCCATGCGGCGGAGG 120
DB 101 AGCGTGGGAGGAGCGGACCTCTCTCCCGGGCTCGGGCCATGCGGCGGAGG 160
QY 121 GAGAGCCCTCGGATGCGGCTCCAGTGGCTCTTTGGGCACTCTGATGCTGCGG 180
DB 161 GAGAGCCCTCGGATGCGGCTCCAGTGGCTCTTTGGGCACTCTGATGCTGCGG 220
QY 181 CGGGCAAGGGGAGCGAGGAGATGGGGTCCAGGCTGTACGCGGATTTGACCTGTA 240
DB 221 CGGGCAAGGGGAGCGAGGAGATGGGGTCCAGGCTGTACGCGGATTTGACCTGTA 280
QY 241 CTTGATTTTGGACAATTCAGAAAGTGTCTGCACTGCACTGGAATGAATCTATTCTTGT 300
DB 281 CTTGATTTTGGACAATTCAGAAAGTGTCTGCACTGCACTGGAATGAATCTATTCTTGT 340
QY 301 GGAACGTTGGCTCAAAATTCACGCCACGTTGAGAAATCTTTATTTGTTTCTC 360
DB 341 GGAACGTTGGCTCAAAATTCACGCCACGTTGAGAAATCTTTATTTGTTTCTC 400
QY 361 CACCCGAGAACCACTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAGAGCTT 420
DB 401 CACCCGAGAACCACTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAGAGCTT 460
QY 421 AGAAGAACTTCAGAAAGTTCTGCCAGAGAGACACTTACATCATGAAGATTGAAAG 480
DB 461 AGAAGAACTTCAGAAAGTTCTGCCAGAGAGACACTTACATCATGAAGATTGAAAG 520
QY 481 GGCACATGAGCAATTTATATGAAAACAGCAAGGTTACAGACAGCGCATCAT 540
DB 521 GGCACATGAGCAATTTATATGAAAACAGCAAGGTTACAGACAGCGCATCAT 580
QY 541 TGGTTTGAATGATGAGAACTCCATGAAAGATCTTTTCTATTCTAGAGAGGAGCTAA 600
DB 581 TGGTTTGAATGATGAGAACTCCATGAAAGATCTTTTCTATTCTAGAGAGGAGCTAA 640
QY 601 TAGGTCCTGAGATCTTGTGCAATTGTTTACTGTGTGTGTGAAAGATTTCATGAGAC 660
DB 641 TAGGTCCTGAGATCTTGTGCAATTGTTTACTGTGTGTGTGAAAGATTTCATGAGAC 700

QY 661 ACAGCTGCGCCGATTTGCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTTCA 720
DB 701 ACAGCTGCGCCGATTTGCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTTCA 760
QY 721 GCGCTGCAAGGATCATCATCTCAATTTTGAAGAAGTCTGATCTGGAATTTACACAG 780
DB 761 GCGCTGCAAGGATCATCATCTCAATTTTGAAGAAGTCTGATCTGGAATTTACACAG 820
QY 781 TGACCATCCACATATGTCAGAGAGTCAATTTCAAGTTGTCTGAGAGAAAAGGCTT 840
DB 821 TGACCATCCACATATGTCAGAGAGTCAATTTCAAGTTGTCTGAGAGAAAAGGCTT 880
QY 841 CCGACATGCCCGCAACGTGACAGAGGCTCTGACAGCTTCAAGATCATGACTCGGTAC 900
DB 881 CCGACATGCCCGCAACGTGACAGAGGCTCTGACAGCTTCAAGATCATGACTCGGTAC 940
QY 901 ACTCAATGAGAGCCCTTTTCTGTGAGAGACCTTATTACTGTGTCCAGCGCTTACTT 960
DB 941 ACTCAATGAGAGCCCTTTTCTGTGAGAGATCTTATTACTGTGTCCAGCGCTTACTT 1000
QY 961 AAAAGAGTTGAGTAAGAACTGCACTCCAGGTGAGATGAAGATGAGCTCTTTTAT 1020
DB 1001 AAAAGAGTTGAGTAAGAACTGCACTCCAGGTGAGATGAAGATGAGCTCTTTTAT 1060
QY 1021 CTCAGATTCTGATCATCATCACCACACACACTGTTTGAAGGTTCCATCTTGCCATTCG 1080
DB 1061 CTCAGATTCTGATCATCATCACCACACACACTGTTTGAAGGTTCCATCTTGCCATTCG 1120
QY 1081 CTTGCTGATCTCTGTTCTCTGCTCTGAGCCCTGCTCTCTCTGTTGTTTCTGCGCCCTCTG 1140
DB 1121 CTTGCTGATCTCTGTTCTCTGCTCTGAGCCCTGCTCTCTCTGTTGTTTCTGCGCCCTCTG 1180
QY 1141 CTGCACTGATATATCAAGAGAGTCCCTCCACCCCTGCGGAGAGATGAGAAA 1197
DB 1181 CTGCACTGATATATCAAGAGAGTCCCTCCACCCCTGCGGAGAGATGAGAAA 1237

RESULT 10
AAD05303
ID AAD05303 standard; cDNA; 2447 BP.
XX
AC AAD05303;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human secreted protein-encoding gene 4 cDNA clone HMLFR02, SEQ ID NO:14.
XX
XX Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiotensin disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery; cell culture;
KW chemotaxis; food additive; gene therapy; binding partner identification;
KW chromosome 19; 88.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 140..1351
FT /tag= a
FT /product= "Human secreted protein"
FT sig_peptide 140..220
FT /tag= b
FT mat_peptide 221..1348
FT /tag= c
FT /product= "Mature human secreted protein"
XX
PN MO200134626-A1.

XX 17-MAY-2001.
PD 01-NOV-2000; 2000MO-US030045.
PF 05-NOV-1999; 99US-0163581P.
PR 30-JUN-2000; 2000US-0215133P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Ruben SM, Komatsoulis GA, Moore PA, Birse CE, Ni J;
PI WPI; 2001-308778/32.
DR P-PSDB; AAE01439.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 1; Page 425-426; 562pp; English.
XX
XX AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE01436-AAE01513 represent the proteins they encode.
CC AAE01514-AAE01544 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 28 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumors, foetal and developmental abnormalities,
CC hematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein-encoding cDNA of the
CC invention
XX
XX Sequence 2447 BP; 673 A; 562 C; 587 G; 625 T; 0 U; 0 Other;
SQ
Query Match 84.4%; Score 1193.6; DB 4; Length 2447;
Best Local Similarity 99.7%; Pred. No. 1.9e-285;
Matches 1196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AGGACCCGCGAGGAGGCGCGATGCGCGTCCCTGAGAGGCTGTCGCGAGTTCCGG 60
DB 37 AGGACCCGCGAGGAGGCGCGATGCGCGTCCCTGAGAGGCTGTCGCGAGTTCCGG 96
QY 61 AGCGTGGAGAGGAGCGGACCTGCTCTCCCGGCGCTGCGGCGCATGCGCGAGGCG 120
DB 97 AGCGTGGAGAGGAGCGGACCTGCTCTCCCGGCGCTGCGGCGCATGCGCGAGGCG 156
QY 121 GAGAGCCCTGGGCGATCGGCTTCCAGTGCGCTCTTTTGCGCACTGTGTCATCTGCGC 180
DB 157 GAGAGCCCTGGGCGATCGGCTTCCAGTGCGCTCTTTTGCGCACTGTGTCATCTGCGC 216
QY 181 CGGCGAAGGGGAGCGCAGGAGGATGGGGATCCAGCCTGCTTACGCGGATTTGACTGTA 240
DB 217 CGGCGAAGGGGAGCGCAGGAGGATGGGGATCCAGCCTGCTTACGCGGATTTGACTGTA 276

QY 241 CTTCATTTTGGACCAATCAGGAAGTGCTGCGACCACTGGAATGAATCTATTCTTGT 300
DB 277 CTTCATTTTGGACCAATCAGGAAGTGCTGCGACCACTGGAATGAATCTATTCTTGT 336
QY 301 GGAAAGTTGGCTCACAATTTTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 360
DB 337 GGAAAGTTGGCTCACAATTTTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 396
QY 361 CACCGGAGAAACAACCTTAATGAACTGACAGAAAGCAGAGAACAAATCGTCAAGCCT 420
DB 397 CACCGGAGAAACAACCTTAATGAACTGACAGAAAGCAGAGAACAAATCGTCAAGCCT 456
QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATGATGAAGATTGAAAG 480
DB 457 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATGATGAAGATTGAAAG 516
QY 481 GGCAGTAGAGCAGATTATTTATGAAACAGACAGAGGTACAGACAGCCAGCTCATAT 540
DB 517 GGCAGTAGAGCAGATTATTTATGAAACAGACAGAGGTACAGACAGCCAGCTCATAT 576
QY 541 TGCTTTGACTGATGAGAACTCCATGAGATCTTTTCTATTCAGAGGGAGGCTAA 600
DB 577 TGCTTTGACTGATGAGAACTCCATGAGATCTTTTCTATTCAGAGGGAGGCTAA 636
QY 601 TAGGTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTAAGATTTCATAGAGAC 660
DB 637 TAGGTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTAAGATTTCATAGAGAC 696
QY 661 ACAGCTGCGCCGGATTCGCGACAGTAAGATCATGTTTCCGTGAATGACGCTTTCA 720
DB 697 ACAGCTGCGCCGGATTCGCGACAGTAAGATCATGTTTCCGTGAATGACGCTTTCA 756
QY 721 GGTCTGCAAGGATCATCATCTCAATTTTGAAGAGTCTGATGAAATCTATACAGC 780
DB 757 GGTCTGCAAGGATCATCATCTCAATTTTGAAGAGTCTGATGAAATCTATACAGC 816
QY 781 TGAACCATCAACCATATGTCAGAGAGTCAATTTCAAGTTGTCGTAGAGAAACGACTT 840
DB 817 TGAACCATCAACCATATGTCAGAGAGTCAATTTCAAGTTGTCGTAGAGAAACGACTT 876
QY 841 CGGACATGCCCGGACAGTGGACAGGCTCTCTGACGCTTCATGATCAATGCTGGTCA 900
DB 877 CGGACATGCCCGGACAGTGGACAGGCTCTCTGACGCTTCATGATCAATGCTGGTCA 936
QY 901 ACTCAATGAGAAACCTTTTCTGTGGAAGACACTTTATCTGTCCAGCGCTATCTT 960
DB 937 ACTCAATGAGAAACCTTTTCTGTGGAAGACTTTATCTGTGTCCAGCGCTATCTT 996
QY 961 AAAAGAAATTGGATGAAGAGCTGCACTCCAGTCAAGATGAAGATGAGCTCTTTTAT 1020
DB 997 AAAAGAAATTGGATGAAGAGCTGCACTCCAGTCAAGATGAAGATGAGCTCTTTTAT 1056
QY 1021 CTCAGTTCTGTATCATATCAACACACACTGTTTGAAGGTTCCATCTCTGCGCATGCG 1080
DB 1057 CTCAGTTCTGTATCATATCAACACACACTGTTTGAAGGTTCCATCTCTGCGCATGCG 1116
QY 1081 CTGCTGATCTGTTCTGCTCTCTTACGCTGCTCTCTCTGTTGTTCTGCGCCCTCTG 1140
DB 1117 CTGCTGATCTGTTCTGCTCTCTTACGCTGCTCTCTCTGTTGTTCTGCGCCCTCTG 1176
QY 1141 CTGCACTGATATATCAAGAGGTCCTCCACCCCTGCGAGAGAGTGAAGAAATAA 1200
DB 1177 CTGCACTGATATATCAAGAGGTCCTCCACCCCTGCGAGAGAGTGAAGTAAGTGA 1236
RESULT 11
AAD05334
ID AAD05334 standard; cDNA; 2086 BP.
XX
XX AAD05334;
XX
DT 17-JUL-2001 (first entry)
XX

| | |
|----|--|
| DE | Human secreted protein-encoding gene 4 cDNA clone HMLFR02, SEQ ID NO:45. |
| XX | |
| KW | Human; secreted protein; proliferative disorder; cancer; tumour; |
| KW | foetal abnormality; developmental abnormality; haematopoietic disorder; |
| KW | immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; |
| KW | inflammation; allergy; neurological disorder; Alzheimer's disease; |
| KW | Parkinson's disease; cognitive disorder; schizophrenia; acutia; |
| KW | skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; |
| KW | cardiovascular disorder; angiogenic disorder; kidney disorder; |
| KW | gastrointestinal disorder; pregnancy-related disorder; |
| KW | endocrine disorder; infection; wound healing; vulnerability; cell culture; |
| KW | chemotaxis; food additive; gene therapy; binding partner identification; |
| KW | chromosome 19; se. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PH | Key |
| FT | location/Qualifiers |
| FT | 166..1377 |
| FT | CDS |
| FT | /*tag= a |
| FT | /product= "Human secreted protein" |
| FT | /transl_except= (pos:68..690, aa:Xaa) |
| FT | /transl_except= (pos:1123..1125, aa:Xaa) |
| FT | /transl_except= (pos:1156..1158, aa:Xaa) |
| FT | /transl_except= (pos:1267..1269, aa:Xaa) |
| FT | /note= "Xaa equals any of the twenty naturally occurring L |
| FT | -amino acids" |
| FT | 166..246 |
| FT | /*tag= b |
| FT | 247..1374 |
| FT | /*tag= c |
| FT | /product= "Mature human secreted protein" |
| XX | |
| PN | WO200134626-A1. |
| XX | |
| PD | 17-MAY-2001. |
| XX | |
| PF | 01-NOV-2000; 2000MO-US030045. |
| XX | |
| PR | 05-NOV-1999; 99US-0163581P. |
| PR | 30-JUN-2000; 2000US-0215133P. |
| XX | |
| PA | (HUMA-) HUMAN GENOME SCI INC. |
| XX | |
| PI | Ruben SM, Komatsoulis GA, Moore PA, Birse CE, Ni J; |
| XX | |
| DR | WPI; 2001-308778/32. |
| XX | |
| DR | P-PEDB; AAE01469. |
| XX | |
| PT | New nucleic acid molecules encoding 28 human secreted proteins for |
| PT | diagnosing, preventing, treating or ameliorating medical conditions and |
| PT | used as food additives or preservatives. |
| XX | |
| PS | Claim 1; Page 449; 562pp; English. |
| XX | |
| CC | AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted |
| CC | protein genes, and AAE01436-AAE01513 represent the proteins they encode. |
| CC | AAE01514-AAE01544 represent human secreted protein fragments or variants. |
| CC | The genes and their secreted proteins are useful for preventing, treating |
| CC | or ameliorating medical conditions, e.g., by protein or gene therapy. |
| CC | Pathological conditions can be diagnosed by determining the amount of the |
| CC | new protein in a sample or by determining the presence of mutations in |
| CC | the new genes. Specific uses are described for each of the 28 genes, |
| CC | based on the tissues in which they are most highly expressed, and include |
| CC | developing products for the diagnosis or treatment of proliferative |
| CC | disorders, cancer, tumours, foetal and developmental abnormalities, |
| CC | haematopoietic disorders, diseases of the immune system, AIDS, autoimmune |
| CC | diseases (e.g., rheumatoid arthritis), inflammation, allergies, |
| CC | neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), |
| CC | cognitive disorders, schizophrenia, asthma, skin disorders (e.g., |
| CC | psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, |
| CC | angiogenic disorders, kidney disorders, gastrointestinal disorders, |
| CC | pregnancy-related disorders, endocrine disorders, and infections. The |
| CC | proteins can also be used to aid wound healing and epithelial cell |

CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or a
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein-encoding cDNA of the
CC invention
XX
SQ Sequence 2086 BP, 544 A, 491 C, 538 G, 501 T, 0 U; 12 Other;

| | Query Match | 84.3% | Score 1192.4; | DB 4; | Length 2086; |
|--|----------------------------|-------|---------------------|-----------|--------------|
| | Best Local Similarity | 99.4% | Pred. No. 3.5e-285; | | |
| | Matches 1193; Conservative | 3; | Mismatches 4; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|--|-----|
| OY | 1 | GGAGACCCGCGAGAAAGGGCCCGCGGATAGGGGGGATCCCTGAGAGGATGTGTGGCGATTCCGGCG | 60 |
| Db | 63 | AGGACCCGCGAGAAAGGGCCCGCGGATAGGGGGGATCCCTGAGAGGATGTGTGGCGATTCCGGCG | 122 |
| OY | 61 | AGCGTGGGAAAGAGACCGGACCCCTGCCTCTCCCGGGCTGCGGGCCATGAGCCACCGCGAGAGCG | 120 |
| Db | 123 | AGCGTGGGAAAGAGACCGGACCCCTGCCTCTCCCGGGCTGCGGGCCATGAGCCACCGCGAGAGCG | 182 |
| OY | 121 | GAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGTGTCTCATCTTGGC | 180 |
| Db | 183 | GAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGTGTCTCATCTTGGC | 242 |
| OY | 181 | CGGGCAAGGGGGAGCGACGAGAGAGATGAGGGGGTCCAGCCTGTGATCGGCGGATTTGACCTGTG | 240 |
| Db | 243 | CGGGCAAGGGGGAGCGACGAGAGAGATGAGGGGGTCCAGCCTGTGATCGGCGGATTTGACCTGTG | 302 |
| OY | 241 | CTTCATTTTGGACAAATCAGGAAGTGTGCTGSCACCACTGGATGGAATCTATTACTTTGT | 300 |
| Db | 303 | CTTCATTTTGGACAAATCAGGAAGTGTGCTGSCACCACTGGATGGAATCTATTACTTTGT | 362 |
| OY | 301 | GGAAACGTTGGCTCACAAATTCAATCAGCCCAAGTTGAGAAATGTCCTTATTTGTTTCTC | 360 |
| Db | 363 | GGAAACGTTGGCTCACAAATTCAATCAGCCCAAGTTGAGAAATGTCCTTATTTGTTTCTC | 422 |
| OY | 361 | CACCCGAGGAAACAACTTAAATGAAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCT | 420 |
| Db | 423 | CACCCGAGGAAACAACTTAAATGAAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCT | 482 |
| OY | 421 | AGAAAGACTCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGATGAAGATTGGAAG | 480 |
| Db | 483 | AGAAAGACTCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGATGAAGATTGGAAG | 542 |
| OY | 481 | GGCCAGTGAAGAAATTTATTTGAAGAAACAGCAAGGGTACAGGACAGCGAGGTATCAT | 540 |
| Db | 543 | GGCCAGTGAAGAAATTTATTTGAAGAAACAGCAAGGGTACAGGACAGCGAGGTATCAT | 602 |
| OY | 541 | TGCTTTGACTATGAGAGAACTCCATGGAAGATCTCTTTTCTAATTCAGAGAGGAGGACTTA | 600 |
| Db | 603 | TGCTTTGACTATGAGAGAACTCCATGGAAGATCTCTTTTCTAATTCAGAGAGGAGGACTTA | 662 |
| OY | 601 | TAGGCTTCGAGATCTTGGTGCAATTTGTTTACTGTGTGGTGTGAAGATTTCAATGAGAC | 660 |
| Db | 663 | TAGGCTTCGAGATCTTGGTGCAATTTGTTTACTGTGTGGTGTGAAGATTTCAATGAGAC | 722 |
| OY | 661 | ACAGGTGGCCCCGGAAATGGGGAACAGTAAGATCATGTGTTCCCGGAATGACGCGCTTCA | 720 |
| Db | 723 | ACAGGTGGCCCCGGAAATGGGGAACAGTAAGATCATGTGTTCCCGGAATGACGCGCTTCA | 782 |
| OY | 721 | GGCTCTGCAAGGACATCATCTCACTCAATTTTGAAGAAAGTCTGCACTGAAATTTCTAGACAC | 780 |
| Db | 783 | GGCTCTGCAAGGACATCATCTCACTCAATTTTGAAGAAAGTCTGCACTGAAATTTCTAGACAC | 842 |
| OY | 781 | TGAACCATCCACCATATGTGACGAGAGTCAATTTCAAGTTGTCGTGAGAGGAAACGGCTT | 840 |
| Db | 843 | TGAACCATCCACCATATGTGACGAGAGTCAATTTCAAGTTGTCGTGAGAGGAAACGGCTT | 902 |

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QY 841 CCGACATGCCGCGACAGTGGACAGGCTCTGTGAGCTTCAAGATCAATGACTGGGAC 900
DB 903 CCGACATGCCGCGACAGTGGACAGGCTCTGTGAGCTTCAAGATCAATGACTGGGAC 962
QY 901 ACTCAATGAGAGCCCTTTCTGTGAGAGACACTTATTTACTGTCTCAGCGCTATCTT 960
DB 963 ACTCAATGAGAGCCCTTTCTGTGAGAGATCTTATTTACTGTCTCAGCGCTATCTT 1022
QY 961 AAAAGAAAGTTGGATGAGAGCTGCACTCCAGGTGAGATGAGATGAGCTCTTTTAT 1020
DB 1023 AAAAGAAAGTTGGATGAGAGCTGCACTCCAGGTGAGATGAGATGAGCTCTTTTAT 1082
QY 1021 CTCAGATTCTGTATCATACACACACACACACTGTTCAGAGGTTTCACTCTGGCAATCGC 1080
DB 1083 CTCAGATTCTGTATCATACACACACACACTGTTCAGAGGTTTCACTCTGGCAATCGC 1142
QY 1081 CCTGCTGATCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1143 CTTGCTGATCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
QY 1141 CTGCACTGTGATTTATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAATA 1200
DB 1203 CTCACATGTGATTTATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGTGA 1262

RESULT 12
ABV73883
ID ABV73883 standard; cDNA; 2112 BP.
AC ABV73883;
XX
XX 08-JAN-2003 (first entry)
XX
XX Human anthrax toxin receptor cDNA.
XX
XX Anthrax; toxin; receptor; human; antibacterial; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 113..1114
XX CDS /*tag= a
XX FT /*tag= b
XX FT 113..193
XX FT /*tag= b
XX FT 194..1111
XX FT /*tag= c
XX FT mac_peptide
XX
XX PN M0200246228-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 03-OCT-2001; 2001WO-US030941.
XX
XX PR 05-DEC-2000; 2000US-0251481P.
XX
XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX PI Young JAT, Bradley KA, Collier RJ, Mogridge JS;
XX
XX DR WPI; 2002-713235/77.
XX
XX DR P-PSDB; ABP54905.
XX
XX PT Novel isolated polypeptide useful for identifying agent that prevents or
XX PT reduces effect of anthrax toxin on host cell, for treating human or non-
XX PT human animal suffering from anthrax.
XX
XX PS Disclosure; Page 39-41; 45pp; English.
XX
XX CC The present sequence is that of cDNA encoding a human anthrax toxin
XX CC receptor (ATR). The cDNA, previously designated IMAGE CLONE 4563020,
XX CC encodes a polypeptide that is identical to amino acids 1-317 of a newly
XX CC identified ATR (see ABP54904), differing thereafter at the C-terminus. No
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CC function was previously known for this polypeptide, nor was there any
CC prior indication that it is a complete or partial ATR. The invention
CC provides ATR polypeptides and polynucleotides, host cells, vectors, and
CC transgenic and knock-out animals. It also provides methods for
CC identifying molecules that bind the ATR and which reduce the toxicity of
CC anthrax toxin. A claimed method for treating anthrax in a human or animal
CC involves administering an agent that inhibits binding between anthrax
CC toxin protective antigen (PA) and ATR at a level effective to reduce the
CC severity of anthrax. Suitable agents include the 4563020 polypeptide or a
CC PA-binding fragment of it, a PA-binding polypeptide at least 80%
CC identical to these, a fusion protein, a monoclonal or polyclonal
CC antibody, a polysaccharide, a lipid or a nucleic acid. ATR
CC polynucleotides can also be used in the recombinant production of ATR
CC polypeptides, and as molecular probes

SQ Sequence 2112 BP; 573 A; 522 C; 515 G; 502 T; 0 U; 0 Other;

Query Match 74.4%; Score 1052.4; DB 6; Length 2112;
Best Local Similarity 99.9%; Pred. No. 1.9e-250;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGAGAGGCGCCCGGATGCGGCTCCCTGAGGGTCTGGCGAGTTGGCG 60
DB 10 AGGACCCGCGAGAGAGGCGCCCGGATGCGGCTCCCTGAGGGTCTGGCGAGTTGGCG 69
QY 61 AGCGTGGAGAGAGGCGGACCTGCTCCCGGGGCTGGGGGCGATGGCCACGCGGAGCG 120
DB 70 AGCGTGGAGAGAGGCGGACCTGCTCCCGGGGCTGGGGGCGATGGCCACGCGGAGCG 129
QY 121 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTGGCCACTGTGGTCTCATCTGCGC 180
DB 130 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTGGCCACTGTGGTCTCATCTGCGC 189
QY 181 CCGGCAAGGGGAGCGAGAGAGATGGGGTCCAGCTCTGACGGCGGATTGACTGTGA 240
DB 190 CCGGCAAGGGGAGCGAGAGAGATGGGGTCCAGCTCTGACGGCGGATTGACTGTGA 249
QY 241 CTTGATTTTGGACAATTCAGGAAGTGTGCTGACCACTGGAATGAAATCTTACTTTG 300
DB 250 CTTGATTTTGGACAATTCAGGAAGTGTGCTGACCACTGGAATGAAATCTTACTTTG 309
QY 301 GGAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATGCTTATGTTTCTC 360
DB 310 GGAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATGCTTATGTTTCTC 369
QY 361 CACCCGAGAAACAACCTTAATGAACCTGACAGAAACAGAAACAATCCGTGAAGCCT 420
DB 370 CACCCGAGAAACAACCTTAATGAACCTGACAGAAACAAGAAACAATCCGTGAAGCCT 429
QY 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATGATGAAGATTGAAAG 480
DB 430 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATGATGAAGATTGAAAG 489
QY 481 GGCAGTGAAGCAGATTTATGAAACAGACAAGGTTACAGAGACCCAGCTCATCAT 540
DB 490 GGCAGTGAAGCAGATTTATGAAACAGACAAGGTTACAGAGACCCAGCTCATCAT 549
QY 541 TGCCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTATTCAGAGAGGAGCTTA 600
DB 550 TGCCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTATTCAGAGAGGAGCTTA 609
QY 601 TAGGTCTCAGAGATCTTGTGCAATTTTAACTGTGTGAGTGAAGATTGCAATGAGAC 660
DB 610 TAGGTCTCAGAGATCTTGTGCAATTTTAACTGTGTGAGTGAAGATTGCAATGAGAC 669
QY 661 ACAGCTGGCCCGGATGGGACAGTAAGATCATGTGTTCCCGTGAATGACCGCTTTTCA 720
DB 670 ACAGCTGGCCCGGATGGGACAGTAAGATCATGTGTTCCCGTGAATGACCGCTTTCA 729
QY 721 GGCCTTGCAAGGATCATTCATCAATTTTGAAGAGTCTGATGGAATTTAGACGC 780
DB 730 GGCCTTGCAAGGATCATTCATCAATTTTGAAGAGTCTGATGGAATTTAGACGC 789
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QY 781 TGAACCATCCACCATATGTGTCAGAGAGTCAATTCAAGTTGTCGTGAGAGAAACGGCTT 840
DB 790 TGAACCATCCACCATATGTGTCAGAGAGTCAATTCAAGTTGTCGTGAGAGAAACGGCTT 849
QY 841 CCGACATGCCCCGCAAGCTGAGACAGGGTCTCTTCAGCTTCAAGATTAATGATCTGGTCA 900
DB 850 CCGACATGCCCCGCAAGCTGAGACAGGGTCTCTTCAGCTTCAAGATTAATGATCTGGTCA 909
QY 901 ACTCAATGAGAAAGCCCTTTTCTGTGAGAAACACTTATTACTGTGTCCAGCGCTATCTT 960
DB 910 ACTCAATGAGAAAGCCCTTTTCTGTGAGAAACTTATTACTGTGTCCAGCGCTATCTT 969
QY 961 AAAAGAGTTGGCATGAGAAAGCTGCACTCCAGTCCAGCATGAGAAAGATGCGCTCTTTTAT 1020
DB 970 AAAAGAGTTGGCATGAGAAAGCTGCACTCCAGTCCAGCATGAGAAAGATGCGCTCTTTTAT 1029
QY 1021 CTCGAGTTCTGTCATCATCAACCAACCACTGT 1054
DB 1030 CTCGAGTTCTGTCATCATCAACCAACCACTGT 1063

RESULT 13
AAA47455
ID AAA47455 standard; cDNA, 2272 BP.
XX
AC AAA47455;
XX
DT 20-OCT-2000 (first entry)
XX
DE Human TANGO 197 coding sequence.
XX
KW TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
KW graft versus-host disease; rheumatoid arthritis; psoriasis;
KW inflammatory bowel disease; septic shock; ulcerative colitis;
KW Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
KW Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia;
KW autoimmune disease; myasthenia gravis; autoimmune diabetes;
KW systemic lupus erythematosus; transgenic animal; diagnosis; prognosis;
KW prophylactic; therapeutic; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 213..1214
FT /*tag= a
FT /product= "TANGO 197"
XX
PN WO200039284-A1.
XX
PD 06-JUL-2000.
XX
PF 23-DEC-1999; 99WO-US031025.
XX
PR 30-DEC-1998; 98US-00223546.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Holzman DA;
XX
PI WPI; 2000-465743/40.
XX
DR P-PSDB; AAB01422.
XX
PT Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224
PT and 239 polypeptides useful for the treatment of asthma, rheumatoid
PT arthritis, psoriasis and autoimmune diseases.
XX
PS Claim 1; Fig 4; 209pp; English.
XX
CC Nucleic acids encoding TANGO polypeptides are useful as modulating agents
CC for regulating cellular processes like asthma, graft versus-host
CC diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease,
CC septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous
CC leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
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CC Lyme's disease, cachexia and autoimmune diseases e.g. myasthenia gravis,
CC autoimmune diabetes and systemic lupus erythematosus. The nucleic acids
CC are also useful for producing transgenic animals and the TANGO
CC polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239
CC sequences are useful in forensic biology, for diagnostic assays.
CC prognostic assays, pharmacogenomics and for monitoring clinical trials.
CC TANGO polypeptides are suitable for both prophylactic and therapeutic
CC methods for treating a subject at risk of a disorder or having a disorder
CC associated with aberrant TANGO expression. A wide range of cellular
CC disorders can be treated
XX
SQ Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 U; 0 Other;
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Query Match 74.4%; Score 1052.4; DB 3; Length 2272;
Best Local Similarity 99.9%; Pred. No. 2e-250;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 AGAAGCCCGAGAGAAAGGCGCCGCGATGCGCGCTCCCTGAGGGTGTGGCGAGTTCCGG 60
DB 110 AGAAGCCCGAGAGAAAGGCGCCGCGATGCGCGCTCCCTGAGGGTGTGGCGAGTTCCGG 169
QY 61 AGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 170 AGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 229
QY 121 GAGAGCCCTCGGCACTCGGCTTCCAGTGGCTCTCTTTGGCACTGTGCTCATCTGCGC 180
DB 230 GAGAGCCCTCGGCACTCGGCTTCCAGTGGCTCTCTTTGGCACTGTGCTCATCTGCGC 289
QY 181 CGGGCAAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 290 CGGGCAAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 349
QY 241 CTTCATTTTGGCAAAATCAGAAAGTGTGCTGACACACTGGAATGAATCTATTACTTGT 300
DB 350 CTTCATTTTGGCAAAATCAGAAAGTGTGCTGACACACTGGAATGAATCTATTACTTGT 409
QY 301 GGAAAGTTGGCTCAAAATTCATCAGGCCACAGTTGGAATGTCCTTATTTGTTTCTC 360
DB 410 GGAAAGTTGGCTCAAAATTCATCAGGCCACAGTTGGAATGTCCTTATTTGTTTCTC 469
QY 361 CACCCGAGAGAACACTTATGAAACTGACAGAAACAGAAACAAATCCGTCAAGGCTT 420
DB 470 CACCCGAGAGAACACTTATGAAACTGACAGAAACAGAAACAAATCCGTCAAGGCTT 529
QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTACATGATGAAGATTGAAG 480
DB 530 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTACATGATGAAGATTGAAG 589
QY 481 GGCCAGTGAAGAGATTTTATGAAAGAGCAAGAGGATACAGAGACAGCCAGGTCATCAT 540
DB 590 GGCCAGTGAAGAGATTTTATGAAAGAGCAAGAGGATACAGAGACAGCCAGGTCATCAT 649
QY 541 TGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTTCAGAGAGGAGGCTTA 600
DB 650 TGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTTCAGAGAGGAGGCTTA 709
QY 601 TAGATCTGAGATCTTGTGCAATGTTACTGTGTGTGGAAGATTTCAATGAGAC 660
DB 710 TAGATCTGAGATCTTGTGCAATGTTACTGTGTGTGGAAGATTTCAATGAGAC 769
QY 661 ACAGCTGGCCCGAGATTTGGGACAGTAAAGATCATGTTTCCCGTAATGACGAGCTTTCA 720
DB 770 ACAGCTGGCCCGAGATTTGGGACAGTAAAGATCATGTTTCCCGTAATGACGAGCTTTCA 829
QY 721 GGCTCTGCAAGGCACTCATCTCAATTTTGAAGAGTCTGATCAGAAATCTTGACAGC 780
DB 830 GGCTCTGCAAGGCACTCATCTCAATTTTGAAGAGTCTGATCAGAAATCTTGACAGC 889
QY 781 TGAACCATCCACCATATGTGTCAGAGAGTCAATTCAAGTTGTCGTGAGAGAAACGGCTT 840
DB 890 TGAACCATCCACCATATGTGTCAGAGAGTCAATTCAAGTTGTCGTGAGAGAAACGGCTT 949
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| | | | | |
|--|--|---|---|------|
| Oy | | 841 | CCGACATCCTCCCGCAACGTGGAGCAGGGTCTCTGCAGCTTTCAAATCATATGACTGGTCAC | 900 |
| Dd | | 950 | CCGACATCCTCCCGCAACGTGGAGCAGGGTCTCTGCAGCTTTCAAATCATATGACTGGTCAC | 1009 |
| Oy | | 901 | ACTCAATGAGAAGCCCTTTTTCTGTGGAAAGACATTATTACTGTGCAGGCCATCTT | 960 |
| Dd | | 1010 | ACTCAATGAGAAGCCCTTTTTCTGTGGAAAGATATTATTATTACTGTGTCCAAGGCCATTCTT | 1069 |
| Oy | | 961 | AAAAGAGTTGGCATGAAGCTGCATCTCAGGTGAGCATGAAGATGGCCCTCTCTTTTAT | 1020 |
| Dd | | 1070 | AAAAGAGTTGGCATGAAGCTGCATCTCAGGTGAGCATGAAGATGGCCCTCTCTTTAT | 1129 |
| Oy | | 1021 | CTCCAGTTCTGTGCATCATCACACACACACTGT | 1054 |
| Dd | | 1130 | CTCCAGTTCTGTGCATCATCACACACACACTGT | 1163 |
| RESULT 14 ADI00533 ID ADI00533 standard; cDNA, 2272 BP. | | | | |
| XX | | AD100533; | | |
| XX | | AD100533; | | |
| XX | | 22-APR-2004 (first entry) | | |
| DE | | Human TANGO 197 cDNA. | | |
| DE | | fusion; von Willebrand factor A-like domain; vWF; antibacterial; | | |
| KW | | cutaneous; inhalation anthrax; human; TANGO 197; ss; gene. | | |
| XX | | Homo sapiens. | | |
| OS | | US2003144193-A1. | | |
| XX | | 31-JUL-2003. | | |
| PD | | 24-JUL-2002; 2002US-00201292. | | |
| PF | | 20-DEC-2001; 2001US-00038307. | | |
| PR | | (ROTT/) ROTTMAN J B. | | |
| XX | | (OKEE/) O'KEEFE T L. | | |
| PA | | (OZKA/) OZKAYNAK E. | | |
| PA | | (HEAL/) HEALEY J J. | | |
| PI | | Rottman JB, O'keefe TL, Ozkaynak E, Healey JJ; | | |
| XX | | WPI: 2003-720708/68. | | |
| DR | | P-PSDB; AD100534. | | |
| PT | | New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or | | |
| PT | | ameliorating symptoms of anthrax comprises a von Willebrand factor A-like | | |
| PT | | domain (vWF) amino acid sequence and an amino acid sequence heterologous | | |
| PT | | to the vWF. | | |
| PS | | Example: SEQ ID NO 1; 86pp; English. | | |
| XX | | The invention relates to a novel fusion polypeptide comprising a von | | |
| CC | | Willebrand factor A-like domain (vWF) amino acid sequence and an amino | | |
| CC | | acid sequence heterologous to the vWF. The polypeptide of the invention | | |
| CC | | demonstrates antibacterial activities whilst the composition and method | | |
| CC | | may be useful in preventing or ameliorating the symptoms of cutaneous | | |
| CC | | and/or inhalation anthrax. The current sequence is that of the human | | |
| CC | | TANGO 197 cDNA of the invention. | | |
| SQ | | Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 U; 0 Other; | | |
| Query Match 74.4%; Score 1052.4; DB 10; Length 2272; Best Local Similarity 99.9%; Pred. No. 2e-250; Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | | | |
| Oy | | 1 AGAGCCCCGAGAGAGGCCCGCGGATGGCGGCTCTTGAGGGTGTGAGGTTGCGGG | 60 | |

| | | | |
|----|------|---|------|
| Db | 110 | AGGACCCGCGAGAAAGGAGCCCGCGAGATGGAGCGTCCCTGAGAGGAGTCGTGGCAGATTCCGCG | 160 |
| QY | 61 | AGCGTGGAGAGAGCGGACCTCTGCTCTCCCGGGCTGCGGACATGGCCACGCGGGAGCG | 120 |
| Db | 170 | AGCGTGGAGAGAGAGCGGACCTCTGCTCTCCCGGGCTGCGGACATGGCCACGCGGGAGCG | 229 |
| QY | 121 | GAGAGCCCTGGGACATCGGCTTCGATGGAGCTCTCTTTGAGCACTGTGGTGCTCATCTGAGC | 180 |
| Db | 230 | GAGAGCCCTGGGACATCGGCTTCGATGGAGCTCTCTTTGAGCACTGTGGTGCTCATCTGAGC | 289 |
| QY | 181 | CGGGCAAGGGGGAGCGAGGAGAGATGGGGGGTCCAGCTGTGCTACGGCGGATTTGA | 240 |
| Db | 290 | CGGGCAAGGGGGAGCGAGGAGAGATGGGGGGTCCAGCTGTGCTACGGCGGATTTGA | 349 |
| QY | 241 | CTTCATTTTGGACAATTCAGAGAGTGTGTGCACTCATGATGAAATCTATTA | 300 |
| Db | 350 | CTTCATTTTGGACAATTCAGAGAGTGTGTGCACTCATGATGAAATCTATTA | 409 |
| QY | 301 | GGAACTGTGGCTCAAAATTCATCAGCCCACTGTGAGAAATGTCCTTTATTTGTTCTC | 360 |
| Db | 410 | GGAACTGTGGCTCAAAATTCATCAGCCCACTGTGAGAAATGTCCTTTATTTGTTCTC | 469 |
| QY | 361 | CACCCGAGGAACAACCTTAATGAATAGTACAGAGACAGAGAACAAATCCGTCAAGGCT | 420 |
| Db | 470 | CACCCGAGGAACAACCTTAATGAATAGTACAGAGACAGAGAACAAATCCGTCAAGGCT | 529 |
| QY | 421 | AGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGAAAGATTTGAAAG | 480 |
| Db | 530 | AGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGAAAGATTTGAAAG | 589 |
| QY | 481 | GGCCAGTGAAGCATTTATTTGAAAACAGACAAAGGATACAGACATCCAGCGTCATCAT | 540 |
| Db | 590 | GGCCAGTGAAGCATTTATTTGAAAACAGACAAAGGATACAGACATCCAGCGTCATCAT | 649 |
| QY | 541 | TGCTTTGATCTATGGAGAACTCCATGGAAGATCTCTTTTCAATTCAGAGAGGAGGCTAA | 600 |
| Db | 650 | TGCTTTGATCTATGGAGAACTCCATGGAAGATCTCTTTTCAATTCAGAGAGGAGGCTAA | 709 |
| QY | 601 | TAGGTCTCGAATCTTGTGTGCAATTTGTTTACTGTGTGTGTAAGAATTTCAATGAGAC | 660 |
| Db | 710 | TAGGTCTCGAATCTTGTGTGCAATTTGTTTACTGTGTGTGTAAGAATTTCAATGAGAC | 769 |
| QY | 661 | ACAGCTGGCCCGGATTTGGGACATGTAAGATCATGTGTTCCTGGTGAATGACGGCTTTCA | 720 |
| Db | 770 | ACAGCTGGCCCGGATTTGGGACATGTAAGATCATGTGTTCCTGGTGAATGACGGCTTTCA | 829 |
| QY | 721 | GGCTCTGGAAGGACATCCACTCAATTTTGAAGAAGCTCGATCGAAATTTCTAGACGC | 780 |
| Db | 830 | GGCTCTGGAAGGACATCCACTCAATTTTGAAGAAGCTCGATCGAAATTTCTAGACGC | 889 |
| QY | 781 | TGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGGAAACGGCTT | 840 |
| Db | 890 | TGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGGAAACGGCTT | 949 |
| QY | 841 | CCGACATGCCCGCAACGTGGAACAGGGTCTCTGCAAGCTTCAAGATCAATGACTGGTAC | 900 |
| Db | 950 | CCGACATGCCCGCAACGTGGAACAGGGTCTCTGCAAGCTTCAAGATCAATGACTGGTAC | 1009 |
| QY | 901 | ACTCAATGAGAAGCCCTTTTCTGTGGAAGACATTAATTTACTGTGTCCAGGCGCTATCTT | 960 |
| Db | 1010 | ACTCAATGAGAAGCCCTTTTCTGTGGAAGATTAATTTACTGTGTCCAGGCGCTATCTT | 1069 |
| QY | 961 | AAAAGAATTTGGCATGAAGAGTGCACCTCAGAGTACAGATGAACAGATGGCTCTCTTTTAT | 1020 |
| Db | 1070 | AAAAGAATTTGGCATGAAGAGTGCACCTCAGAGTACAGATGAACAGATGGCTCTCTTTTAT | 1129 |
| QY | 1021 | CTCCAGTTCTGTCAATCATCACACCAACACTGT | 1054 |
| Db | 1130 | CTCCAGTTCTGTCAATCATCACACCAACACTGT | 1163 |

ID ADM64567 standard; cDNA; 2272 BP.
 XX
 AC ADM64567;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human von Willebrand factor A-like domain protein TANGO197 cDNA.
 XX
 KW antibacterial; gene therapy;
 KM von Willebrand factor A-like domain amino acid sequence;
 KM vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
 KM inhalation anthrax; human; TANGO197; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003134786-A1.
 XX
 PD 17-JUL-2003.
 XX
 PF 20-DEC-2001; 2001US-00038307.
 XX
 PR 20-DEC-2001; 2001US-00038307.
 XX
 PA (ROTT/) ROTTMAN J B.
 PA (OKEE/) O'KEEFE T L.
 PA (OZKA/) OZKAYNAK E.
 PA (HEAL/) HEALEY J J.
 XX
 PI Rotman JB, O'keefe TL, Ozkaynak E, Healey JJ;
 XX
 DR WPI; 2003-829643/77.
 DR P-PSDB; ADM64568.
 XX
 PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
 PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
 PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
 PT to the vWF.
 XX
 PS Disclosure; SEQ ID NO 1; 64pp; English.
 XX
 CC The invention describes a fusion polypeptide comprising a von Willebrand
 CC factor A-like domain (vWF) amino acid sequence and an amino acid sequence
 CC heterologous to the vWF. Also described are: a method of preventing or
 CC ameliorating a symptom of anthrax in a subject thought to be at risk for
 CC exposure to or suspected of having been exposed to Bacillus anthracis;
 CC and a pharmaceutical composition comprising the novel fusion polypeptide.
 CC The composition and method are useful in preventing or ameliorating
 CC symptoms of cutaneous and/or inhalation anthrax. This sequence encodes
 CC human von Willebrand factor A-like domain (vWF) amino acid sequence
 CC TANGO197.
 XX
 SQ Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 U; 0 Other:
 Query Match 74.4%; Score 1052.4; DB 11; Length 2272;
 Best Local Similarity 99.9%; Pred. No. 2e-250; Indels 0; Gaps 0;
 Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGGACCCGCGAGGAAGGCGCCGCGAGTGGCGCTCCCTGAGGCTGCGGAGTTGCGG 60
 DB 110 AGGACCCGCGAGGAAGGCGCCGCGAGTGGCGCTCCCTGAGGCTGCGGAGTTGCGG 169
 QY 61 AGCGTGGGAAGAGCGAGCCCTGCTCTCCCGGGGCTGCGGAGCCATGGCCAGCGGAGCG 120
 DB 170 AGCGTGGGAAGAGCGAGCCCTGCTCTCCCGGGGCTGCGGAGCCATGGCCAGCGGAGCG 229
 QY 121 GAGAGCCCTCGGCGATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGTGTCTCATCTGGCG 180
 DB 230 GAGAGCCCTCGGCGATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGTGTCTCATCTGGCG 289
 QY 181 CGGCGAAGGGGAGCGAGGAGATGGGGGTCCAGGCTGTACGGGGATTGAACCTGTA 240
 DB 290 CGGCGAAGGGGAGCGAGGAGATGGGGGTCCAGGCTGTACGGGGATTGAACCTGTA 349

QY 241 CTTCATTTTGGACAAATCAGGAAGTGTCTGCACCACTGGAAATGAATCTATTTACTTTGT 300
 DB 350 CTTCATTTTGGACAAATCAGGAAGTGTCTGCACCACTGGAAATGAATCTATTTACTTTGT 409
 QY 301 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGGAATGTCCTTATTTGTTTCTC 360
 DB 410 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGGAATGTCCTTATTTGTTTCTC 469
 QY 361 CACCCGAGAAACAACTTAAATGAACATGACAGAAAGACAGAGAACAAATCCGCAAGGCT 420
 DB 470 CACCCGAGAAACAACTTAAATGAACATGACAGAAAGACAGAGAACAAATCCGCAAGGCT 529
 QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAATGATGATGAAGATTGAAG 480
 DB 530 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAATGATGATGAAGATTGAAG 589
 QY 481 GGCAGTAGAGATTTATTTATGAAAACAGACAAAGGTACAGGACAGCCAGGCTCATCT 540
 DB 590 GGCAGTAGAGATTTATTTATGAAAACAGACAAAGGTACAGGACAGCCAGGCTCATCT 649
 QY 541 TGCTTTGACTGATGAGAACTCCATGAAGATCTTTTCTATTGAGAGAGGAGCTTA 600
 DB 650 TGCTTTGACTGATGAGAACTCCATGAAGATCTTTTCTATTGAGAGAGGAGCTTA 709
 QY 601 TAGGTCTGAGATCTTGGTGCAATTTGTTACTGTGTGTGTGAAGATTTCATGAGAC 660
 DB 710 TAGGTCTGAGATCTTGGTGCAATTTGTTACTGTGTGTGTGAAGATTTCATGAGAC 769
 QY 661 ACAGCTGCCCCGGATTTGGGACAGTAAGATCATGTGTTCCCGGAATGAGAGGCTTCA 720
 DB 770 ACAGCTGCCCCGGATTTGGGACAGTAAGATCATGTGTTCCCGGAATGAGAGGCTTCA 829
 QY 721 GGCTCTGCAAGGATCATCTCAATTTTGAAGATCTCTGATCGAAATTTCTAGACAC 780
 DB 830 GGCTCTGCAAGGATCATCTCAATTTTGAAGATCTCTGATCGAAATTTCTAGACAC 889
 QY 781 TGAACCATCCACCATATGTGACAGAGAGTCATTCAAGTTGTGTGAGAGAAACGGCTT 840
 DB 890 TGAACCATCCACCATATGTGACAGAGAGTCATTCAAGTTGTGTGAGAGAAACGGCTT 949
 QY 841 CCGAATGCCCCGCAACGTGACAGGGTCTCTGCAAGCTTTCMAAGATCATGATCTCGTCA 900
 DB 950 CCGAATGCCCCGCAACGTGACAGGGTCTCTGCAAGCTTTCMAAGATCATGATCTCGTCA 1009
 QY 901 ACTCAATGAAAGCCCTTTTCTGTGAAGACACTTATTTACTGTGTCCAGCCCTATCTT 960
 DB 1010 ACTCAATGAAAGCCCTTTTCTGTGAAGACACTTATTTACTGTGTCCAGCCCTATCTT 1069
 QY 961 AAAAGAACTGGCATGAAGAGCTGCACTCCAGGTCAAGATGAACGATGAGCTCTCTTTAT 1020
 DB 1070 AAAAGAACTGGCATGAAGAGCTGCACTCCAGGTCAAGATGAACGATGAGCTCTCTTTAT 1129
 QY 1021 CTCGAGTTCTGATCATCATCAGCACACACACTGT 1054
 DB 1130 CTCGAGTTCTGATCATCATCAGCACACACACTGT 1163

Search completed: December 17, 2005, 19:22:59
 Job time : 947.731 secs

QY 1 AGAACCAGGAGAAAGGCGCGGATGCGCGCTCCCTGAGGAGCTGTGCGAGTTTCGCGG 60
DB 92 AGGACCCCGGAGAAAGGCGCGCGATGCGCGTCCCTGAGGAGTGTGCGAGTTTCGCGG 151
QY 61 AGCGTGGAGAGAGCGGAGCTGTCTCTCCCGGCGCTGCGGCGCATGCGCACGCGGAGCG 120
DB 152 AGCGTGGAGAGAGCGGAGCTGTCTCTCCCGGCGCTGCGGCGCATGCGCACGCGGAGCG 211
QY 121 GAGAGCCCTCGGAGATGCGGCTCCAGTGGGCTCTTTGGGCACTGTGGTCTGATCTGCGG 180
DB 212 GAGAGCCCTCGGAGATGCGGCTCCAGTGGGCTCTTTGGGCACTGTGGTCTGATCTGCGG 271
QY 181 CGGCGAGAGGAGAGCGGAGAGATGGGGGTCCAGGCTCTACGCGGATTTGACCTGTA 240
DB 272 CGGCGAGAGGAGAGCGGAGAGATGGGGGTCCAGGCTCTACGCGGATTTGACCTGTA 331
QY 241 CTTTCATTTTGGACAATTCAGAAAGTGTCTGCACTCTGGAATGAAATCTATTACTTTGT 300
DB 332 CTTTCATTTTGGACAATTCAGAAAGTGTCTGCACTCTGGAATGAAATCTATTACTTTGT 391
QY 301 GGAACAGTTGGCTCACAATTCATGACGCCACAGTTGAGAAATGCTTTATTGTTTCTC 360
DB 392 GGAACAGTTGGCTCACAATTCATGACGCCACAGTTGAGAAATGCTTTATTGTTTCTC 451
QY 361 CACCCGAGAGACACCTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAGGCGCT 420
DB 452 CACCCGAGAGACACCTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAGGCGCT 511
QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACATTCATGTCATGAAAGATTGGAAG 480
DB 512 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACATTCATGTCATGAAAGATTGGAAG 571
QY 481 GGCAGTGGAGCATTTATTAAGAAACAGCAAGGGTACAGACAGCCAGGCTCATCAT 540
DB 572 GGCAGTGGAGCATTTATTAAGAAACAGCAAGGGTACAGACAGCCAGGCTCATCAT 631
QY 541 TGCCTTGAATGAGAACTCCATGAGATCTCTTTTCTATTGAGAGAGGAGGCTTA 600
DB 632 TGCCTTGAATGAGAACTCCATGAGATCTCTTTTCTATTGAGAGAGGAGGCTTA 691
QY 601 TAGGCTCGAGATCTTGGTGCATTTGTTTACTGTGTGTGAAAGATTTCATGATGAC 660
DB 692 TAGGCTCGAGATCTTGGTGCATTTGTTTACTGTGTGTGAAAGATTTCATGATGAC 751
QY 661 ACAGCTGGCGCGGATGGGAGCATGATCATGTTTCCCGTAATGACGGCTTTCA 720
DB 752 ACAGCTGGCGCGGATGGGAGCATGATCATGTTTCCCGTAATGACGGCTTTCA 811
QY 721 GGCCTGCAAGGATCATCATCTCAATTTTGAAGAGTCCGTCATCGAAATCTTAGCAGC 780
DB 812 GGCCTGCAAGGATCATCATCTCAATTTTGAAGAGTCCGTCATCGAAATCTTAGCAGC 871
QY 781 TGAACCATCAACCATATGTGCGAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTT 840
DB 872 TGAACCATCAACCATATGTGCGAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTT 931
QY 841 CGGACATGGCCGCAAGTGGAGCAAGGGTCCCTGCGACCTCAAGATCAATGACTCGGTAC 900
DB 932 CGGACATGGCCGCAAGTGGAGCAAGGGTCCCTGCGACCTCAAGATCAATGACTCGGTAC 991
QY 901 ACTCATAGAAAGCCCTTTTCTGTGAAAGACATTATTTACTGTGTCCAGCGGCTATCTT 960
DB 992 ACTCATAGAAAGCCCTTTTCTGTGAAAGTACTATTTTACTGTGTCCAGCGGCTATCTT 1051
QY 961 AAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCAGATGAAAGATGCGCTCTTTTAT 1020
DB 1052 AAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCAGATGAAAGATGCGCTCTTTTAT 1111
QY 1021 CTCGAGTTCTGTCATCATCACCAACCAACACCTGT 1054
DB 1112 CTCGAGTTCTGTCATCATCACCAACCAACACCTGT 1145

RESULT 2
AK031465
LOCUS
DEFINITION

AK031465 3161 bp mRNA linear HTC 03-APR-2004
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030436P19 product:ANTAX TOXIN RECEPTOR
PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], full
insert sequence.

ACCESSION
AK031465
VERSION
KEYWORDS
SOURCE
ORGANISM

AK031465.1 GI:26082340
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

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PUBMED
REFERENCE
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P.,
Komuro, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Yamamoto, R., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A.,
Sumi, N., Ishii, Y., Nakamura, S., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wachihi, M.,
Yoneda, Y., Iehikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

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PUBMED
REFERENCE
AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3161)

JOURNAL
PUBMED
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komuro, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Morita, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-ees@gscc.riken.jp,
URL: http://genome.gscc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cdna library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

Source

Location/Qualifiers

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1.3161
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM,DB:6030436P19"
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/clone="6030436P19"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
1.3161
/notes="ANTHRAX TOXIN RECEPTOR PRECURSOR (TUMOR ENDOTHELIAL
MARKER 8) homolog [Mus musculus] (SWISSPROT|Q9CZ52,
evidence: FASTA, 100%ID, 84.6%length, match=1428)"
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ORIGIN

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Query Match      60.4%; Score 853.4; DB 4; Length 3161;
Best Local Similarity 87.3%; Pred. No. 1e-196;
Matches 935; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

127 CCTCGGCGATGGGCTTCAGTGGCTCTCTTGGCCACTGCTGCTCATCTGCCCGGACA 186
187 AGGGGAGCGAGGAGGAGTGGGGTCCAGCTCGTACGCGGAGTTGACCTGTATTCAT 246
401 CGGGGGCGCGCGAGGATGGGGGACCAAGCTTGCTACGAGAGATTGACCTTATTCAT 460
247 TTGGGACAAATCAGGAAGTGTGCTGCACTCGAATGAATGAAATCTTATTCATGGA 306
461 CTTGGACAAATCAGGAAGTGTGCTGCACTCGAATGAATGAAATCTTATTCATGGA 520
307 GTTGGCTCACAAATTCATGAGCCGACGTTGAGAAATGCTTATTCATTCACCCG 366
521 GTTGGCTCACAAATTCATGAGCCGACGTTGAGAAATGCTTATTCATTCACCCG 580
367 AGGAACAACCTTAATGAAGTGAAGACAGAGAAACAATTCGTCAGGCTTGAAGA 426
581 AGGAACAACCTTAATGAAGTGAAGTGAAGACAGAGAAACAATTCGTCAGGCTTGA 640
427 ACTTCAGAAAGTTTCTCCAGAGAGACACTTACATGATGAAGAGATTGAAAGGCG 486
641 GCTTCAGAAAGTTTCTCCAGAGAGACACTTACATGATGAAGAGATTGAAAGGCG 700
487 TGAACAAATTTACTATGAAGCACTCAAGATACAGACGCGCTCATCTCGGTT 546
701 TGAACAAATTTACTATGAAGCACTCAAGATACAGACGCGCTCATCTCGGTT 760
547 GACTGATGAGAACTCCATGAAAGTCTTTTCTATTCAGAGAGGCTTAATAGTTC 606
761 GAGGAGTGGGAGAGTGAACGAGACCTTCTTCTACAGAGAGGAGGCTTAACGATC 820
607 TCGAGATCTTGTGTCATTTGTTTCTGTGTGTGTGAAGATTTCAATGAGACAGCT 666
821 CCGAGACCTTGTGTCATTTGTTTCTGTGTGTGTGAAGATTTCAATGAGACAGCT 880
667 GGCCCGGATTTGCGAGACAGTATGATCATGTGTTCCGTCGATGACGCTTTCAGGCT 726
881 GGCTCGGATTTGCGAGACAGTATGATCATGTGTTCCGTCGATGACGCTTTCAGGCT 940
727 GCAAGGATCATTCATCAATTTTGAAGAGTCTGTCGATGCAAAATTCAGACGTTGAC 786
941 CCAAGGATCATTCATCAATTTTGAAGAGTCTGTCGATGCAAAATTCAGACGTTGAC 1000
787 ATCCACCATATGTGAGAGAGTCAATTCAGAGTGTGTCGAGAGAGAAAGGCTTCGACA 846
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Db 1001 ATCCACCATATGTGAGAGAGTCAATTCAGAGTGTGTCGAGAGAGAAATGGCTTCGACA 1060
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Qy 907 TGAAGAGCCCTTTCTGTGGAAGACACTAATTTACTGTGTCCAGGCTATCTTAAGA 966
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Qy 967 AGTTGCGATGAAGAGTCACTCCAGTCAAGATGAAGAGATGAGCTCTTTATTCACAG 1026
Db 1181 AGTTGCGATGAAGAGTCACTCCAGTCAAGATGAAGAGATGAGCTCTTTATTCACAG 1240
Qy 1027 TTCTGTATCATCAACACACACACTGTTCTGACAGGTTCCATTCCTGCGCATGCCCTGCT 1086
Db 1241 TTCTGTATCATCAACACACACACTGTTCTGACAGGTTCCATTCCTGCGCATGCCCTGCT 1300
Qy 1087 GATCCGTTCCTGCTCTCTAAGCCCTGAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 1146
Db 1301 GATCCGTTCCTGCTCTCTAAGCCCTGAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 1360
Qy 1147 TGTGATTATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1197
Db 1361 AGTGATCATCAAGAGAGTCCCTCCACCCCTGTTGAGAGAGTGAAGAAA 1411
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RESULT 3
AL542724 1006 bp mRNA linear EST 24-MAR-2004
LOCUS AL542724 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YL09
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL542724
VERSION AL542724 GI:45718299
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1006)
REFERENCE 1 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
AUTHORS Pull-length cDNA libraries and normalization.
TITLE Unpublished (2001)
JOURNAL On Feb 15, 2001 this sequence version replaced gi:30548161.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1660.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DE011Y050P1&c=1660.f.
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FEATURES

Source

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/clone="CS0DE011YL09"
/tissue_type="PLACENTA"
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double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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ORIGIN

Query Match 55.0%; Score 778.2; DB 1; Length 1006;
 Best Local Similarity 98.9%; Pred. No. 1.8e-178;
 Matches 804; Conservative 1; Mismatches 4; Indels 4; Gaps 2;

1 AAGAACCCGGAGGAGGAGGCGCGGATGGCGGCTCCCTGAGGATGGTGGCGAGTTGCGCG 60
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 192 AAGAACCCGGAGGAGGAGGCGCGGATGGCGGCTCCCTGAGGATGGTGGCGAGTTGCGCG 251
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 61 ACCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
 252 A--GTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 309
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 121 GAGAGCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 310 GAGAGCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 369
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 181 CCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 370 CCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 429
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 241 CTTTATTTTGGACAAATCAGAAAGTGTGTCACCACTGAAATGAATCTATTACTTTGT 300
 430 CTTTATTTTGGACAAATCAGAAAGTGTGTCACCACTGAAATGAATCTATTACTTTGT 489
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 301 GGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAAGTCTTTATTTGTTTCTC 360
 490 GGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAAGTCTTTATTTGTTTCTC 549
 |||||
 361 CACCCGAGAACCACTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
 550 CACCCGAGAACCACTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 609
 |||||
 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACATTCATGATGAAAGATTTGAAAG 480
 610 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACATTCATGATGAAAGATTTGAAAG 669
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 481 GGCAGTGAAGCAGATTTATTTAAGAAACAGACAGAGGTAACAGAGCAGCCATCATCAT 540
 670 GGCAGTGAAGCAGATTTATTTAAGAAACAGACAGAGGTAACAGAGCAGCCATCATCAT 729
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 541 TGGTTGACGATGAGAGACTCCATGAAGTCTTTTCTATTGAGAGGAGGCTAA 600
 730 TGGTTGACGATGAGAGACTCCATGAAGTCTTTTCTATTGAGAGGAGGCTAA 789
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 601 TAGGTCTGAGATCTTGTCAGATTTGTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
 790 TAGGTCTGAGATCTTGTCAGATTTGTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 849
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 661 ACAGCTGGCCCGGATTCGAGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 720
 850 ACAGCTGGCCCGGATTCGAGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 909
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 721 GGCTTCGAGAGGATCATCTCAATTTTGAAGATCCTGATGAAATTTCTACACG 780
 910 GGCTTCGAGAGGATCATCTCAATTTTGAAGATCCTGATGAAATTTCTACACG 967
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 781 TGAACCATCCACCATATGTCAGAGAGTCATT 813
 968 CTGAACATCCACCATATGTCAGAGAGTCATT 1000
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RESULT 4
 BM800898 1054 bp mRNA linear EST 05-MAR-2002
 LOCUS BM800898
 DEFINITION AGENCOURT_6420797 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5541228
 5', mRNA sequence.
 ACCESSION BM800898
 VERSION BM800898.1 GI:19117721
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE Homiidae; Homo.
 1 (bases 1 to 1054)
 AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Place: LLNL12238 row: j column: 13
 High quality sequence stop: 595.
 Location/Qualifiers
 1..1054
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 /db_xref="taxon:9606"
 /clone="IMAGE:5541228"
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 52.9%; Score 748; DB 3; Length 1054;
 Best Local Similarity 97.8%; Pred. No. 4.2e-171;
 Matches 790; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

18 GCCCGCGATGGCGGCTCCCTGAGGATGCTGGCGAGTTGCCGAGCGTGGAGAGCGCG 77
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 11 GCCCGCGATGGCGGCTCCCTGAGGATGCTGGCGAGTTGCCGAGCGTGGAGAGCGCG 70
 |||||
 78 ACCGTCTCTCCCGGAGCTGCGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 137
 71 ACCGTCTCTCCCGGAGCTGCGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 130
 |||||
 138 GCTTCAGTGGCTCTCTTTGGCACTGTGCTCATCTGCGCCGCGGCAAGGAGGAGCGCA 197
 131 GCTTCAGTGGCTCTCTTTGGCACTGTGCTCATCTGCGCCGCGGCAAGGAGGAGCGCA 190
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 198 GGAAGATGGGAGTCCAGCTGCTACGCGGATTTGAACCTGATCTTATTTTGGACAAAT 257
 191 GGAAGATGGGAGTCCAGCTGCTACGCGGATTTGAACCTGATCTTATTTTGGACAAAT 250
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 258 CAGAAAGTGTGTCACCACTGAATGAATCTATTACTTTGGAACAGTTGGCTCACA 317
 251 CAGAAAGTGTGTCACCACTGAATGAATCTATTACTTTGGAACAGTTGGCTCACA 310
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 318 AATTATCAGCCACAGTTGAGATGTCCTTATTTGTTTCTCCACCGAGAACAACT 377
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 378 TATGAAATGACAGAAACAGAGAACAAATCCGTCAAGGCTTGAAGAACTCCAGAAAG 437
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 438 TTCTGACAGAGAGACACTTACATGATGAGATTTTGAAGGCGCAGTGAAGATTT 497
 431 TTCTGACAGAGAGACACTTACATGATGAGATTTTGAAGGCGCAGTGAAGATTT 490
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 498 ATTATGAAACAGACAGAGGTAACAGACAGCCAGCGTCATCTTGTGATGATGAG 557
 491 ATTATGAAACAGACAGAGGTAACAGACAGCCAGCGTCATCTTGTGATGATGAG 550
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 558 AACTCATGAAGATCTTTTCTATTGAGAGGAGGCTAATAGTCTCGAGATCTTG 617
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| | | | |
|-----------------------|--|---|-----------------------------|
| Db | 551 | AACCTCATGAAAGATCTCTTTTTCATTATTCAGAGAGGGAGGCTAATAATGAATCTTG | 610 |
| Oy | 618 | GTGCATATTGTTACTGTGTGTGGTGTGAAGAATTTCAATCAGACAAGCTGGCCCGAATG | 677 |
| Db | 611 | GTGCATATTGTTACTGTGTGTGGTGTGAAGAATTTCAATCAGACAAGCTGGCCCGAATG | 670 |
| Oy | 678 | CGACAGTAAGAGATCATGTGTGTTCCCGTAATGACGCGCTTTCAGGCTCTGCAAGGATCA | 737 |
| Db | 671 | CGACAGTAAGAGATCATGTGTGTTCCCGTAATGACGCGCTTTCAGGCTCTGCAAGGATCA | 729 |
| Oy | 738 | TCCACTCAATTTGAAAGAGTCCTGCATCGAAATTCGTACAGCTGACACCATCACCAT-A | 796 |
| Db | 730 | TCCACTCCAGTTTAAAGAGTCCTGCATCGAAATTCGTACAGCTGACACCATCACCATGA | 789 |
| Oy | 797 | TGTGCA-CGAGAGTCATTTCAAGTTGTC | 823 |
| Db | 790 | TGTGCAAGGAGAGACATTTCCAGGTC | 817 |
| RESULT 5 | | | |
| B1823853 | | 878 bp | mRNA linear EST 04-OCT-2001 |
| LOCUS | | | |
| DEFINITION | B1823853 | 603039031.1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179974 5', | |
| ACCESSION | | mRNA sequence. | |
| VERSION | B1823853 | | |
| KEYWORDS | B1823853.1 | GI:15935416 | |
| SOURCE | EST. | | |
| ORGANISM | Homo sapiens (human) | | |
| REFERENCE | Homo sapiens | | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; | | |
| TITLE | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | |
| JOURNAL | Homidae; Homo. | | |
| COMMENT | 1 (bases 1 to 878) NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Place: LLM11448 row: n column: 07 High quality sequence stop: 804. Location/Qualifiers 1..878 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5179974" /lab_host="DH10B" /clone_1fb="NIH MGC 115" /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: This is a NIH_MGC Library." | | |
| FEATURES | source | | |
| ORIGIN | | | |
| Query Match | 52.4% | Score 740.6; | DB 3; Length 878; |
| Best Local Similarity | 95.4%; | Pred. No. 2.6e-169; | |
| Matches 839; | Conservative 0; | Mismatches 29; | Indels 11; Gaps 7; |
| 48 | GCGCAGTTGCCGAGCGTGGAGAGCGGACCTTGCTCCCGGCGCTGCGGSCCATGG | | 107 |

| Db | 1 | GGCGAGTTCCGCGAGCGCTGGGGAAGAGACGGACCCCTGCTCTCCCGGGCTCGGGCCATGG | 60 |
|------------|-----|---|-----------------------------|
| Qy | 108 | CCACGCGCGAGACCGGAGAGCCCTTCGCGCATCG3CTTCCAGTGGCTCTCTTTGGCCACTCTGG | 167 |
| Db | 61 | CCACGCGCGAGACCGGAGAGCCCTCGCGCATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGG | 120 |
| Qy | 168 | TGCTCATCTGCGCCGGGCAAGGGGGAAGCGAGGAGAGATGGGGGTCGACCTGCTAGCGGCG | 227 |
| Db | 121 | TGCTCATCTGCGCGGGGCAAGGGGGAAGCGAGGAGAGATGGGGGTCGACCTGCTAGCGGCG | 180 |
| Qy | 228 | GATTGACCTGTACTTCAATTTTGGACAATATCAGGAAATGTGCTSCACCACTGGAATGAAA | 287 |
| Db | 181 | GATTGACCTGTACTTCAATTTTGGACAATATCAGGAAATGTGCTSCACCACTGGAATGAAA | 240 |
| Qy | 288 | TCTATTACTTGTGTGGAACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAAATGTCCT | 347 |
| Db | 241 | TCTATTACTTGTGTGGAACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAAATGTCCT | 300 |
| Qy | 348 | TTATTGTTTCTCCACCCGAGGAACAACCTTTAATGAAAATGACAGAAACAGAGAACAAA | 407 |
| Db | 301 | TTATTGTTTCTCCACCCGAGGAACAACCTTTAATGAAAATGACAGAAACAGAGAACAAA | 360 |
| Qy | 408 | TCCGTCGAAGGCTTGAAGAACTCCAGAAAGTTCTCCAGGAGGAGACACTTACATGTCATG | 467 |
| Db | 361 | TCCGTCGAAGGCTTGAAGAACTCCAGAAAGTTCTCCAGGAGGAGACACTTACATGTCATG | 420 |
| Qy | 468 | AAGGATTTGAAAAGGCGCAGTGAGCAGATTTATATGAAAAACAGCAAAGGTTACAGACAG | 527 |
| Db | 421 | AAGGATTTGAAAAGGCGCAGTGAGCAGATTTATATGAAAAACAGCAAAGGTTACAGACAG | 480 |
| Qy | 528 | CCAGCGTCATGATTCCTTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAG | 587 |
| Db | 481 | CCAGCGTCATGATTCCTTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAG | 540 |
| Qy | 588 | AGAGGGAGGCTTAATAGGCTCGAGATCTGGTGCATTTGTTTACTGTGTTGGTGTGAAG | 647 |
| Db | 541 | AGAGGGAGGCTTAATAGGCTCGAGATCTGGTGCATTTGTTTACTGTGTTGGTGTGAAG | 599 |
| Qy | 648 | ATTTCATATGAGACACAGCTGGCCCGGATTTGCGGACAGTAAGATCATGTGTTTCCGCTGA | 707 |
| Db | 600 | ATTTCATATGAGACACAGCTGGCCCGGATTTGCGGACAGTAAGATCATGTGTTTCCGCTGA | 659 |
| Qy | 708 | ATGACGCTTTCAAGGCTCTGCAAGGATCATCTCACTCAATTTTG-AAAGAGTCTGTCATC | 766 |
| Db | 660 | ATGACGCTTTCAAGGCTCTGCAAGGATCATCTCACTCAATTTTAAAGAGTCTGTCATC | 719 |
| Qy | 767 | -GAAATTTACACACTGAACCATCCACATATGTGACAGGAGAGTC-ATTTCAGTTGTCG | 824 |
| Db | 720 | GGAATTTACACACTGAACCATCCACATATGTGACAGGAGAGTCATTTCCAATTTGTCG | 779 |
| Qy | 825 | TGAGAGG--AAACGGCTTCCGACATGCGCG--CAACGTGACACAGG--TCTCTGACGC | 877 |
| Db | 780 | TGAGAGGGAACCGGTTTCCGACATGCGCGGCAACGTGACACAGGAGTCTCTTTGAGGT | 839 |
| Qy | 878 | TTCAAGATCAATGACTCGGTCAACTCACTCAATGAGAAGCC 916 | |
| Db | 840 | TTCCAGATCATGACTCGGTCAACTCACTCAATGAGAAGCC 878 | |
| RESULT 6 | | | |
| CX872420 | | | |
| LOCUS | | 744 bp | mRNA linear EST 03-FEB-2005 |
| DEFINITION | | HESC4.68.H01.g1.A037 NIH MGC 262 Homo sapiens cDNA clone | |
| ACCESSION | | IMAGE17487092.57, mRNA sequence. | |
| VERSION | | CX872420 | |
| KEYWORDS | | CX872420.1 GI:58555594 | |
| SOURCE | | EST. | |
| ORGANISM | | Homo sapiens (human) | |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | |
| | | Homnidae; Homo. | |
| REFERENCE | | 1 (bases 1 to 744) | |

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: BresaGen, Inc.
 cDNA Library Preparation: Express Genomics, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
 University of Georgia
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Place: LLNL15815 row: p column: 02
 Seq primer: JENREV (CAGGAACAGCTATGACC)
 High quality sequence stop: 744.
 Location/Qualifiers

FEATURES

source

```

1..744
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7487092"
/sex="male"
/tissue_type="embryonic stem"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_1ib="NIH_MGC_262"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BG01.
Positive for Nestin and Musashi expression. Passage number
18. cDNA primed using oligo-dT primer:
5'-pgactgttcttagatcgccgagccgccccc(7)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC_259). It was constructed by Express Genomics
(Federick, MD). Sequence ends have been trimmed to
exclude vector and regions below phred quality 16. Note:
this is a Mammalian Gene Collection library."

```

ORIGIN

Query Match 50.7%; Score 717; DB 8; Length 744;
 Best Local Similarity 100.0%; Pred. No. 1,4e-163;
 Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGGACCCGGAGGAGAGGCGCGGATGCGGCTCCCTAGAGGTGCGGAGTTGGCGG 60
DB 28 AGGACCCGGAGGAGAGGCGCGGATGCGGCTCCCTAGAGGTGCGGAGTTGGCGG 87
QY 61 AGCGTGGAGAGAGCGGAGCTCTCTCCCGGGGCTGCGGAGCATGCGGCGGAGCG 120
DB 88 AGCGTGGAGAGAGCGGAGCTCTCTCCCGGGGCTGCGGAGCATGCGGCGGAGCG 147
QY 121 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTTGGCCACTTGTGTCTATCTGGC 180
DB 148 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTTGGCCACTTGTGTCTATCTGGC 207
QY 181 CGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGCTGACGGGGATTTGACCTGTA 240
DB 208 CGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGCTGACGGGGATTTGACCTGTA 267
QY 241 CTTGATTTTGGACAATTCAGAGAGTGTGTGCACTGCAATGAATGTAATCTTATCTTGT 300
DB 268 CTTGATTTTGGACAATTCAGAGAGTGTGTGCACTGCAATGAATGTAATCTTATCTTGT 327
QY 301 GGAACGTTGGCTCACAATTCATCAAGCCCAAGTTGAGAAATGCTTTATGTTTTCTC 360

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DB 328 GGAACGTTGGCTCACAATTCATCAAGCCCAAGTTGAGAAATGCTTTATGTTTTCTC 387
QY 361 CACCCGAGGAACAACCTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAGAGCCT 420
DB 388 CACCCGAGGAACAACCTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAGAGCCT 447
QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAATCATGATGAGATTTGAAG 480
DB 448 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAATCATGATGAGATTTGAAG 507
QY 481 GGGCAGTAGAGAGATTTTATGAAACAGACAAAGGTACAGAGACAGCAGGTCATCAT 540
DB 508 GGGCAGTAGAGAGATTTTATGAAACAGACAAAGGTACAGAGACAGCAGGTCATCAT 567
QY 541 TGCCTTGAAGTAGAGAGATTCATGAGATCTCTTTTCTTATTCAGAGAGGAGCTTAA 600
DB 568 TGCCTTGAAGTAGAGAGATTCATGAGATCTCTTTTCTTATTCAGAGAGGAGCTTAA 627
QY 601 TAGGTCGAGATCTTGGTGCAATGTTTACTGTGTGTGTGAAAGATTTCAATGAGAC 660
DB 628 TAGGTCGAGATCTTGGTGCAATGTTTACTGTGTGTGTGAAAGATTTCAATGAGAC 687
QY 661 ACAAGTGGCCCGAGATTTGGCGACAGTAAGATCATGTTTCCCGAATGAGGCTT 717
DB 688 ACAAGTGGCCCGAGATTTGGCGACAGTAAGATCATGTTTCCCGAATGAGGCTT 744

```

RESULT 7

LOCUS

CO245219

DEFINITION

AGENCOURT_26524177 NIH_MGC_212 Homo sapiens cDNA clone

IMAGE:30924322 5', mRNA sequence.

ACCESSION

CO245219

VERSION

CO245219.1 GI:49108057

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 833)

REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Mary Hendrix
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM1166 row: j column: 11
 High quality sequence start: 6
 High quality sequence stop: 688.
 Location/Qualifiers

1..833

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30924322"

/tissue_type="Chondrosarcoma Lung Metastasis cell lines"

/lab_host="DH10B (T1 phage resistant)"

/clone_1ib="NIH_MGC_212"

/note="Organ: Lung; Vector: pYX-AseI; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT

FEATURES

source

| | | | |
|----|-----|---|-----|
| Db | 433 | AGAAAGACTCCAGAAAGTTCTGCCAGGAGGAGACACTTAACTGATGAAAGATTCCGAAAG | 490 |
| Qy | 481 | GGCCAGTAGCAGATTATTTATGAAAACAGACAAAGGTTACAGGACACGCCAGCTCATCAT | 540 |
| Db | 491 | GGCCAGTAGCAGATTATTTATGAAAACAGAAAGGTTACAGGACACGCCAGCTCATCAT | 550 |
| Qy | 541 | TGCTTTGACTAGTGAGAACTCCATGAAAGATCTCTTTTCTAATTACAGAGAGGAGGCTTAA | 600 |
| Db | 551 | TGCTTTGACTAGTGAGAACTCCATGAAAGATCTCTTTTCTAATTACAGAGAGGAGGCTTAA | 610 |
| Qy | 601 | TAGGCTTCGAAATCTTGGTGGCAATTGTTTACCTGTGTTGGTGTGAAAGATTTCAATGAAGAC | 660 |
| Db | 611 | TAGGCTTCGAAATCTTGGTGGCAATTGTTTACCTGTGTTGGTGTGAAAGATTTCAATGAAGAC | 670 |
| Qy | 661 | ACAGCTGGCCCCGAGATTGCGGACAGTAAGAGATCATGTGTTCCCGTGAATGACGCGCTTTCA | 720 |
| Db | 671 | AAGTTTGGCC--GAGTGGCGGACAGTAAGAGATCATGTGATATCCCGTAATGACGG--TTTAA | 726 |
| Qy | 721 | GGCTTTCGAAAGGCATCATCCACTCAATT | 748 |
| Db | 727 | AGATCTGGAAGGCATCATCCACTCAATT | 754 |

| RESULT 9 | |
|------------|---|
| LOCUS | 820 bp mRNA linear EST 21-FEB-2001 |
| DEFINITION | 602402121 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:4544691 5' - 3' mRNA sequence. |

| | | |
|----------|----------------------|-------------|
| VERSION | BG281561.1 | GI:13030486 |
| KEYWORDS | EST. | |
| SOURCE | Homo sapiens (human) | |
| ORGANISM | Homo sapiens | |

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Email: csapabs-r@mail.nih.gov
Tissue Procurement: ATCC/DC/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: image.llnl.gov
Plate: L10CM128 row: h column: 04
High quality sequence stop: 815.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .820 |

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4544631"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_l1b="NH MGC 20"
/notes="organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
insert: GGCAAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

| ORIGIN | | | |
|---------------------------|-------|--------------------|------------|
| Query Match | 48.5% | Score 685.6 | DB 2 |
| Best Local Similarity | 96.6% | Pred. No. 6.5e-15c | length 820 |
| Matches 786; Conservative | 0 | Indels 9 | Gaps 8 |

| | | | |
|----|-----|---|-----|
| OY | 1 | AGGACCCGCGAGAGAGGGGCCCGCGGAATGGGCGCTCCCTGAGAGGCTGTGGCGAATTGCGCG | 60 |
| Db | 9 | AGGACCCGCGAGAGAGGGGCCCGCGGAATGGGCGCTCCCTGAGAGGCTGTGGCGAATTGCGCG | 68 |
| OY | 61 | AGCGTGGGAAGAGACGCGACCCCTGCTCTCCCGGGCTGCGGGCCATGGCCACCGCGGAGCG | 120 |
| Db | 69 | AGCGTGGGAAGAGACGCGACCCCTGCTCTCCCGGGCTGCGGGCCATGGCCACCGCGGAGCG | 128 |
| OY | 121 | GAGAGCCCTGGGCAATGGGCTTCCAGTGGGCTCTCTTGGGCCACTCTGGTGGCTCATCTGGCG | 180 |
| Db | 129 | GAGAGCCCTGGGCAATGGGCTTCCAGTGGGCTCTCTTGGGCCACTCTGGTGGCTCATCTGGCG | 188 |
| OY | 181 | CGGGCAAGGGGGAGCGACGAGAGATGGGGGTCCAGCGCTGCAACGCGCGAATTGGACTGTGA | 240 |
| Db | 189 | CGGGCAAGGGGGAGCGACGAGAGATGGGGGTCCAGCGCTGCTACGCGCGAATTGGACTGTGA | 248 |
| OY | 241 | CTTCATTTTGGACAAATCAGAACTGTGCTGCACCACTGAAATGAATCTATTACTTTGT | 300 |
| Db | 249 | CTTCATTTTGGACAAATCAGAACTGTGCTGCACCACTGAAATGAATCTATTACTTTGT | 308 |
| OY | 301 | GGAAACAGTT -GGCTCACAATTAACAAGCCACAGTTGAAGATGCT -TTATGTGTTT | 357 |
| Db | 309 | GGAAACAGTTGGGTTCACAATTTCAACGCCACAGTTGAAGATGCTCTTATATGTGTTT | 368 |
| OY | 358 | CTCCACCCGAGGAACAACCTTATATGAACCTGACAGAGACAGAGACAAATCCGTCAGG | 417 |
| Db | 369 | CTCCACCCGAGGAACAACCTTATATGAACCTTAAAGAACTGACAGAGACAGAGACAAATCCGTCAGG | 428 |
| OY | 418 | CTTGAAGAACTCCAGAAAAGTTCTGCCAGAGAGACACTTACATGATGAGAGATTGGA | 477 |
| Db | 429 | CTTGAAGAACTCCAGAAAAGTTCTGCCAGAGAGACACTTAACTATGATGAGAGATTGGA | 488 |
| OY | 478 | AAGGGCCAGTGAAGAGATTATT -ATGAAAACAGACAAGGGTACAGGACAGCCAGCTCA | 536 |
| Db | 489 | AAGGGCCAGTGAAGAGATTATTATGATGAAAACAGACAAGGGTACAGGACAGCCAGCTCA | 548 |
| OY | 537 | TCATTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTACAGAGGAGG | 596 |
| Db | 549 | TCATTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTGCTATTACAGAGGAGG | 608 |
| OY | 597 | CTAATAGTCTCCGAGATCTTGATGCAATTTGTTATCTGTGTGGGTGA -AGATTTCAAT | 655 |
| Db | 609 | CTAATAGTCTCCGAGATCTTGATGCAATTTGTTATCTGTGATGGGTGAACGATTTCAAT | 668 |
| OY | 656 | GAGACACAGCTGCGCCGGATTGCGGACAGT -AAGATCATGTGTTCCTCCGTAATGACGG | 714 |
| Db | 669 | GAGACACAGCTGCGCCGGATTGCGGACAGTAAAGATCATGTGTTCCTCCGTAATGACGG | 728 |
| OY | 715 | CTTTCAAGCTCTGCAAGGCATCATCACTCAATTTTGAAGAGTCTGCAATCGAAATCT | 774 |
| Db | 729 | -TTTCAAGCTCTGCG -AGGCATCATCTCAATCTTGAACGAAGTCTGCTCGAAATCT | 786 |
| OY | 775 | AGCAGCTGAACCATCAACCAATATGACGAGAG | 808 |
| Db | 787 | AGCAGCTGAACCATCAACCAATATGACGAGAG | 819 |

RESULT 10
AKO13005
LOCUS AKO13005 1614 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810405N18 product:ANPRAX TOXIN RECEPTOR
PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], full
insert sequence.
AKO13005
ACCESSION AKO13005.1 GI:12850099
VERSION
KEYWORDS HTC; CAP trapper..
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1

DB 542 AAGCCCTTGCTGTGGAGACACTTATTGCTGTGCCAGACCAATCTTGAAGAAGTT 601
QY 971 GGCATGAAGCTGCACTCCAGGTCAGCATGAAGAGGGCTCTCTTTATTCCTACTTCT 1030
DB 602 GGCATGAAGCTGCACTCCAGGTCAGCATGAAGAGGGCTCTCTTTATTCCTACTTCT 661
QY 1031 GTCATCATGACCAACCACTGTTTGAAGGTTCCATCCCTGCGCCCTGCTGATC 1090
DB 662 GTCATCATGACCAACCACTGTTTGAAGGTTCCATCCCTGCGCCCTGCTGATC 721
QY 1091 CTGTTCTGCTCTAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1150
DB 722 CTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
QY 1151 ATTATGAAGAGGTCCCTCCACCCCTGCGCGAGAGAGTGAAGAAA 1197
DB 782 ATCATGAAGAGGTCCCTCCACCCCTGTTGAGAGAGTGAAGAGA 828

RESULT 11
CP126791 780 bp mRNA linear EST 05-AUG-2003
LOCUS CP126791
DEFINITION UI-HF-E70-5V-O-15-0-UI.r1 NIH_MGC_214 Homo sapiens cDNA clone
IMAGE:30560510 5', mRNA sequence.
ACCESSION CP126791
VERSION CP126791.1 GI:33204381
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 780)
Normalisation and subtractions: two approaches to facilitate gene
discovery

REFERENCE
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5.

FEATURES
source Location/Qualifiers

1..780
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30560510"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH MGC 214"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATTAAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN

Query Match 45.6%; Score 644.4; DB 6; Length 780;
Best Local Similarity 99.8%; Pred. No. 7.2e-146;
Matches 645; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGACCCCGGAGAAAGGGCCCGGAGATGGCGGCTCCCTGAGGGTCGTGGCGAGTTGCGG 60
DB 135 AGGACCCCGGAGAAAGGGCCCGGAGATGGCGGCTCCCTGAGGGTCGTGGCGAGTTGCGG 194
QY 61 AGCGTGGAGAGAGGCGGACCTGCTCCCGGGCTCGGGGCGAGTGGCCAGCGGAGG 120
DB 195 AGCGTGGAGAGAGGCGGACCTGCTCCCGGGCTCGGGGCGAGTGGCCAGCGGAGG 254
QY 121 GAGAGCCCTCGGACATCGGCTTCAGTGGCTCTTTTGGCCACTGTGGTCTGATCTGCGC 180
DB 255 GAGAGCCCTCGGACATCGGCTTCAGTGGCTCTTTTGGCCACTGTGGTCTGATCTGCGC 314
QY 181 CGGGCAAGGGGAGCGAGGAGGATGGGGGTCAAGCTGTCTACGGGATTTGACCTGTA 240
DB 315 CGGGCAAGGGGAGCGAGGAGGATGGGGGTCAAGCTGTCTACGGGATTTGACCTGTA 374
QY 241 CTTCAATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAGTGAATCTATTACTTCT 300
DB 375 CTTCAATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAGTGAATCTATTACTTCT 434
QY 301 GGAACAGTTGGCTCAAAATTCATCAGCCCACTGAGAAATGTCCTTATTGTTTCTC 360
DB 435 GGAACAGTTGGCTCAAAATTCATCAGCCCACTGAGAAATGTCCTTATTGTTTCTC 494
QY 361 CACCGGAGAACACCTTAATGAAACTGACAGAAACAGAGAACAAATCGTCAAGGCT 420
DB 495 CACCGGAGAACACCTTAATGAAACTGACAGAAACAGAGAACAAATCGTCAAGGCT 554
QY 421 AAGAAGATCCCGAAGATTCGCGAGAGAACCTTCATGCAATGAGATTTGAAG 480
DB 555 AAGAAGATCCCGAAGATTCGCGAGAGAACCTTCATGCAATGAGATTTGAAG 614
QY 481 GGCAGTGAAGCATTTATTATGAAGAACAGAAAGGTCACAGACAGCGCTCATCAT 540
DB 615 GGCAGTGAAGCATTTATTATGAAGAACAGAAAGGTCACAGACAGCGCTCATCAT 674
QY 541 TCGTTGACTGATGAGAACTCCATGAGATCTTTTCTATTCAGAGGAGGCTTA 600
DB 675 TCGTTGACTGATGAGAACTCCATGAGATCTTTTCTATTCAGAGGAGGCTTA 734
QY 601 TAGGTCGAGATCTTGTCGCAATGTTTACTGCTGTGGTGGAA 646
DB 735 TAGGTCGAGATCTTGTCGCAATGTTTACTGCTGTGGTGGAA 780

RESULT 12

BE741333 725 bp mRNA linear EST 15-SEP-2000
LOCUS BE741333
DEFINITION 601594179F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948114 5',
mRNA sequence.
ACCESSION BE741333
VERSION BE741333.1 GI:10155325
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 725)
NIH-MGC http://mgi.nci.nih.gov/.
Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rsemail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at: Image.lim.gov
 Plate: LCM810 row: n column: 19
 High quality sequence stop: 711.
 Location/Qualifiers

FEATURES

Source

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1..725
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3948114"
/issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_9"
/notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 45.1%; Score 637.8; DB 2; Length 725;
 Best Local Similarity 98.8%; Pred. No. 2.9e-144;
 Matches 653; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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395 GACGAGAGAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGAC 454
Db 1 GACGAGAGAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGAC 60
QY 455 ACTTACATGATGAGAGATTGAAAAGGCCAGTGAAGATTATTGAAAACAGACAA 514
Db 61 ACTTACATGATGAGAGATTGAAAAGGCCAGTGAAGATTATTGAAAACAGACAA 120
QY 515 GGGTACAGGACAGCAGCTCATGTTGACTGATGAGAACTCCATGAAGATCTC 574
Db 121 GGGTACAGGACAGCAGCTCATGTTGACTGATGAGAACTCCATGAAGATCTC 180
QY 575 TTTTCTATTGAGAGAGAGGCTAATAGTCTCGAATCTTGATGCAATTTGTTACTGT 634
Db 181 TTTTCTATTGAGAGAGAGGCTAATAGTCTCGAATCTTGATGCAATTTGTTACTGT 240
QY 635 GTTGTGTGAAGATTTCATGAGACACAGCTGCGGATTCGGAAGTGAAGATCAT 694
Db 241 GTTGTGTGAAGATTTCATGAGACACAGCTGCGGATTCGGAAGTGAAGATCAT 300
QY 695 GTTGTTCCTGATGAGAGGCTTTCAGGCTTGAAGGATCATCCATTTTGAAG 754
Db 301 GTTGTTCCTGATGAGAGGCTTTCAGGCTTGAAGGATCATCCATTTTGAAG 360
QY 755 AAGTCTGATGAGAAATTCAGAGCTGAACATTCACATATGTCAGAGAGATCTT 814
Db 361 AAGTCTGATGAGAAATTCAGAGCTGAACATTCACATATGTCAGAGAGATCTT 420
QY 815 CAACTGTGATGAGAGAAAGGCTTCGACATCCCGCAAGTGAAGAGGCTCTTGC 874
Db 421 CAACTGTGATGAGAGAAAGGCTTCGACATCCCGCAAGTGAAGAGGCTCTTGC 480
QY 875 AGCTTCAAGATCATGATCGGTCACTCAATGAGAAAGCCCTTTTCTGGAAGACAT 934
Db 481 AGCTTCAAGATCATGATCGGTCACTCAATGAGAAAGCCCTTTTCTGGAAGATCAT 540
QY 935 TATTACTGTGTCAGGCTATCTTAA-AGAAGTTGTCATGAAGTGCATCCAGT 993
Db 541 TATTACTGTGTCAGGCTATCTTAA-AGAAGTTGTCATGAAGTGCATCCAGT 600
QY 994 CAGCATGAAGATGAGCTCTCTTTTATCTCAAGTTCTGTCATCATCACACACACTG 1053
Db 601 CAGCATGAAGATGAGCTCTCTTTTATCTCAAGTTCTGTCATCATCACACACACTG 660
QY 1054 T 1054
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Db 661 T 661

RESULT 13
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 LOCUS CFI32432
 DEFINITION UI-HF-P00-two-m-16-0-UI.r1 NIH_MGC_215 Homo sapiens cDNA clone
 IMAGE:30560079 5', mRNA sequence.

ACCESSION CFI32432
 VERSION CFI32432.1 GI:33215693
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bernaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548

COMMENT
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: bento-soares@uiowa.edu
 Tissue Procurement: Mary Hendrix
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/humanfl.html
 Seq primer: pyx-5.

FEATURES

Source

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1..641
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30560079"
/issue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/notes="Organ: Lung; Vector: pyx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATTAAGCCA. Tissue was provided by Mary Hendrix."
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ORIGIN

Query Match 44.8%; Score 630; DB 6; Length 641;
 Best Local Similarity 99.8%; Pred. No. 2.2e-142;
 Matches 641; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 61 CTCCCGGCGTGGCGGCTATGCGCAGCGGAGCGAGAGAGAGAGAGAGAGAGAGAG 120
QY 146 TGGCTCTTTGGCACTGTGCTCATCTGCGCCCGGCAAGAGGAGACCGAGGAGAT 205
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| Db | 121 | TGGCTCTCTTTGGCCACTCTGGTGTCTACTCTGGCCGGGCAAGGGGAGACGAGGAGAGAT | 180 |
| OY | 206 | GGGGGTCCAGCCTGCTGACGGCGGATTTGACTCTGACTTCAATTTTGGACAAATCAGGAAGT | 265 |
| Db | 181 | GGGGGTCCAGCCTGCTGCTACGGCGGATTTTGGACTCTGACTTCAATTTTGGACAAATCAGGAAGT | 240 |
| OY | 266 | GTGCTGCACCACTGGGAATGAAATCTATTACTTTGTGTGGAACAGTGGCTACACAAATTCATC | 325 |
| Db | 241 | GTGCTGCACCACTGGGAATGAAATCTATTACTTTGTGTGGAACAGTGGCTACACAAATTCATC | 300 |
| OY | 326 | AGCCCACTTGAGAAATGTCCTTTATTTGTCTTCACCCGAGGAACAACCTTAAATGAAA | 385 |
| Db | 301 | AGCCCACTTGAGAAATGTCCTTTATTTGTCTTCACCCGAGGAACAACCTTAAATGAAA | 360 |
| OY | 386 | CTGACAGAAAGACAGAGAAACAATTCGCTCAAGGCTTGAAAGAACTCCAGAAAGTCTGGCA | 445 |
| Db | 361 | CTGACAGAAAGACAGAGAAACAATTCGCTCAAGGCTTGAAAGAACTCCAGAAAGTCTGGCA | 420 |
| OY | 446 | GGAGAGACACTTACATGATGATGAGGATTTGAAAAGGCCAGTGACAGATTTATATGAA | 505 |
| Db | 421 | GGAGAGACACTTACATGATGATGAGGATTTGAAAAGGCCAGTGACAGATTTATATGAA | 480 |
| OY | 506 | AACAGACAAAGGTTACAGGACAGCCAGCTGATCATTTGCTTTGACTGATGAGAACTTCAT | 565 |
| Db | 481 | AACAGACAAAGGTTACAGGACAGCCAGCTGATCATTTGCTTTGACTGATGAGAACTTCAT | 540 |
| OY | 566 | GAAGATCTCTTTTCTATTCAAGAGAGGAGGCTTAATAGGCTCTCGAATCTTGGTGCAAAT | 625 |
| Db | 541 | GAAGATCTCTTTTCTATTCAAGAGAGGAGGCTTAATAGGCTCTCGAATCTTGGTGCAAAT | 600 |
| OY | 626 | GTTTACTGTGTGGTGATGAAAATTTCAATAGACACAGCTG | 667 |
| Db | 601 | GTTTACTGTGTGGTGATGAAAATTTCAATAGACACAGCTG | 641 |

| | | | | | | |
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| | RESULT | 14 | | | | |
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| | DEFINITION | BG281831 | 964 bp | mRNA | linear | EST 21-FEB-2001 |
| | | 602403057P1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4545302 5 , | | | | |
| | ACCESSION | rNA sequence. | | | | |
| | VERSION | BG281831 | | | | |
| | KEYWORDS | BG281831.1 GI:13030757 | | | | |
| | SOURCE | EST. | | | | |
| | ORGANISM | Homo sapiens (human) | | | | |
| | | Homo sapiens | | | | |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| | | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | | | |
| | | Homidae; Homo. | | | | |
| | REFERENCE | 1 (bases 1 to 964) | | | | |
| | AUTHORS | NIH-MGC http://mgc.nci.nih.gov/. | | | | |
| | TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | |
| | JOURNAL | Unpublished (1999) | | | | |
| | COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/TRP | | | | |
| | | cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA library Arrayed By: The I.M.A.G.E. Consortium (ULNL) DNA Sequencing by: Incyte Genomics, inc. Data distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at: image.lnl.gov Plate: LILMLI230 row: a column: 15 High quality sequence stop: 659. Location/Qualifiers 1..964 | | | | |
| FEATURES | | | | | | |
| bsource | | | | | | |

| FEATURES | source | Location/Qualifiers |
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| | /clone="IMAGE:4545302" | |
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| | /clone_1lb="NH MGC 20" | |
| | /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally | |

cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). "

| | | | | |
|---------------------------|-------|--------------------|----------|------------|
| Query Match | 41.2% | Score 582 | DB 2 | Length 964 |
| Bsect Local Similarity | 98.3% | Pred. No. 1.2e-130 | | |
| Matches 641; Conservative | 0 | Mismatches 5 | Indels 6 | Gaps 5 |

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| QY | 1 | AGAA | CCCGCAGAGAAAGGGCCCGCGAGATGGCGCGCTCCCTGAAAGGTGCGTGGCAGATTCCCG | 60 |
| Db | 22 | AGAA | CCCGCAGAGAAAGGGCCCGCGAGATGGCGCGCTCCCTGAAAGGTGCGTGGCAGATTCCCG | 81 |
| QY | 61 | AGCG | TGGAGAAAGAACCGGACCCTGCTCTCCCGGGCTCGGGCCATGGCCAC - GGC | 119 |
| Db | 82 | AGCG | TGGAGAAAGAACCGGACCCTGCTCTCCCGGGCTCGGGCCATGGCCACTGGCGGAGC | 141 |
| QY | 120 | GGA | AGCCCTTGGCATGGGCTTCCAGTGGCTCTTTTGGCCACTCTGTGTCTCATCTTGGC | 179 |
| Db | 142 | GGA | AGCCCTTGGCATGGGCTTCCAGTGGCTCTTTTGGCCACTCTGTGTCTCATCTTGGC | 201 |
| QY | 180 | CCGG | GCAAAGGGGACGCAGGGAGATGGGGGTCCAGCTGCTACGGCGGAAATTTGACCTGT | 239 |
| Db | 202 | CCGG | GCAAAGGGGACGCAGGGAGATGGGGGTCCAGCTGCTACGGCGGAAATTTGACCTGT | 261 |
| QY | 240 | ACTT | CATTTTGGACAAATCAGAAAGTGTGCTGCACCACTGGATGAAATCTATTAC - TTT | 298 |
| Db | 262 | ACTT | CATTTTGGACAAATCAGAAAGTGTGCTGCACCACTGGATGAAATCTATTACCTTTT | 321 |
| QY | 289 | GTGA | ACAG - TTGGCTCAAAATTCATCAGCCCACTGAGAAATGACCTTATTTGTTT | 357 |
| Db | 322 | GTGA | ACAGTTTGGCTCAAAATTCATCAGCCCACTGAGAAATGACCTTATTTGTTT | 381 |
| QY | 358 | CTCC | ACCAGGAAACAACCTTATGAAACTGACAGAAACAGAGAACAAATCCGCTCAAG | 417 |
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| QY | 418 | CCTG | AAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAATGAAAGATTGGA | 477 |
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| QY | 478 | AAGG | CCAGTAGAGATTTATTATGAAAAACAGACAAGG - TACAGACACGACGCTC | 535 |
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| QY | 536 | ATCAT | TGCTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCAGAG - AAGGA | 594 |
| Db | 562 | ATCAT | TGCTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCAGAGACAGGA | 621 |
| QY | 595 | GCGT | TAATGGTCTCGAATCTTGGTCAATGTTTACTCTGTGGTGGTGA | 646 |
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| | |
|------------|--|
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| LOCUS | DN993680 |
| DEFINITION | DN993680 672 bp mRNA linear EST 17-MAY-2005 TC113711 Human adult whole brain, large insert, cDNA expression library. Homo sapiens cDNA clone TC113711 5' similar to Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 3, mRNA sequence. |
| ACCESSION | DN993680 |
| VERSION | DN993680.1 GI:5625511 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. |
| REFERENCE | 1 (bases 1 to 672) |

AUTHORS

TITLE

JOURNAL

COMMENT

Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
 Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
 Zhang, X., Yag, G., and He, W.
 High-throughput cloning of full-length human cDNAs directly from
 cDNA libraries optimized for large and rare transcripts
 Unpublished (2005)
 Contact: Kovacs, K.
 High Throughput cDNA Cloning
 Origene Technologies, Inc. (www.origene.com)
 6 Taft Court, Suite 100, Rockville, MD 20850, USA
 Tel: 301 340 3188
 Fax: 301 340 8606
 Email: cDNA@origene.com
 This EST submission is part of an on-going human full-length
 cloning project at Origene Technologies, Inc.
 Please contact Origene for access.
 Origene Technologies, Inc.
 6 Taft Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com
 Seq primer: PCMV6 5prime forward vector primer, Origene
 Technologies Inc.

FEATURES

source

Location/Qualifiers
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 Site 2: XhoI/SalI compatible end ligatio; Oligo-dT primed
 reverse transcription optimized for large and GC rich mRNA
 transcripts, cDNA size selection, optimized ligation for
 large inserts into mammalian expression vector, random
 clones selected for end sequence verification of
 full-length genes"

ORIGIN

Query Match 40.4%; Score 571; DB 8; Length 672;
 Best Local Similarity 100.0%; Pred. No. 5.5e-128; Indels 0; Gaps 0;
 Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 102 AGGACCCGCGAGAGAGGCGCGGATGCGCGTCCCTGAGGGTCTGCGAGTTTCGGG 161
 QY 61 AGCGTGGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGCCATGCGCACGCGAGCG 120
 DB 162 AGCGTGGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGCCATGCGCACGCGAGCG 221
 QY 121 GAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGSCACTGCGTGCATCTGCGC 180
 DB 222 GAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGSCACTGCGTGCATCTGCGC 281
 QY 181 CGGCGAAGGGGAGCGCAGAGAGATGCGGGTCCAGCCTGCTACGCGCGGATTGACTGTA 240
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 QY 301 GGAACAGTTGGCTGCAAAATTCATCAGGCCCAAGTTGAGATGTCCTTATTTGTTCTC 360
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 QY 361 CACCGAGAGAACAACTTATGAAGTGAAGAGACAGAGAACAAATCCGTCAAGGCTT 420
 DB 462 CACCGAGAGAACAACTTATGAAGTGAAGAGACAGAGAACAAATCCGTCAAGGCTT 521

QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCATGAAGATTGAAG 480
 DB 522 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCATGAAGATTGAAG 581
 QY 481 GGCACGTGAGCAGATTATTTATGAACACAGACAGGGTACAGACAGCCAGCGTCATCAT 540
 DB 582 GGCACGTGAGCAGATTATTTATGAACACAGACAGGGTACAGACAGCCAGCGTCATCAT 641
 QY 541 TGCTTTGACTGATGAGAACTCCATGAAGAT 571
 DB 642 TGCTTTGACTGATGAGAACTCCATGAAGAT 672

Search completed: December 19, 2005, 00:48:40
 Job time : 6395.95 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 10:16:44 ; Search time 266.178 Seconds
(Without alignments)
9442.828 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 1414
Sequence: 1 aggaccgcggaggaagggcc.....aaaaaaaaaaaaaaaaaaaa 1414

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 906.8 | 64.1 | 1609 | US-09-620-312D-8 | Sequence 8, Appli |
| 2 | 516.8 | 36.5 | 3981 | US-09-799-451-250 | Sequence 250, App |
| 3 | 346.2 | 24.5 | 2234 | US-10-104-047-669 | Sequence 669, App |
| 4 | 307.4 | 21.7 | 1492 | US-09-774-528-297 | Sequence 297, App |
| 5 | 307.4 | 21.7 | 1492 | US-10-120-988-297 | Sequence 297, App |
| 6 | 79.4 | 5.6 | 450 | US-10-131-827-8330 | Sequence 8330, Ap |
| 7 | 55.2 | 3.9 | 612 | US-09-902-540-1357 | Sequence 1357, Ap |
| 8 | 51.6 | 3.6 | 985 | US-09-322-409-25 | Sequence 25, Appl |
| 9 | 51.6 | 3.6 | 985 | US-09-322-409-27 | Sequence 27, Appl |
| 10 | 51.6 | 3.6 | 985 | US-09-451-527-25 | Sequence 25, Appl |
| 11 | 51.6 | 3.6 | 985 | US-09-451-527-27 | Sequence 27, Appl |
| 12 | 51.6 | 3.6 | 2158 | US-07-602-608-1 | Sequence 1, Appli |
| 13 | 51.6 | 3.6 | 2158 | US-08-261-578-1 | Sequence 1, Appli |
| 14 | 51.4 | 3.6 | 1660 | US-09-722-971-9 | Sequence 9, Appli |
| 15 | 50.8 | 3.6 | 3829 | US-08-631-097-8 | Sequence 8, Appli |
| 16 | 50.8 | 3.6 | 3829 | US-08-810-712-6 | Sequence 6, Appli |
| 17 | 50.2 | 3.6 | 1412 | US-09-614-912-197 | Sequence 197, App |
| 18 | 50.2 | 3.6 | 36311 | US-09-949-016-13627 | Sequence 13627, A |
| 19 | 50 | 3.5 | 1013 | US-09-322-409-6 | Sequence 6, Appli |
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| 23 | 49.8 | 3.5 | 658 | US-08-998-416-595 | Sequence 595, App |
| 24 | 49.8 | 3.5 | 2608 | US-09-618-596A-1 | Sequence 1, Appli |

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| 25 | 49.8 | 3.5 | 2609 | US-09-437-568A-1 | Sequence 1, Appli |
| 26 | 49.4 | 3.5 | 194 | US-09-621-976-801 | Sequence 801, App |
| 27 | 48.8 | 3.5 | 1039 | US-09-902-540-1280 | Sequence 1280, Ap |
| 28 | 48.8 | 3.5 | 4167 | US-09-973-278-700 | Sequence 700, App |
| 29 | 48.6 | 3.4 | 603 | US-10-178-449A-11 | Sequence 11, Appl |
| 30 | 48.6 | 3.4 | 908 | US-09-800-729-25 | Sequence 25, Appl |
| 31 | 48.6 | 3.4 | 2445 | US-09-949-016-781 | Sequence 781, App |
| 32 | 48.6 | 3.4 | 2539 | US-10-144-198-21 | Sequence 21, Appl |
| 33 | 48.4 | 3.4 | 396 | US-09-640-173-53 | Sequence 53, Appl |
| 34 | 48.4 | 3.4 | 396 | US-09-713-550-53 | Sequence 53, Appl |
| 35 | 48.4 | 3.4 | 396 | US-09-825-294-53 | Sequence 53, Appl |
| 36 | 48.4 | 3.4 | 396 | US-09-970-966-53 | Sequence 53, Appl |
| 37 | 48.4 | 3.4 | 1898 | US-08-342-411A-1 | Sequence 1, Appli |
| 38 | 47.8 | 3.4 | 1766 | US-10-142-835-27 | Sequence 27, Appl |
| 39 | 47.6 | 3.4 | 323 | US-09-621-976-10374 | Sequence 10374, A |
| 40 | 47.6 | 3.4 | 530 | US-09-461-325-28 | Sequence 28, Appl |
| 41 | 47.6 | 3.4 | 530 | US-10-012-542-28 | Sequence 28, Appl |
| 42 | 47.6 | 3.4 | 530 | US-10-115-123-28 | Sequence 28, Appl |
| 43 | 47.6 | 3.4 | 1378 | US-09-149-476-208 | Sequence 208, App |
| 44 | 47.6 | 3.4 | 2323 | US-09-149-476-24 | Sequence 24, Appl |
| 45 | 47.4 | 3.4 | 1248 | US-09-489-847-101 | Sequence 101, App |

ALIGNMENTS

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RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aunani, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aildong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhilwei
; APPLICANT: John Tillinghaast
; APPLICANT: Dermanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
US-09-620-312D-8
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Best Local Similarity 99.8%; Pred. No. 5.4e-223;
Matches 908; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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206 AGGACCCGAGAGGAGGCGCGGATGCGCTCCCTGAGGATCGTGGCGAGTTGCGCG 265
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326 GAGAGCCCTGCGGCGGCTTCCAGTGGCTCTTTTGGCGGCGGCGGCGGCGG 385
181 CGGCGAGAGGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
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686 GGCAGTGAAGAGATTTATTAAGAAAGAGAGGAGGAGGAGGAGGAGGAGG 745
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806 TGGGCTGAGAGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 865
661 ACAGTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
866 ACAGTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 925
721 GGCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
926 GGCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 985
781 TGAACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
986 TGAACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1045
841 CCGAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
1046 CCGAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1105
901 ACTCAATGAG 910
1106 ACTCAATGAG 1115

RESULT 2
US-09-799-451-250
Sequence 250, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Aundt, Vinod

APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aiding J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yuning
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Weinman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 67839691 Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_Fl_genes Version 2.0
SEQ ID NO 250
LENGTH: 3981
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)..(1118)
US-09-799-451-250

Query Match 36.5%; Score 516.8; DB 3; Length 3981;
Best Local Similarity 99.6%; Pred. No. 1.6e-122;
Matches 518; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

678 CGAGAGTGAAGATATGTTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 737
1 CGAGAGTGAAGATATGTTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
738 TCACATCAATTTTGAAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 797
61 TCACATCAATTTTGAAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
798 GTGAGAGGAGTCAATTTCAAGTTGTGAGAGGAGGAGGAGGAGGAGGAGG 857
121 GTGAGAGGAGTCAATTTCAAGTTGTGAGAGGAGGAGGAGGAGGAGGAGG 180
858 TGGAGAGGAGTCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 917
181 TGGAGAGGAGTCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
918 TTTCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 977
241 TTTCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
978 AAGTGCATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1037
301 AAGTGCATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
1038 TACACCAACACAGCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1097
361 TACACCAACACAGCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
1098 TGCCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1157
421 TGCCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
1158 AGAGAGTCCCTCAGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1197
481 AGAGAGTCCCTCAGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 520

RESULT 3
US-10-104-047-669


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QY 438 TTCTGCGAGAGAGACACTTATCATGATGAAGATTGTAAGAGCCAGTGCAGATT 497
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   |||
Db 182 TTAGTCCAGTACAGAGACATATATCATGAGAGCTAAGAGTAAAGTAAAGAAAT-- 239
QY 498 ATTATGAAAACAGACAAAGGTACAGAGACAGCCGCTCATCTGTTGTTGATGATGAG 557
   |||
   |||
   |||
Db 240 ----TCAGAAAGCAGAGAGCTGAAAACCTCCAGTATCATATGCTCTGACAGATGGCA 295
QY 558 AACTCCATGAAGATCTTTTCTTATTCAGAGAGAGGCTTAATAGTCTCGAGATCTTG 617
   |||
   |||
   |||
Db 296 AGTTGAGCGGTCTGGGCCATCATATGACAGAAAGCAAGCAAGATCATGATCATCTTG 355
QY 618 GTGCAATTGTTTACTGTGTGTGTGTAAGATTCAATGACACAGCTGCCCCGATG 677
   |||
   |||
   |||
Db 356 GGGCTATGTATGTGTGTGGGCTCTGATTTTGAACAGACAGCTGTAAGAAATTTG 415
QY 678 CGGACGTAAAGATCATGTGTTCCTGTAATGACGGCTTCAAGGCTTCGAAAGATCA 737
   |||
   |||
   |||
Db 416 CTGATTCAGAGAGCAAGTTTCCCTGTCAAGGTGATTTCAAGGCTTTAAAGAAATTA 475
QY 738 TCCACTCAATTTGAAGAAGTCCGTCATGAAATTTAGACGCTGAACCATCCACATAT 797
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   |||
Db 476 TTATTTCTTACTAGCTCATGATCATGTAATCTTAAGATTGACGCTCAAGTGTCT 535
QY 798 GTGCAAGAGATCATTTCAAGTTGTGTGTAAGAGAAACGGCTTCCGACATGCCCGAACG 857
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   |||
Db 536 GTGTGGGGAGAGAAATTTCAAGATGTCTTAAGTGAAGAGAAATTCATGCTGGGACATCGGA 595
QY 858 TGGACAGGGTCTCTGACGCTTCAGATGAAATGATCTGCTCACTCATGTAAGAAAGCTT 917
   |||
   |||
   |||
Db 596 ATGGCAGTGTCTGTGACCTTACATGTAATGAAACATATACACAGATGTAAGAAACGAG 655
QY 918 TTTCTGTGAAGACACTTATTTACTGTGTGACAGCGCTATCTTAAAGAAGTTGCGATGA 977
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   |||
   |||
Db 656 TTAGTGTACAGCTTATTTCTATGCTTGTCTGTGACCTATCTGAAATTAAGCTGAGAGAA 715
QY 978 AAGCTGACATCCAGGTACAGATGAACAGATGCGCTCTTTTATCTTCAAGTTCTGTCATCA 1037
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   |||
Db 716 CTCTGATGTTCAGTGAAGCTTTAATGAGAAATCTGTCATTTCAAGATCATTTAATTG 775
QY 1038 TCACCAACACACACTGTCTGTGAGAGTTCCATCTGCGCATGCGCTGCTGATCTGTTC 1097
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   |||
   |||
Db 776 TCACAGCCACAGAAATTTCTTAACGGGATGCGAGCCATCATTTATTTTGGTGTACTG 835
QY 1098 TGTCTTACGCTGCTGCTCTCTGTGAGTTGTTGAGGCTCTGCTGCTGCTGCTGCTGCTGCT 1157
   |||
   |||
   |||
Db 836 TACTCTGGGATCGGTTGATGTGTGTTGGCCCTTTGCTGCAAGTGTATTATTA 895
QY 1158 AGGAGGTCCCTCCACCCCTGCC 1180
   |||
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Db 896 AGGATCTCCACACACACCCCCC 918
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RESULT 5
US-10-120-988-297
; Sequence 297, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyun
; APPLICANT: Wang, Dunru
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/120,988
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_fl_genes Version 2.0

```

```

; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-10-120-988-297

Query Match      21.7%; Score 307.4; DB 3; Length 1492;
Best Local Similarity 59.2%; Pred. No. 7,3e-69;
Matches 546; Conservative 0; Mismatches 371; Indels 6; Gaps 1;

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QY 258 CAGGAAGTGTGTGACACACATGGAATGAATCTTATTTGTGGAACAGTTGGCTCACA 317
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   |||
Db 2 CAGCGCGCGGCGAATTAATGATTAATTAATTTGTTACAGCAACTTGGGAGAGA 61
QY 318 AATTATCAGCCCAAGTTGAGATGCTTTATTTGTTTCTCCACCCGAGAAACAACCT 377
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   |||
Db 62 GATTTGTAGCGCTGAAATGAGATTTCTTCTATTTGTGTCTTCTCAAGCACTATTTA 121
QY 378 TAAATGAACCTGACAGAGACAGAGAAATCCGTCAGGCTTAGAAGACTCCAGAAAG 437
   |||
   |||
   |||
Db 122 TTTTCCATTAATCTGAGACAGAGGCAAAATCAGTAAGGCTTGAAGATTTAAACGTC 181
QY 438 TTCTGCGAGAGAGACACTTATCATGATGAAGATTGAAAGGCGCAGTGCAGATTT 497
   |||
   |||
   |||
Db 182 TTAGTCCAGTACAGAGACATATATCATGAAAGACTAAGCTACGATGAACAAAT-- 239
QY 498 ATTATGAAAACAGACAAAGGTACAGAGACAGCCGCTCATCTGTTGTTGATGATGAG 557
   |||
   |||
   |||
Db 240 ----TCAGAAAGCAGAGAGCTGAAAACCTCCAGTATCATATTTCTCTGACAGATGGCA 295
QY 558 AACTCCATGAAGATCTTTTCTTATTCAGAGAGAGGAGCTTAATAGTCTCGAGATCTTG 617
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   |||
   |||
Db 296 AGTTGAGCGGTCTGGGCCATCATATGACAGAAAGCAAGCAAGATCATGATCATCTTG 355
QY 618 GTGCAATTGTTTACTGTGTGTGTGTAAGATTTCATATGAGACACAGCTGCGCGATTTG 677
   |||
   |||
   |||
Db 356 GGGCTATGTATGTGTGTGGGCTCTGATTTTGAACAGACAGCTGTAAGAAATTTG 415
QY 678 CGGACGTAAAGATCATGTGTTCCTGTAATGATGAGCGCTTGAAGCTGCTGCAAGGATCA 737
   |||
   |||
   |||
Db 416 CTGATTCAGAGAGCAAGTTTCCCTGTCAAGGTGGAATTCAGGCTCTTAAAGAAATTA 475
QY 738 TCCACTCAATTTGAAGAAGTCCGTCATGAAATTTAGACGCTGAACCATCCACATAT 797
   |||
   |||
   |||
Db 476 TTATTTCTTACTAGCTCATGATCATGTAATCTTAAGATTGACGCTCAAGTGTCT 535
QY 798 GTGCAAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCGACATGCCCGAACG 857
   |||
   |||
   |||
Db 536 GTGTGGGGAGAGAAATTTCAAGATGTCTTAAGTGAAGAGATTCATGCTGGGACATCGGA 595
QY 858 TGGACAGGGTCTCTGACGCTTCAGATGAAATGATCTGCTCACTCATGTAAGAAAGCTT 917
   |||
   |||
   |||
Db 596 ATGGCAGTGTCTGTGACCTTACATGTAATGAAACATATACACAGATGTAAGAAACGAG 655
QY 918 TTTCTGTGAAGACACTTATTTACTGTGTGACAGCGCTATCTTAAAGAAGTTGCGATGA 977
   |||
   |||
   |||
Db 656 TTAGTGTACAGCTTATTTCTATGCTTGTCTGTGACCTATCTGAAATTAAGCTGAGAGAA 715
QY 716 CTCTGATGTTCAGTGAAGCTTTAATGAGAGAAATCTGTCAATTTCAAGATCATTTAATTG 775
QY 776 TCACCAACACACACTGTCTGTGAGAGTTCCATCTGCGCATGCGCTGCTGATCTGTTC 1097
   |||
   |||
   |||
Db 1038 TCACCAACACACACTGTCTGTGAGAGTTCCATCTGCGCATGCGCTGCTGATCTGTTC 1097
   |||
   |||
   |||
Db 776 TCACAGCCACAGAAATTTCTTAACGGGATGCGAGCCATCATTTATTTTGGTGTACTG 835
QY 1098 TGTCTTACGCTGCTGCTCTCTGTGAGTTGTTGAGGCTCTGCTGCTGCTGCTGCTGCTGCT 1157
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   |||
Db 836 TACTCTGGGATCGGTTGATGTGTGTTGGCCCTTTGCTGCAAGTGTATTATTA 895

```



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Patent No.6471957
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Drelitz, Matthew J.
APPLICANT: Wondolting, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 985
TYPE: DNA
ORGANISM: Canis familiaris
US-09-322-409-27

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| | Query Match | 3.6% | Score 51.6; | DB 3, | Length 985; |
|----|--|--------|----------------|-------|----------------------------------|
| | Similarity | 65.8%; | Pred. NO.0037; | | |
| | Best Local | | | | |
| | Matches | 75, | Conservative | 0; | Mismatches 39; Indels 0; Gaps 0; |
| Oy | 1301 CTCAATCAGACAGCTTTTTCCTCAGTGCCCGTAGTCCAATCCAGGTCTAACATTC | | | | 1360 |
| Db | 122 CCCCTGTCACAAAGCTTGGCCCCCAGAAATTGAATTAATCATCTCTTTTCACAGC | | | | 63 |
| Oy | 1361 AATAAATGCTATATGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | | | | 1414 |
| Db | 62 AA | | | | 9 |

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RESULT 10
US-09-451-527-25
; Sequence 25, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Drelitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/122,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (74)..(901)
US-09-451-527-25

```

```

Query Match 3.6% Score 51.6; DB 3, Length 985;
Best Local Similarity 65.8%; Pred. No. 0.0037;
Matches 75; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1301 CTCAATCTAGACAGTCTTTTCTCTAGTTCCTGTATTCAAATCCAGTGCTTAACATTC 1360
Db CCGCTGTAGACAAAGTCTTTGGCCCCAGMAATTGTATTTAATCATCTTTTCTTACGAGC 923
QY 1361 AATAAATGCTATATGAAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
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Db          924 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 977

RESULT 11
US-09-451-527-27/c
; Sequence 27, Application US/09451527
; Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 985
TYPE: DNA
ORGANISM: Canis familiaris
US-09-451-527-27
```

| Query Match | 3.6* | Score 51.6 | DB 3 | Length 985 |
|-----------------------|-------|---|---------------|------------|
| Beet Local Similarity | 65.8* | Pred. No. 0.0037 | | |
| Matches | 75 | Conservative 0 | Mismatches 39 | Indels 0 |
| | | | Gaps 0 | |
| Q7 | 1301 | CTCAATCAGACGCTTTTCCTTAATTCCTGATTCCTCAATCCAGTGTCAACATTC | 1360 | |
| | | | | |
| Db | 122 | CCCTCTGACAAATCCTTGCCCCCAAGAAATGTATATAAATCATCTTTTTCACAGC | 63 | |
| | | | | |
| Q7 | 1361 | AATAAATAGCATATGSAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | 1414 | |
| | | | | |
| Db | 62 | AA | 9 | |
| | | | | |

```

1      RESULT 12
2      US-07-602-608-1
3      ; Sequence 1, Application US/07602608
4      ; Patent No. 5382524
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Desnick, Robert J.
7      ; APPLICANT: Bishop, David F.
8      ; APPLICANT: Ioannou, Yiannis A.
9      ; APPLICANT: Wang, Anne M.
10     ; TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
11     ; TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGLACTOSAMINIDASE
12     ; NUMBER OF SEQUENCES: 24
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: PENNIE & EDMONDS
15     ; STREET: 1155 Avenue of the Americas
16     ; CITY: New York
17     ; STATE: New York
18     ; COUNTRY: U.S.A.
19     ; ZIP: 10036
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Floppy disk
22     ; COMPUTER: IBM PC compatible
23     ; OPERATING SYSTEM: PC-DOS/MS-DOS
24     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: US/07/602,608
27     ; FILING DATE: 24-OCT-1990
28     ; CLASSIFICATION: 435
29     ; ATTORNEY/AGENT INFORMATION:
30     ; NAME: Cortuzzi, Laura A.
31     ; REGISTRATION NUMBER: 30,742

```

```
REFERENCE/DOCKET NUMBER: 6923-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 345..1580
US-07-602-608-1

Query Match
Best Local Similarity 62.3%; DB 2; Length 2158;
Matches 81; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1285 CTCTGAAATCATATGCTCAATCTAGACAGTCTTTCTCTAGTCCCTGTATTCAAATC 1344
    |||||
Db 2025 CACTGGAGTGAAGGTCACAAAGAGACCTTGCTCCCTCAGGTCACTAAACCTGTT 2084

QY 1345 CCAGTGTCTACATTCATTAATGCTATATGAAATCAAAAAAAAAAAAAAAAAAAAA 1404
    |||||
Db 2085 CTTTAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2144

QY 1405 AAAAAAAAAA 1414
Db 2145 AAAAAAAAAA 2154

RESULT 13
US-08-261-578-1
Sequence 1, Application US/08261578
Patent No. 5491075
GENERAL INFORMATION:
APPLICANT: Desnick, Robert J.
APPLICANT: Bishop, David P.
APPLICANT: Ioannou, Yiannis A.
APPLICANT: Wang, Anne M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGLACTOSAMINIDASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261.578
FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/602,608
FILING DATE: 24-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
```

```
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 345..1580
US-08-261-578-1

Query Match
Best Local Similarity 62.3%; DB 2; Length 2158;
Matches 81; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1285 CTCTGAAATCATATGCTCAATCTAGACAGTCTTTCTCTAGTCCCTGTATTCAAATC 1344
    |||||
Db 2025 CACTGGAGTGAAGGTCACAAAGAGACCTTGCTCCCTCAGGTCACTAAACCTGTT 2084

QY 1345 CCAGTGTCTACATTCATTAATGCTATATGAAATCAAAAAAAAAAAAAAAAAAAAA 1404
    |||||
Db 2085 CTTTAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2144

QY 1405 AAAAAAAAAA 1414
Db 2145 AAAAAAAAAA 2154

RESULT 14
US-09-722-971-9
Sequence 9, Application US/09722971
Patent No. 6599408
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Butler, Karla
APPLICANT: Fang, Yiwen
APPLICANT: Helentjaris, Tim
APPLICANT: Macool, Dan
TITLE OF INVENTION: Regulator of Sugar and Hormone Responses
FILE REFERENCE: BB1409 US NA
CURRENT APPLICATION NUMBER: US/09/722,971
CURRENT FILING DATE: 2000-11-27
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/169969
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
LENGTH: 1660
TYPE: DNA
ORGANISM: Zea mays
US-09-722-971-9

Query Match
Best Local Similarity 60.3%; DB 3; Length 1660;
Matches 85; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1274 TTATACATGCTCTGAAATCATATGCTCAATCTAGACAGTCTTTCTCTAGTCCCT 1333
    |||||
Db 1500 TTGGTCCACGCTTTGAAACCTTAGACTGTTCTTTGTGATCTTGCGGTGATTTGAT 1559

QY 1334 GTATTCAAATCCAGTCTCTACATTCATTAATAGCTATATGAATCAAAAAAAAA 1393
    |||||
Db 1560 TATTAACCTTACTTAGTACCTTGACCTCTGCACCTAAAAAAAAAAAAAAAAAAA 1619

QY 1394 AAAAAAAAAAAAAAAAAAAAAA 1414
    |||||
Db 1620 AAAAAAAAAAAAAAAAAAAAAA 1640

RESULT 15
US-08-631-097-8
Sequence 8, Application US/08631097
```

Patent No. 5968816
GENERAL INFORMATION:
APPLICANT: Kimchi, Adi
TITLE OF INVENTION: Tumor Suppressor Genes, and Use of Said Genes and Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wigman, Cohen, Leitner, & Myers, P.C.
STREET: 900 17th Street, N.W., Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,097
FILING DATE: 12-Apr-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11598
FILING DATE: 12-Oct-94
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Herbert
REGISTRATION NUMBER: 25,109
REFERENCE/DOCKET NUMBER: 0744.057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)463-7700
TELEFAX: (202)473-6915
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3829 base pair
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: not applicable
ORIGINAL SOURCE:
ORGANISM: homo sapiens
STRAIN: not applicable
INDIVIDUAL ISOLATE: not applicable
DEVELOPMENTAL STAGE: not applicable
HAPLOTYPE: not applicable
TISSUE TYPE: blood
CELL TYPE: leucocyte
CELL LINE: HeLa
ORGANELLE: not applicable
IMMEDIATE SOURCE:
LIBRARY: not applicable
CLONE: not applicable
POSITION IN GENOME:
CHROMOSOME/SEGMENT: not applicable
MAP POSITION: not applicable
UNITS: not applicable
FEATURE:
NAME/KEY: SEQ ID. NO:8 is the sequence
NAME/KEY: in claim 1(vi) starting at triplet in position 201-203
NAME/KEY: and ending at the triplet 3018-3020
LOCATION: not available
IDENTIFICATION METHOD: experiment-
IDENTIFICATION METHOD: in specification
OTHER INFORMATION: prevention of IFN- γ -induced
OTHER INFORMATION: programmed cell death
PUBLICATION INFORMATION: not available
US-08-631-097-8

Query Match 3.6%; Score 50.8; DB 2; Length 3829;
Best Local Similarity 74.4%; Pred. No. 0.011;

Matches 64; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 1328 TTCCCTGATTCAAAATCCAGTGTCTAACAATTCATTAATAAGCTATGAAATCAAAAA 1387
Db 3736 TGCCCTGATTTTATATATCTGATCTATCAATTAACATTTGTCATCTGAAAAA 3795
Qy 1388 AAAAAAAAAAAAAAAAAAAAAAAAAA 1413
Db 3796 AAAAAAAAAAAAAAAAAAAAAA 3821
Search completed: December 17, 2005, 13:37:32
Job time : 269.178 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 13:22:55 ; Search time 1300.57 Seconds
(without alignments)
8990.628 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 1414
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

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- 10: /cgn2_6/ptodaca/1/pubpna/us11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1414 | 100.0 | 1414 | 10 US-11-047-278-1 | Sequence 1, Appl1 |
| 2 | 1414 | 100.0 | 1454 | 6 US-10-133-937-58 | Sequence 58, Appl1 |
| 3 | 1414 | 100.0 | 1454 | 6 US-10-159-563-58 | Sequence 58, Appl1 |
| 4 | 1193.8 | 84.4 | 5540 | 3 US-09-918-715-176 | Sequence 176, App |
| 5 | 1193.8 | 84.4 | 5540 | 3 US-09-918-715-231 | Sequence 231, App |
| 6 | 1193.8 | 84.4 | 5540 | 6 US-10-301-822-198 | Sequence 198, App |
| 7 | 1193.8 | 84.4 | 5540 | 8 US-10-474-794-176 | Sequence 176, App |
| 8 | 1193.8 | 84.4 | 5540 | 9 US-10-474-794-231 | Sequence 231, App |
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ALIGNMENTS

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; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047, 278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970, 076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251, 481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1

Query Match      100.0%; Score 1414; DB 10; Length 1414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringer, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
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; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-159-563-58

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1201 AATTAATAAACAAGAAAGAAAGAAAGAAATCCACAGAAACAGATTAACCTAACACAGC 1260
Db 1241 AATTAATAAACAAGAAAGAAAGAAAGAAATCCACAGAAACAGATTAACCTAACACAGC 1300
Qy 1261 CCGTGCAAGTATTTTATCAATGCTGCTGAAAATCAATGCTCAATCTGACAGTCTTT 1320
Db 1301 CCGTGCAAGTATTTTATCAATGCTGAAAATCAATGCTCAATCTGACAGTCTTTT 1360
Qy 1321 CCTCTAGTCCCTGATTTCAATCCAGTGTCTAATCAATTAATAGCTATATGAAT 1380
Db 1361 CCTCTAGTCCCTGATTTCAATCCAGTGTCTAATCAATTAATAGCTATATGAAT 1420
Qy 1381 CAAAAAATAAAAAAAAAAAAAAAAAAAAAA 1414
Db 1421 CAAAAAATAAAAAAAAAAAAAAAAAAAAAA 1454

RESULT 4
US-09-918-715-176
; Sequence 176, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-176

Query Match 84.4%; Score 1193.8; DB 3; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACCCGCGAGAGAGGCGCCGCGATGCGCGCTCCCTGAGGTCGTGCGAGTTCGCG 60
Db 41 AGGACCCGCGAGAGAGGCGCCGCGATGCGCGCTCCCTGAGGTCGTGCGAGTTCGCG 100

Qy 61 AGCGTGGAGAGAGCGGACCCCTGCTCTCCCGGGCTGCGGGCCATGCGCACCGGCGAGCG 120
Db 101 AGCGTGGAGAGAGCGGACCCCTGCTCTCCCGGGCTGCGGGCCATGCGCACCGGCGAGCG 160
Qy 121 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGCACTCTGTGTCTATCTGGCC 180
Db 161 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGCACTCTGTGTCTATCTGGCC 220
Qy 181 CGGGCAAGGGGGAGCGCAGGAGGATGGGGGTCCAGCTGCTACGGCGGATTTGACCTGTA 240
Db 221 CGGGCAAGGGGGAGCGCAGGAGGATGGGGGTCCAGCTGCTACGGCGGATTTGACCTGTA 280
Qy 241 CTTCAATTTTGGACAATGAGAAAGTGTGCTGACCACTGGAATGAATCTATTAATCTTGT 300
Db 281 CTTCAATTTTGGACAATGAGAAAGTGTGCTGACCACTGGAATGAATCTATTAATCTTGT 340
Qy 301 GGAACAGTTGGCTCAAAATTCATGACGCCACAGTTGAGAAATGCTTTATGTTTCTC 360
Db 341 GGAACAGTTGGCTCAAAATTCATGACGCCACAGTTGAGAAATGCTTTATGTTTCTC 400
Qy 361 CACCGAGAGAACACCTTAATGAACTGACAGAAACAGAGAACAAATCCGCAAGGCT 420
Db 401 CACCGAGAGAACACCTTAATGAACTGACAGAGAACAGAGAACAAATCCGCAAGGCT 460
Qy 421 AGAAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTACATGCAATGAAGATTGAAAG 480
Db 461 AGAAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTACATGCAATGAAGATTGAAAG 520
Qy 481 GGCAGTGAAGCATTTATTAATGAAAACAGACAGAGGTACAGAGACACCGCTCATAT 540
Db 521 GGCAGTGAAGCATTTATTAATGAAAACAGACAGAGGTACAGAGACACCGCTCATAT 580
Qy 541 TGCTTGAAGTGAAGAACTCCATGAAAGATCTCTTTTCTAATGAGAGGAGGCTAA 600
Db 581 TGCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTAATGAGAGGAGGCTAA 640
Qy 601 TAGGCTCGAGATCTTGGTGCATTTGTTTACTGTGTGTGTAAGAAATTTCAATGAGAC 660
Db 641 TAGGCTCGAGATCTTGGTGCATTTGTTTACTGTGTGTGTAAGAAATTTCAATGAGAC 700
Qy 661 ACAGCTGGCCGGATTCGGAGACATGATGATGTTTCCCGTAATGACGGCTTCA 720
Db 701 ACAGCTGGCCGGATTCGGAGACATGATGATGTTTCCCGTAATGACGGCTTCA 760
Qy 721 GGCTCGAAGGCATCATCTCAATTTTGAAGAGCTGACATGGAATTTAGACAGC 780
Db 761 GGCTCGAAGGCATCATCTCAATTTTGAAGAGCTGACATGGAATTTAGACAGC 820
Qy 781 TGAACCATCAACATATGTCAGAGAGTCAATTTCAAGTTGTCTGAGAGAAACGGCTT 840
Db 821 TGAACCATCAACATATGTCAGAGAGTCAATTTCAAGTTGTCTGAGAGAAACGGCTT 880
Qy 841 CCGACATGCCCGAACGTGAGACAGGTCTCTGACGCTTCAAGATCAATGATCTGGTCA 900
Db 881 CCGACATGCCCGAACGTGAGACAGGTCTCTGACGCTTCAAGATCAATGATCTGGTCA 940
Qy 901 ACTCAATGAGAGCCCTTTCTGTGGAAGACCTATTATCAATGTCAGGCGCTATCTT 960
Db 941 ACTCAATGAGAGCCCTTTCTGTGGAAGATCTATTATCAATGTCAGGCGCTATCTT 1000
Qy 961 AAAAGAGTGGCATGAAGCTGCACTCCAGGTCAAGATGAAGAGTGGCTCTCTTTAT 1020
Db 1001 AAAAGAGTGGCATGAAGCTGCACTCCAGGTCAAGATGAAGAGTGGCTCTCTTTAT 1060
Qy 1021 CTCAGTTCTGTATCATATCAACACACATGTTCTGACGGTTCATCTTGCCATCGC 1080
Db 1061 CTCAGTTCTGTATCATATCAACACACATGTTCTGACGGTTCATCTTGCCATCGC 1120
Qy 1081 CCTGCTGATCCCTGCTCCCTGCTCCAGCTGCTCCCTGCTCCCTGCTCCCTGCTCC 1140
Db 1121 CCTGCTGATCCCTGCTCCCTGCTCCAGCTGCTCCCTGCTCCCTGCTCCCTGCTCC 1180

ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)...(1838)
US-10-301-822-198

Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 AAGACCCGAGAGAGAGGCGCCGCGATGCGCGCTCCCTGAGAGGTGCGGAGTTGCGCG 60
DB 41 AAGACCCGAGAGAGAGGCGCCGCGATGCGCGCTCCCTGAGAGGTGCGGAGTTGCGCG 100
QY 61 AAGCGTGGAGAGAGCGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 120
DB 101 AAGCGTGGAGAGAGCGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 160
QY 121 AAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACTCTGCTCATCTGCGC 180
DB 161 AAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACTCTGCTCATCTGCGC 220
QY 181 CGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTCAAGCGGATTTGACTGTG 240
DB 221 CGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTCAAGCGGATTTGACTGTG 280
QY 241 CTTGATTTTGAACAATCAGAAAGTGTGCTGACCACTGGAATGAATCTAATTCTTGT 300
DB 281 CTTGATTTTGAACAATCAGAAAGTGTGCTGACCACTGGAATGAATCTAATTCTTGT 340
QY 301 GGAACGTTGGCTCACAAATTCATCAGCCCAAGTTGAAGATGCTTTATGTTTCTC 360
DB 341 GGAACGTTGGCTCACAAATTCATCAGCCCAAGTTGAAGATGCTTTATGTTTCTC 400
QY 361 CACCCGAGAGAACCTTAATGAATGACAGAAAGCAGAAACAAATCCGTCAAGCCT 420
DB 401 CACCCGAGAGAACCTTAATGAATGACAGAAAGCAGAAACAAATCCGTCAAGCCT 460
QY 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATCATGAAGATTTGAAG 480
DB 461 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATCATGAAGATTTGAAG 520
QY 481 GGCAGTAGAGCAGATTTATTAAGAAACAGACAAAGGTAACAGACAGCCAGCCTCAT 540
DB 521 GGCAGTAGAGCAGATTTATTAAGAAACAGACAAAGGTAACAGACAGCCAGCCTCAT 580
QY 541 TGTCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTATTCAGAGAGGAGCTTA 600
DB 581 TGTCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTATTCAGAGAGGAGCTTA 640
QY 601 TAGGTCTGAGATCTTGTGCAATGTTTACTGTGTGTGTAAGATTTCAATGAGAC 660
DB 641 TAGGTCTGAGATCTTGTGCAATGTTTACTGTGTGTGTAAGATTTCAATGAGAC 700
QY 661 AAGAGTGGCCCGGATTTGCGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTCA 720
DB 701 AAGAGTGGCCCGGATTTGCGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTCA 760
QY 721 GGTCTGCAAGGATCATCTCAATTTTGAAGAACTCTGATGTAAGATTTTACAGAC 780
DB 761 GGTCTGCAAGGATCATCTCAATTTTGAAGAACTCTGATGTAAGATTTTACAGAC 820
QY 781 TGAACCATCAACCATATGTGACAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTT 840
DB 821 TGAACCATCAACCATATGTGACAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTT 880
QY 841 CCGACATGCCCCGCAAGTGGACAGGGTCTCTGACAGCTTCAGATCAATGACTCGGTCA 900
DB 881 CCGACATGCCCCGCAAGTGGACAGGGTCTCTGACAGCTTCAGATCAATGACTCGGTCA 940
QY 901 ACTCAATGAGAGCCCTTTTCTGTGAGAGACATTTATTTCTGTGTCCAGCGCTTCTT 960
DB 941 ACTCAATGAGAGCCCTTTTCTGTGAGAGATTTATTTTACTGTGTCCAGCGCTTCTT 1000
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QY 961 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAACGATGGCCTCTTTTAT 1020
DB 1001 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAACGATGGCCTCTTTTAT 1060
QY 1021 CTCGAGTTCTGATCATATACCAACACACACTGTTCTGACGGTTCATCTCGCCATCGC 1080
DB 1061 CTCGAGTTCTGATCATATACCAACACACACTGTTCTGACGGTTCATCTCGCCATCGC 1120
QY 1081 CCTGAGATCTGTTCTGCTCTGCTCTGAGCCCTGAGCTCTCTGAGGTTCTGAGCCCTCTG 1140
DB 1121 CCTGAGATCTGTTCTGCTCTGCTCTGAGCCCTGAGCTCTCTGAGGTTCTGAGCCCTCTG 1180
QY 1141 CTGCACTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAGAGATGAGAGAAA 1197
DB 1181 CTGCACTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAGAGATGAGAGAAA 1237
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RESULT 7
US-10-474-794-176
; Sequence 176, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelsstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PaedSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-176
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Query Match 84.4%; Score 1193.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 AAGACCCGAGAGAGAGGCGCCGCGATGCGCGCTCCCTGAGAGGTGCGGAGTTGCGCG 60
DB 41 AAGACCCGAGAGAGAGGCGCCGCGATGCGCGCTCCCTGAGAGGTGCGGAGTTGCGCG 100
QY 61 AAGCGTGGAGAGAGCGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 120
DB 101 AAGCGTGGAGAGAGCGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 160
QY 121 AAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACTCTGAGTCTCATCTGCGC 180
DB 161 AAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACTCTGAGTCTCATCTGCGC 220
QY 181 CGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTCAAGCGGATTTGACTGTG 240
DB 221 CGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTCAAGCGGATTTGACTGTG 280
QY 241 CTTGATTTTGAACAATCAGAAAGTGTGACCACTGGAATGAATCTAATTCTTGT 300
DB 281 CTTGATTTTGAACAATCAGAAAGTGTGACCACTGGAATGAATCTAATTCTTGT 340
QY 301 GGAACGTTGGCTCAACAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 360
DB 341 GGAACGTTGGCTCAACAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 400
QY 361 CACCCGAGAGAACCTTAATGAATGACAGAGACAGAGAACAAATCCGTCAAGCCT 420
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Db 401 CACCCGAGAACACTTAATGAAACAGAGAACAGAACAAATCCGTCAGGCT 460
Qy 421 AGAAGAACTCAGAAAATTCTGCCAGAGAGACCTTAATGATGATAGAGATTGAAAG 480
Db 461 AGAAGAACTCAGAAAATTCTGCCAGAGAGAGACCTTAATGATGATAGAGATTGAAAG 520
Qy 481 GGCAGAGAGACAGATTATATGAAAACAGACAGAGGATACAGGACAGCCGATCAT 540
Db 521 GGCAGAGAGAGATTATATGAAAACAGACAGAGGATACAGGACAGCCGATCAT 580
Qy 541 TGCCTTGATGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAGAGAGGCTAA 600
Db 581 TGCTTTGATGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAGAGAGGCTAA 640
Qy 601 TAGGCTCGAGATTTGGTGCATTTGTTTACTGTGTGGTGTGAAAGATTCAATGAGC 660
Db 641 TAGGCTCGAGATTTGGTGCATTTGTTTACTGTGTGGTGTGAAAGATTCAATGAGC 700
Qy 661 ACAGCTGGCCGGGATGGGACAGTAAGATCATGTGTTCCGTTGAATGACGGCTTCA 720
Db 701 ACAGCTGGCCGGGATGGGACAGTAAGATCATGTGTTCCGTTGAATGACGGCTTCA 760
Qy 721 GGCCTGCAAGGATCATCACTCAATTTTGAAGAGTCCGATCGAAATTTAGCAGC 780
Db 761 GGCCTGCAAGGATCATCACTCAATTTTGAAGAGTCCGATCGAAATTTAGCAGC 820
Qy 781 TGAACATCCACCATATGTGAGAGAGTCAATTTCAAGTTGCTGTGAGAGAAAGGCTT 840
Db 821 TGAACATCCACCATATGTGAGAGAGTCAATTTCAAGTTGCTGTGAGAGAAAGGCTT 880
Qy 841 CCGACATGCCCGGACAGTGGACAGGGTCTCTGAGCTTCAAGATCAATGACTGGCTAC 900
Db 881 CCGACATGCCCGGACAGTGGACAGGGTCTCTGAGCTTCAAGATCAATGACTGGCTAC 940
Qy 901 ACTCAATGAGAGCCCTTTTCTGTGAAAGACCTTATTTACTGTGCAGGCTATCTT 960
Db 941 ACTCAATGAGAGCCCTTTTCTGTGAAAGACTTATTTACTGTGCAGGCTATCTT 1000
Qy 961 AAAAGAGTTGGCATGAAAGCTGCACTCCAGCTCAGATGAAAGATGAGCTCTTTTAT 1020
Db 1001 AAAAGAGTTGGCATGAAAGCTGCACTCCAGCTCAGATGAAAGATGAGCTCTTTTAT 1060
Qy 1021 CTCAGTTCTGTATCATCAACACACACACACTGTTTCAAGGTTCCATCCGCGCATGCG 1080
Db 1061 CTCAGTTCTGTATCATCAACACACACACACTGTTTCAAGGTTCCATCCGCGCATGCG 1120
Qy 1081 CCTGCTATCTGTCTCTGCTCTAGGCTGAGCTCTCTCTGTGTGTTCTGAGCCCTCTG 1140
Db 1121 CCTGCTATCTGTCTCTGCTCTAGGCTGAGCTCTCTCTGTGTGTTCTGAGCCCTCTG 1180
Qy 1141 CTGCACTGTGATTATCAAGAGAGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1197
Db 1181 CTGCACTGTGATTATCAAGAGAGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1237

RESULT 8

US-10-474-794-231
Sequence 231, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00179
CURRENT APPLICATION NUMBER: US/10/474,794
PRIORITY FILING DATE: 2003-10-14
PRIORITY FILING DATE: 2001-04-11
PRIORITY FILING DATE: 2001-04-11
PRIORITY FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-474-794-231
Query Match 84.4%; Score 1193.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACCCGCGAGAGAGGCGCCGCGATGCGCTGCTGAGGATGAGGATGAGGATGAGG 60
Db 41 AGGACCCGCGAGAGAGGCGCCGCGATGCGCTGCTGAGGATGAGGATGAGGATGAGG 100
Qy 61 AGCGTGGAGAGAGAGGCGGCTCTCTCCCGGGCTGCGGGCCATGAGCCAGCGGAGCG 120
Db 101 AGCGTGGAGAGAGAGGCGGCTCTCTCCCGGGCTGCGGGCCATGAGCCAGCGGAGCG 160
Qy 121 GAGAGCCCTCGGATGCGGCTTCCAGTGGCTCTCTTGGCACTCTGATGCTCATGCGC 180
Db 161 GAGAGCCCTCGGATGCGGCTTCCAGTGGCTCTCTTGGCACTCTGATGCTCATGCGC 220
Qy 181 CCGGCAAGGGGAGCGAGAGAGATGGGGTCCAGCTGCTAGCGCGGATTTGACCTGTA 240
Db 221 CCGGCAAGGGGAGCGAGAGAGATGGGGTCCAGCTGCTAGCGCGGATTTGACCTGTA 280
Qy 241 CTTCATTTTGGACAAATCAGAAAGTGTGTCACCACTGGAATGAAATCTATTAATTGT 300
Db 281 CTTCATTTTGGACAAATCAGAAAGTGTGTCACCACTGGAATGAAATCTATTAATTGT 340
Qy 301 GGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 360
Db 341 GGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 400
Qy 361 CACCCGAGAACCACTTATGAACTGACAGAAAGACAGAAACAAATCCGTCAGGCT 420
Db 401 CACCCGAGAACCACTTATGAACTGACAGAAAGACAGAAACAAATCCGTCAGGCT 460
Qy 421 AGAAGAACTCAGAAAATTCTGCCAGAGAGACCTTAATGATGATAGAGATTGAAAG 480
Db 461 AGAAGAACTCAGAAAATTCTGCCAGAGAGACCTTAATGATGATAGAGATTGAAAG 520
Qy 481 GGCAGAGAGACAGATTATATGAAAACAGACAGAGGATACAGGACAGCCGATCAT 540
Db 521 GGCAGAGAGACAGATTATATGAAAACAGACAGAGGATACAGGACAGCCGATCAT 580
Qy 541 TGCCTTGATGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAGAGAGGCTAA 600
Db 581 TGCCTTGATGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAGAGAGGCTAA 640
Qy 601 TAGGCTCGAGATTTGGTGCATTTGTTTACTGTGTGGTGTGAAAGATTCAATGAGC 660
Db 641 TAGGCTCGAGATTTGGTGCATTTGTTTACTGTGTGGTGTGAAAGATTCAATGAGC 700
Qy 661 ACAGCTGGCCGGGATGGGACAGTAAGATCATGTGTTCCGTTGAATGACGGCTTCA 720
Db 701 ACAGCTGGCCGGGATGGGACAGTAAGATCATGTGTTCCGTTGAATGACGGCTTCA 760
Qy 721 GGCCTGCAAGGATCATCACTCAATTTTGAAGAGTCCGATCGAAATTTAGCAGC 780
Db 761 GGCCTGCAAGGATCATCACTCAATTTTGAAGAGTCCGATCGAAATTTAGCAGC 820
Qy 781 TGAACATCCACCATATGTGAGAGAGTCAATTTCAAGTTGCTGTGAGAGAAAGGCTT 840
Db 821 TGAACATCCACCATATGTGAGAGAGTCAATTTCAAGTTGCTGTGAGAGAAAGGCTT 880
Qy 841 CCGACATGCCCGGACAGTGGACAGGGTCTCTGAGCTTCAAGATCAATGACTGGCTAC 900
Db 881 CCGACATGCCCGGACAGTGGACAGGGTCTCTGAGCTTCAAGATCAATGACTGGCTAC 940
Qy 901 ACTCAATGAGAGCCCTTTTCTGTGAAAGACCTTATTTACTGTGTCAGGCTATCTT 960

| | | | |
|----|------|--|------|
| Db | 941 | ACTCAATGAGAAAGCCCTTTTCGTGGAAGATACATTATTACGTGTGTCCAGAGCCATCTT | 1000 |
| Qy | 961 | AAAAGAGTTGGCATGAAGCTGCACCTCCAGTCAAGATGAACGATGGCCCTCTCTTTAT | 1020 |
| Db | 1001 | AAAAGAGTTGGCATGAAGAGCTGCACCTCCAGTCAAGATGAACGATGGCCCTCTCTTTAT | 1060 |
| Qy | 1021 | CTCCAGTTCGTGCATCATCACCAACAACGTGTTCTAGACGGTTCATCTCGGCATGCG | 1080 |
| Db | 1061 | CTCCAGTTCGTGCATCATCACCAACAACGTGTTCTAGACGGTTCATCTCGGCATGCG | 1120 |
| Qy | 1081 | CTGCTGATCTCTGTCCTGCTCTGAGCCCTGCTCTCTCTGATGGTTCGAGCCCTCTG | 1140 |
| Db | 1121 | CTGCTGATCTCTGTCCTGCTCTGAGCCCTGCTCTCTCTGATGGTTCGAGCCCTCTG | 1180 |
| Qy | 1141 | CTGCACCTGTATTATCAGAGAGGTCCCTCCACCCCTGCGCAGAGAGATGAGGAAAA | 1197 |
| Db | 1181 | CTGCACCTGTATTATCAGAGAGGTCCCTCCACCCCTGCGCAGAGAGATGAGGAAAA | 1237 |

```

RESULT 9
US-10-979-159-176
; Sequence 176, Application US/10979159
; Publication No. US2005042138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918, 715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-979-159-176

```

| | | | | |
|----------------------------|--------|---------------|-----------|--------------|
| Query Match | 84.4%; | Score 1193.8; | DB 9; | Length 5540; |
| Best Local Similarity | 99.8%; | Pred. No. 0; | | |
| Matches 1195; Conservative | 0; | Mismatches 2; | Indels 0; | Gaps 0; |

QY 1 AGGACCCCGAGAGAGGGCCCGGATGGCGGTCCCTGAGGGGTGTGGCAGATTCCGGG 60

Db 41 AGGACCCCGAGAGAGGGCCCGGATGGCGGTCCCTGAGGGGTGTGGCAGATTCCGGG 100

QY 61 AGCGTGGGAAAGGAGCGGACCTGTCTCTCCCGGAGTGCAGGCAAGCCGAGGACG 120

Db 101 AGCGTGGGAAAGGAGCGGACCTGTCTCTCCCGGAGTGCAGGCAAGCCGAGGACG 160

QY 121 GAGAGCCCTCGGCATTCGGCTTCCATGGCTCTCTTTGGCACTGTGTGCTCATTTGGGC 180

Db 161 GAGAGCCCTCGGCATTCGGCTTCCATGGCTCTCTTTGGCACTGTGTGCTCATTTGGGC 220

QY 181 CGGGCAAGGGGAGCGCAGGAGAGATGGGGGTCCAGCTGTCTACGCGGATTTGACCTGTA 240

Db 221 CGGGCAAGGGGAGCGCAGGAGAGATGGGGGTCCAGCTGTCTACGCGGATTTGACCTGTA 280

QY 241 CTTCAATTTTGGCAAAATCAGAAAGTGTGTGTGCACCATGTGAATGAATCTAATTAATTGT 300

Db 281 CTTCAATTTTGGCAAAATCAGAAAGTGTGTGTGCACCATGTGAATGAATCTAATTAATTGT 340

QY 301 GGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATGTCTTATATGTTTCTC 360

| | | | |
|----|------|--|------|
| Db | 341 | GGAAcAGTGGCTCAcAAATTCATCAcGCCCAAGTGAAGATGTCCTTTATGTTTCTC | 400 |
| QY | 361 | CAcCCGAGGAACAACCTTTATGAACTGACAGAAAGACAAATTCCTGCAAGGCT | 420 |
| Db | 401 | CACCCGAGGAACAACCTTTATGAACTGACAGAAAGACAAATTCCTGCAAGGCT | 460 |
| QY | 421 | AGAAGAACTCCAGAAAGTTCTGCCAGAGGAGACACTTACATGCATAGAGATTTGAAAG | 480 |
| Db | 461 | AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCATAGAGATTTGAAAG | 520 |
| QY | 481 | GGCCAGTGAAGATTTATTATGAAAACAGCAAGGGTACAGACACGCTCATCAT | 540 |
| Db | 521 | GGCCAGTGAAGATTTATTATGAAAACAGCAAGGGTACAGACACGCTCATCAT | 580 |
| QY | 541 | TGCTTTACATGATGGAACCTCCATGAAAGTCTTTTTCATTCAGAGAGGGGCTAA | 600 |
| Db | 581 | TGCTTTACATGATGGAACCTCCATGAAAGTCTTTTTCATTCAGAGAGGGGCTAA | 640 |
| QY | 601 | TAGGTCCTGAGATCTTGATGCAATTTGTTTACTGTGTGTGTGAAGATTTCAATGAGAC | 660 |
| Db | 641 | TAGGTCCTGAGATCTTGATGCAATTTGTTTACTGTGTGTGAAGATTTCAATGAGAC | 700 |
| QY | 661 | ACAGCTGGCCCGGATTTGCCGACAGTAAAGATCATGTGTTTCCGTGAATGACGGCTTCA | 720 |
| Db | 701 | ACAGCTGGCCCGGATTTGCCGACAGTAAAGATCATGTGTTTCCGTGAATGACGGCTTCA | 760 |
| QY | 721 | GGCTCTGCAAGGCAATCATCCACATTTTGAAGAAGTCCGATCGAAATTTCTAGCAGC | 780 |
| Db | 761 | GGCTCTGCAAGGCAATCATCCACATTTTGAAGAAGTCCGATCGAAATTTCTAGCAGC | 820 |
| QY | 781 | TGAACATCCACCATATGTGACAGAGAGTCATTTCAAGTTGTGCTGAGAGAAACGGCTT | 840 |
| Db | 821 | TGAACATCCACCATATGTGACAGAGAGTCATTTCAAGTTGTGCTGAGAGAAACGGCTT | 880 |
| QY | 841 | CCGACATGCCCCGCAACGTGACAGGGTCTCTGACGTTCAAGATTCATGTGCTGAC | 900 |
| Db | 881 | CCGACATGCCCCGCAACGTGACAGGGTCTCTGACGTTCAAGATTCATGTGCTGAC | 940 |
| QY | 901 | ACTCAATGAGAAGCCCTTTTCTGTGAAAGACACTTATTTACTGTGCAGGCGCTATCTT | 960 |
| Db | 941 | ACTCAATGAGAAGCCCTTTTCTGTGAAAGATCTTATTTACTGTGTCAAGGCGCTATCTT | 1000 |
| QY | 961 | AAAAAGAAATTGGCATGAAGCTGCACTCCAGCTCAGCATGAACGATGGCTCTCTTTTAT | 1020 |
| Db | 1001 | AAAAAGAAATTGGCATGAAGCTGCACTCCAGCTCAGCATGAACGATGGCTCTCTTTTAT | 1060 |
| QY | 1021 | CTCAGATTCGTCAATCAATCAACAACAACAACACTGTTCTGAAGGTTCAATCCTGGGCATGCG | 1080 |
| Db | 1061 | CTCAGATTCGTCAATCAATCAACAACAACAACAACACTGTTCTGAAGGTTCAATCCTGGGCATGCG | 1120 |
| QY | 1081 | CTGTGCTGATCTGTGTTCTGTCTCTTAGGCTTGAGCTTGCTCTCTGTGATGTTCTTGACCCTCTG | 1140 |
| Db | 1121 | CTGTGCTGATCTGTGTTCTGTCTCTTAGGCTTGAGCTTGCTCTCTGTGATGTTCTTGACCCTCTG | 1180 |
| QY | 1141 | CTGCACTGTGATTTCAAGAAGGTCTCTCAACCCCTGCGCAGAGAGATGAGAAAA | 1197 |
| Db | 1181 | CTGCACTGTGATTTCAAGAAGGTCTCTCAACCCCTGCGCAGAGAGATGAGAAAA | 1237 |

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/ RESULT 10
/ US-10-979-159-231
/ Sequence 231, Application US/10979159
/ Publication No. US20050142138a1
/ GENERAL INFORMATION:
/ APPLICANT: Brad St. Croix
/ APPLICANT: Bert Vogelstein
/ APPLICANT: Kenneth Kinzler
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00134
/ CURRENT APPLICATION NUMBER: US/10/979,159
/ CURRENT FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US/09/918,715
/ PRIOR FILING DATE: 2001-08-01

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; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-979-159-231

Query Match      84.4%; Score 1193.8; DB 9; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGAGAGGCGCGGAGTGGGCGTCCCTGAGGGTCTGAGGAGTTGGCGG 60
DB 41 AGGACCCGCGAGAGAGGCGCGGAGTGGGCGTCCCTGAGGGTCTGAGGAGTTGGCGG 100
QY 61 AGGCTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGGAGCG 120
DB 101 AGGCTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGGAGCG 160
QY 121 GAGAGCCCTCGGAGTCGGCTTCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 180
DB 161 GAGAGCCCTCGGAGTCGGCTTCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 220
QY 181 CGGGCAAGGGGAGCGGAGGAGATGGGGGTCCAGCCTGCTAGCGGAGTTTGAACCTGTA 240
DB 221 CGGGCAAGGGGAGCGGAGGAGATGGGGGTCCAGCCTGCTAGCGGAGTTTGAACCTGTA 280
QY 241 CTTCATTTTGGACAAATCAGAAAGTGTGTGTCACACCTGAGATGAAATCTATTACTTTGT 300
DB 281 CTTCATTTTGGACAAATCAGAAAGTGTGTGTCACACCTGAGATGAAATCTATTACTTTGT 340
QY 301 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCTTTATTTGTTTCTC 360
DB 341 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCTTTATTTGTTTCTC 400
QY 361 CACCCGAGGAAACAACTTAATGAAACAGAGAAAGAGAAACAAATCCGTCAAGGCTT 420
DB 401 CACCCGAGGAAACAACTTAATGAAACAGAGAAAGAGAAACAAATCCGTCAAGGCTT 460
QY 421 AGAAGAACTCAGAAAGTTCTGCGAGAGAGACACTTAATGATGAGATTTGAAG 480
DB 461 AGAAGAACTCAGAAAGTTCTGCGAGAGAGACACTTAATGATGAGATTTGAAG 520
QY 481 GGGCAGTGAGCAGATTTATATGAAAACAGCAAGGGTACAGGACAGCGCTCATCAT 540
DB 521 GGGCAGTGAGCAGATTTATATGAAAACAGCAAGGGTACAGGACAGCGCTCATCAT 580
QY 541 TGCCTTACGTATGAGAAATCTCCATGAAAGTCTCTTTTCTATTCAAGAGGGAGCTAA 600
DB 581 TGCCTTACGTATGAGAAATCTCCATGAAAGTCTCTTTTCTATTCAAGAGGGAGCTAA 640
QY 601 TAGGCTCGAGATCTTGATGCAATTTGTTTACTGTGTGTGTAAGATTTCAATGAGAC 660
DB 641 TAGGCTCGAGATCTTGATGCAATTTGTTTACTGTGTGTGTAAGATTTCAATGAGAC 700
QY 661 ACAGCTGGCCCGGATTCGGAACAGTAAAGATCATGTGTTTCCGCTGAATGACGGCTTCA 720
DB 701 ACAGCTGGCCCGGATTCGGAACAGTAAAGATCATGTGTTTCCGCTGAATGACGGCTTCA 760
QY 721 GGGCTTCGAAAGGATCATCTCAATTTTGAAGAAATCCGTCATTCGAAATTTCAAGAGC 780
DB 761 GGGCTTCGAAAGGATCATCTCAATTTTGAAGAAATCCGTCATTCGAAATTTCAAGAGC 820
QY 781 TGAACATTCACATATGTGAGAGAGATCATTTCAAGTTGTCTGTGAGAGAAACGGCTT 840
DB 821 TGAACATTCACATATGTGAGAGAGATCATTTCAAGTTGTCTGTGAGAGAAACGGCTT 880
```

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QY 841 CGGACATGCCCCGCAAGTGGAGAGGCTCTCTGACACTTCAAGATCATGACTCGGTAC 900
DB 881 CGGACATGCCCCGCAAGTGGAGAGGCTCTCTGACACTTCAAGATCATGACTCGGTAC 940
QY 901 ACTCAATGAGAAAGCCCTTTTCTGTGAGAGACATTATTTACTGTGTCCAGCGCTATCTT 960
DB 941 ACTCAATGAGAAAGCCCTTTTCTGTGAGAGATTTATTTACTGTGTCCAGCGCTATCTT 1000
QY 961 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAAGAGTGGCTCTTTTAT 1020
DB 1001 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAAGAGTGGCTCTTTTAT 1060
QY 1021 CTCGACTGTCATCATATACACACACACACTGTTTGAAGGTTCCATCCCTGAGCATGCG 1080
DB 1061 CTCGACTGTCATCATATACACACACACTGTTTGAAGGTTCCATCTGAGCATGCG 1120
QY 1081 CCGTGTGATCTGTTCTGCTCTCTAGCCCTGAGCTCTCTCTGTGTGTCTGAGCCCTCTG 1140
DB 1121 CCGTGTGATCTGTTCTGCTCTCTAGCCCTGAGCTCTCTCTGTGTGTCTGAGCCCTCTG 1180
QY 1141 CTGCACTGTGATTTATCAAGAGGTCCTTCAACCCCTGCGAGAGAGTGAAGAAA 1197
DB 1181 CTGCACTGTGATTTATCAAGAGGTCCTTCAACCCCTGCGAGAGAGTGAAGAAA 1237

RESULT 11
US-11-047-278-5
; Sequence 5, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31/970,076
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)..(1835)
US-11-047-278-5

Query Match      84.4%; Score 1193.8; DB 10; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGAGAGGCGCGGATGGGCGTCCCTGAGGGTCTGAGGAGTTGGCGG 60
DB 41 AGGACCCGCGAGAGAGGCGCGGATGGGCGTCCCTGAGGGTCTGAGGAGTTGGCGG 100
QY 61 AGGCTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGGAGCG 120
DB 101 AGGCTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGGAGCG 160
QY 121 GAGAGCCCTCGGAGTCGGCTTCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 180
DB 161 GAGAGCCCTCGGAGTCGGCTTCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 220
QY 181 CGGGCAAGGGGAGCGGAGGAGATGGGGGTCCAGCCTGCTAGCGGAGTTTGAACCTGTA 240
DB 221 CGGGCAAGGGGAGCGGAGGAGATGGGGGTCCAGCCTGCTAGCGGAGTTTGAACCTGTA 280
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OY 241 CTTCAATTTTGA CAAATCAGAGTGTGTCACCACTGGAATGAATCTATTCTTGT 300
| | | | |
DB 281 CTTCAATTTTGA CAAATCAGAGTGTGTCACCACTGGAATGAATCTATTCTTGT 340
OY 301 GGAACGTTGGCTCACAATTTCACTGACCCACAGTTGAGATGTCTTTATGTTTTCTC 360
| | | | |
DB 341 GGAACGTTGGCTCACAATTTCACTGACCCACAGTTGAGATGTCTTTATGTTTTCTC 400
OY 361 CACCCGAGGAACAACCTTAATGAAATGACAGAAACAGAAACAAATCCGTCAAGGCT 420
| | | | |
DB 401 CACCCGAGGAACAACCTTAATGAAATGACAGAAACAGAAACAAATCCGTCAAGGCT 460
OY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATGATGAAGATTTGAAG 480
| | | | |
DB 461 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATGATGAAGATTTGAAG 520
OY 481 GGCCAGTGAAGCAGATTTATTTATGAAAACAGACAGAGGTAACAGACACCGCTCATCAT 540
| | | | |
DB 521 GGCCAGTGAAGCAGATTTATTTATGAAAACAGACAGAGGTAACAGACACCGCTCATCAT 580
OY 541 TGCCTTGAAGTGAAGTCAATGAAATCTCTTTTCTATTCTAGAGAGGAGCTTA 600
| | | | |
DB 581 TGCCTTGAAGTGAAGTCAATGAAATCTCTTTTCTATTCTAGAGAGGAGCTTA 640
OY 601 TAGGTCTGAGATCTTGTCGCAATGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 660
| | | | |
DB 641 TAGGTCTGAGATCTTGTCGCAATGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 700
OY 661 ACAAGTGGCCCGGATTCGGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 720
| | | | |
DB 701 ACAAGTGGCCCGGATTCGGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 760
OY 721 GGCTCGAAGGATCATCATCAATTTTGAAGAACTCTGTCATGAAATTTAGACAG 780
| | | | |
DB 761 GGCTCGAAGGATCATCATCAATTTTGAAGAACTCTGTCATGAAATTTAGACAG 820
OY 781 TGAACCATCCACCATATGTCAGAGAGATCATTTCAAGTTGTCTGAGAGAAACGGCTT 840
| | | | |
DB 821 TGAACCATCCACCATATGTCAGAGAGATCATTTCAAGTTGTCTGAGAGAAACGGCTT 880
OY 841 CCGACATGCCCGGACAGTGAACAGGTCCTCTGACGCTTCAGATCAATGATCTCGGTCA 900
| | | | |
DB 881 CCGACATGCCCGGACAGTGAACAGGTCCTCTGACGCTTCAGATCAATGATCTCGGTCA 940
OY 901 ACTCAATGAAAGCCCTTTTCTGTGAAAGACATTTATTTATGTCGACGCGCTATCTT 960
| | | | |
DB 941 ACTCAATGAAAGCCCTTTTCTGTGAAAGATTTATTTATGTCGACGCGCTATCTT 1000
OY 961 AAAAAGATTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAGATGCGCTCTTTTAT 1020
| | | | |
DB 1001 AAAAAGATTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAGATGCGCTCTTTTAT 1060
OY 1021 CTCACATTTCTGATCATCATCAACCAACAACATGTTTCTGACGGTTCATCTCGGCATCG 1080
| | | | |
DB 1061 CTCACATTTCTGATCATCATCAACCAACAACATGTTTCTGACGGTTCATCTCGGCATCG 1120
OY 1081 CCGTCGATCTCTGTCCTGCTAGCCCTGAGCTCTCTCTGCTGCTGCTGCTGCTGCTG 1140
| | | | |
DB 1121 CCGTCGATCTCTGTCCTGCTAGCCCTGAGCTCTCTCTGCTGCTGCTGCTGCTGCTG 1180
OY 1141 CTCGACTGTGATTAATCAAGAGAGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1197
| | | | |
DB 1181 CTCGACTGTGATTAATCAAGAGAGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1237
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RESULT 12

US-11-047-278-7

; Sequence 7, Application US/11047278

; Publication No. US20050196407A1

; GENERAL INFORMATION:

; APPLICANT: Young, John A.T.

; APPLICANT: Bradley, Kenneth A.

```
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113) .. (1111)
US-11-047-278-7
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Query Match 74.4%; Score 1052.4; DB 10; Length 2112;
Best Local Similarity 99.9%; Pred. No. 1.6e-279;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 AGAAGCCGAGAGAGAGGCGCCGAGATGCGCGCTCTGAGGAGTGTGCGAGTTGCGCG 60
| | | | |
DB 10 AGAAGCCGAGAGAGAGGCGCCGAGATGCGCGCTCTGAGGAGTGTGCGAGTTGCGCG 69
OY 61 ACGGTGGAGAGAGAGGAGCCCTGCTCTCCCGGGGCTGCGGGCCATGAGCCAGGAGAG 120
| | | | |
DB 70 ACGGTGGAGAGAGAGGAGCCCTGCTCTCCCGGGGCTGCGGGCCATGAGCCAGGAGAG 129
OY 121 GAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTTGAGCACTCTGAGTCTCATCTGCGC 180
| | | | |
DB 130 GAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTTGAGCACTCTGAGTCTCATCTGCGC 189
OY 181 CGGAGAGGAGGAGCGAGAGAGATGGGGTCAAGCTGCTCAAGCGAATTTGACCTGTA 240
| | | | |
DB 190 CGGAGAGGAGGAGCGAGAGAGATGGGGTCAAGCTGCTCAAGCGAATTTGACCTGTA 249
OY 241 CTTCAATTTTGA CAAATCAGAGTGTGTCACCACTGGAATGAATCTATTCTTGT 300
| | | | |
DB 250 CTTCAATTTTGA CAAATCAGAGTGTGTCACCACTGGAATGAATCTATTCTTGT 309
OY 301 GGAACGTTGGCTCACAATTTATGATGAGCCACAGTTGAGAAATGCTTATTGTTTCTC 360
| | | | |
DB 310 GGAACGTTGGCTCACAATTTATGATGAGCCACAGTTGAGAAATGCTTATTGTTTCTC 369
OY 361 CACCGAGAGAACACTTAATGAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCT 420
| | | | |
DB 370 CACCGAGAGAACACTTAATGAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCT 429
OY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGAAGATTTGAAG 480
| | | | |
DB 430 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGAAGATTTGAAG 489
OY 481 GGCCAGTGAAGCAGATTTATTTATGAAAACAGACAGAGGTAACAGACACCGCTCATCAT 540
| | | | |
DB 490 GGCCAGTGAAGCAGATTTATTTATGAAAACAGACAGAGGTAACAGACACCGCTCATCAT 549
OY 541 TGCCTTGAAGTGAAGTCAATGAAATCTCTTTTCTATTCTAGAGAGGAGCTTA 600
| | | | |
DB 550 TGCCTTGAAGTGAAGTCAATGAAATCTCTTTTCTATTCTAGAGAGGAGCTTA 609
OY 601 TAGGTCTGAGATCTTGTCGCAATGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 660
| | | | |
DB 610 TAGGTCTGAGATCTTGTCGCAATGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 669
OY 661 ACAAGTGGCCCGGATTCGGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 720
| | | | |
DB 670 ACAAGTGGCCCGGATTCGGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 729
```



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Db 770 |ACAGCTGGCCCGATTGCGGACGATGATCATGTGTTCCCTGMAATGACGGCTTTTCA| 829
Qy 721 |GGCTCGAAGGATCATCACTCAATTTTGAAGAAGTCTCGATCGAAATCTAGCAGC| 780
Db 830 |GGCTCGAAGGATCATCACTCAATTTTGAAGAAGTCTCGATCGAAATCTAGCAGC| 889
Qy 781 |TGAACCATCCACCATATGTGTCAGAGAGATCATTTCAAGTTGTCTGAGAGAAACGGCTT| 840
Db 890 |TGAACCATCCACCATATGTGTCAGAGAGATCATTTCAAGTTGTCTGAGAGAAACGGCTT| 949
Qy 841 |CGACATGCCCCGACAGTGAAGGGTCTCTGACAGCTTCAAGATCAATGAATCTGGTAC| 900
Db 950 |CGACATGCCCCGACAGTGAAGGGTCTCTGACAGCTTCAAGATCAATGAATCTGGTAC| 1009
Qy 901 |ACTCAATGAGAAGCCCTTTTCTGTGGAAGACATTTATTTACTGTGTCAGCGCTATCTT| 960
Db 1010 |ACTCAATGAGAAGCCCTTTTCTGTGGAAGATCTTTATTTACTGTGTCAGCGCTATCTT| 1069
Qy 961 |AAAAGAAGTTGGATGAAGAGCTGCACTCGAGTCAAGATGAAGAGATGCGCTCTTTTAT| 1020
Db 1070 |AAAAGAAGTTGGATGAAGAGCTGCACTCGAGTCAAGATGAAGAGATGCGCTCTTTTAT| 1129
Qy 1021 |CTCCAGTTCTGTCAATCATCAACCAACCACTGT 1054
Db 1130 |CTCCAGTTCTGTCAATCATCAACCAACCACTGT 1163
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RESULT 14
US-10-038-307-1
/ Sequence 1, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2272
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: CDS
/ LOCATION: (213) .. (1211)
US-10-038-307-1
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Query Match 74.4%; Score 1052.4; DB 6; Length 2272;
Best Local Similarity 99.9%; Pred. No. 1.7e-279;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 |AGGACCCGCGAGGAAGGCGCGGATGGCGCTCCCTGAGGATCGTGGCAGATTGCGCG| 60
Db 110 |AGGACCCGCGAGGAAGGCGCGGATGGCGCTCCCTGAGGATCGTGGCAGATTGCGCG| 169
Qy 61 |ACGCTGGAGGAAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGCGGACGCGGAGCG| 120
Db 170 |ACGCTGGAGGAAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGCGGACGCGGAGCG| 229
Qy 121 |GAGAGCCCTCGGATGCGCTTCCAGTGGCTCTTTTGGCAGCTCTGCTGCTCATCTGCC| 180
Db 230 |GAGAGCCCTCGGATGCGCTTCCAGTGGCTCTTTTGGCAGCTCTGCTGCTCATCTGCC| 289
Qy 181 |CGGCAAGGGGAGCGGAGGAGATGGGGTCCAGGCTGTACGGCGGATTTGACCTGTA 240
Db 290 |CGGCAAGGGGAGCGGAGGAGATGGGGTCCAGGCTGTACGGCGGATTTGACCTGTA 349
Qy 241 |CTTCATTTTGAACAAATCAGGAAGTGTGTGCAACCACTGGAATGAATCTATTACTTTGT| 300
```

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Db 350 |CTTCATTTTGAACAAATCAGGAAGTGTGTGCAACCACTGGAATGAATCTATTACTTTGT| 409
Qy 301 |GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCTTTATTTGTTTCTC| 360
Db 410 |GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCTTTATTTGTTTCTC| 469
Qy 361 |CACCCGAGGAACAACTTAAATGAACCTGAAGAGATCAAGAGAGAGAGAAATCCGCAAGGCTT| 420
Db 470 |CACCCGAGGAACAACTTAAATGAACCTGAAGAGATCAAGAGAGAGAGAAATCCGCAAGGCTT| 529
Qy 421 |AGAAACATCCGAAAGTTTCTGCGAGAGAGACATTAACATGCAATGAAAGATTTGAAG| 480
Db 530 |AGAAACATCCGAAAGTTTCTGCGAGAGAGACATTAACATGCAATGAAAGATTTGAAG| 589
Qy 481 |GGCAGTGAAGATTTTATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG| 540
Db 590 |GGCAGTGAAGATTTTATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG| 649
Qy 541 |TGCCTTGAATGAGAACTTCATGAAGATCTTTTCTATTCAGAGAGAGAGAGAGAGAG| 600
Db 650 |TGCCTTGAATGAGAACTTCATGAAGATCTTTTCTATTCAGAGAGAGAGAGAGAGAG| 709
Qy 601 |TAGGTCGAGATCTTTGTCATTTGTTTACTGTGTGTTGTTGTTGTTGTTGTTGTTGTTG| 660
Db 710 |TAGGTCGAGATCTTTGTCATTTGTTTACTGTGTGTTGTTGTTGTTGTTGTTGTTGTTG| 769
Qy 661 |ACAGCTGGCCCGGATGGGACAGTAAAGATCATGTTTCCCGTAATGACGGCTTTCA 720
Db 770 |ACAGCTGGCCCGGATGGGACAGTAAAGATCATGTTTCCCGTAATGACGGCTTTCA 829
Qy 721 |GGCTCGAAGGATCATCACTCAATTTTGAAGAAGTCTGATCGAAATCTAGCAGC 780
Db 830 |GGCTCGAAGGATCATCACTCAATTTTGAAGAAGTCTGATCGAAATCTAGCAGC 889
Qy 781 |TGAACCATCCACCATATGTGTCAGAGAGATCATTTCAAGTTGTCTGAGAGAAACGGCTT| 840
Db 890 |TGAACCATCCACCATATGTGTCAGAGAGATCATTTCAAGTTGTCTGAGAGAAACGGCTT| 949
Qy 841 |CGACATGCCCCGACAGTGAAGGGTCTCTGACAGCTTCAAGATCAATGAATCTGGTAC 900
Db 950 |CGACATGCCCCGACAGTGAAGGGTCTCTGACAGCTTCAAGATCAATGAATCTGGTAC 1009
Qy 901 |ACTCAATGAGAAGCCCTTTTCTGTGGAAGACATTTATTTACTGTGTGCGCGCTATCTT| 960
Db 1010 |ACTCAATGAGAAGCCCTTTTCTGTGGAAGATCTTTATTTACTGTGTGCGCGCTATCTT| 1069
Qy 961 |AAAAGAAGTTGGATGAAGAGCTGCACTCGAGTCAAGATGAAGAGATGCGCTCTTTTAT| 1020
Db 1070 |AAAAGAAGTTGGATGAAGAGCTGCACTCGAGTCAAGATGAAGAGATGCGCTCTTTTAT| 1129
Qy 1021 |CTCCAGTTCTGTCAATCATCAACCAACCACTGT 1054
Db 1130 |CTCCAGTTCTGTCAATCATCAACCAACCACTGT 1163
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RESULT 15
US-10-201-292-1
/ Sequence 1, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2272
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; TYPE: DNA
; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213) ... (1211)
;
US-10-201-292-1

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| | | | | |
|----------------------------|--------|---------------------|-----------|--------------|
| Query Match | 74.4% | Score 1052.4; | DB 6; | Length 2272; |
| Best Local Similarity | 99.9%; | Pred. No. 1.7e-279; | | |
| Matches 1053; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|--|------|
| Oy | 1 | AGAACCCGCGAAGAAAGGCGCCGCGGATGGCGGTCCTCGAAGAGTGTGGCAGATTCCGGG | 60 |
| Db | 110 | AGAACCCGCGAAGAAAGGCGCCGCGGATGGCGGTCCTCGAAGAGTGTGGCAGATTCCGGG | 169 |
| Oy | 61 | AGCGTGGAGAGAGCGGACCCCTGCTCTCCCGGCGTGGCGCCATGACGCGCGAGCG | 120 |
| Db | 170 | AGCGTGGAGAGAGCGGACCCCTGCTCTCCCGGCGTGGCGCCATGAGCACGCGCGAGCG | 229 |
| Oy | 121 | GAGAGCCCTCGGCATCCGGCTTCCAGTGGCTCTTTGGGCCACTGTGGTGTCAATCTGGC | 180 |
| Db | 230 | GAGAGCCCTCGGCATCCGGCTTCCAGTGGCTCTTTGGGCCACTGTGGTGTCAATCTGGC | 289 |
| Oy | 181 | CGGCGAAGGGGACCGCAGAGAGATGGGGGTCTCAGCTGCTACCGCGGATTTGACTGT | 240 |
| Db | 290 | CGGCGAAGGGGACCGCAGAGAGATGGGGGTCTCAGCTGCTACCGCGGATTTGACTGT | 349 |
| Oy | 241 | CTTCAATTTTGGCAAAATCAGGAAGTGTCTGCAACCATGGATGAAATCTAATCTTTGT | 300 |
| Db | 350 | CTTCAATTTTGGCAAAATCAGGAAGTGTCTGCAACCATGGATGAAATCTAATCTTTGT | 409 |
| Oy | 301 | GGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGATGTCCTTAATGTTTCTC | 360 |
| Db | 410 | GGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGATGTCCTTAATGTTTCTC | 469 |
| Oy | 361 | CACCCGAGGAAACAACCTTAAATGAACTGACAGAAACAGAGAACAAATCCGTCAAGGCT | 420 |
| Db | 470 | CACCCGAGGAAACAACCTTAAATGAACTGACAGAAACAGAGAACAAATCCGTCAAGGCT | 529 |
| Oy | 421 | AGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTAATGCTGAAGATTTGAAG | 480 |
| Db | 530 | AGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTAATGCTGAAGATTTGAAG | 589 |
| Oy | 481 | GGCCAGTGGAGATTTAATGAAACAGACAAGGGTACAGGACAGCGAGGTCAAT | 540 |
| Db | 590 | GGCCAGTGGAGATTTAATGAAACAGACAAGGGTACAGGACAGCGAGGTCAAT | 649 |
| Oy | 541 | TGCTTTGACTGATGAGAACTCCATGAAAGTCTTTTTTCAATTCAGAGAGGAGCTTA | 600 |
| Db | 650 | TGCTTTGACTGATGAGAACTCCATGAAAGTCTTTTTTCAATTCAGAGAGGAGCTTA | 709 |
| Oy | 601 | TAGTCTCGAAGTCTTGGTGCAATTGTTTACTGTGTGGTGTGAAAGATTTCAATGAAAC | 660 |
| Db | 710 | TAGTCTCGAAGTCTTGGTGCAATTGTTTACTGTGTGGTGTGAAAGATTTCAATGAAAC | 769 |
| Oy | 661 | AAGCTGGCGCGGATTTGGCGGACAGTAAGGATCATGATGTTCCCGAATGACGGCTTCA | 720 |
| Db | 770 | AAGCTGGCGCGGATTTGGCGGACAGTAAGGATCATGATGTTCCCGAATGACGGCTTCA | 829 |
| Oy | 721 | GGCTCTGCAAGGCATCATCACTCAATTTGAAAGAGTCTTGCAATCGAAATTTCTAGACG | 780 |
| Db | 830 | GGCTCTGCAAGGCATCATCACTCAATTTGAAAGAGTCTTGCAATCGAAATTTCTAGACG | 889 |
| Oy | 781 | TGAACCATCAACCTAATGTGCAAGAGAGTCAATTTCAAGTGTCTGTAAGAGAAACGGCTT | 840 |
| Db | 890 | TGAACCATCAACCTAATGTGCAAGAGAGTCAATTTCAAGTGTCTGTAAGAGAAACGGCTT | 949 |
| Oy | 841 | CCGACATGCCCCGAAGTGGACAGGGTCTCTGCAAGCTTCAAGATCAATGACTCCGTAC | 900 |
| Db | 950 | CCGACATGCCCCGAAGTGGACAGGGTCTCTGCAAGCTTCAAGATCAATGACTCCGTAC | 1009 |
| Oy | 901 | ACTCAATGAAAGCCCTTTTCTGTGGAAGACTTAATTTACTGTGTCCAGCCCTAATCTT | 960 |

Search completed: December 17, 2005, 18:47:10
Job time : 1305.57 secs

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QY 61 AGCGTGGAGGAGCGGAGCCCTGCTCCCGGGCTGCGGGCCATGAGCCAGCGGAGCG 120
 DB 101 AGCGTGGAGGAGCGGAGCCCTGCTCCCGGGCTGCGGGCCATGAGCCAGCGGAGCG 160
 QY 121 GAGAGCCCTCGGCGATGCGCTTCCAGTGGCTCTCTTTGGGCACTCTGGTCTCATCTGGCG 180
 DB 161 GAGAGCCCTCGGCGATGCGCTTCCAGTGGCTCTCTTTGGGCACTCTGGTCTCATCTGGCG 220
 QY 181 CGGCGAAGGGGAGCGAGGAGGATGGGGATCCAGGCTCTCAAGCGGATTTGACCTGTA 240
 DB 221 CGGCGAAGGGGAGCGAGGAGGATGGGGATCCAGGCTCTCAAGCGGATTTGACCTGTA 280
 QY 241 CTTCAATTTTGAAGAAATGAGGATGTCGCACTCAATGAAATGAAATCTTATCTTTGT 300
 DB 281 CTTCAATTTTGAAGAAATGAGGATGTCGCACTCAATGAAATCTTATCTTTGT 340
 QY 301 GGAACAGTTGGCTCACAATTTCAAGCCCAAGTTGAAATGCTTTATGTTTCTC 360
 DB 341 GGAACAGTTGGCTCACAATTTCAAGCCCAAGTTGAAATGCTTTATGTTTCTC 400
 QY 361 CACCCGAGGACCACTTAATGAACTGACAGAGACAGAGAACTCCGTCAGGCGCT 420
 DB 401 CACCCGAGGACCACTTAATGAACTGACAGAGACAGAGAACTCCGTCAGGCGCT 460
 QY 421 AGAAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTAATGATGAAGATTGAAAG 480
 DB 461 AGAAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTAATGATGAAGATTGAAAG 520
 QY 481 GGGCAGTGGAGCATTTTATTAAGAAACAGACAGAGGATCAGAGACGCCAGCTCATCT 540
 DB 521 GGGCAGTGGAGCATTTTATTAAGAAACAGACAGAGGATCAGAGACGCCAGCTCATCT 580
 QY 541 TGGTTGATGATGAGAACTCATGAAGTCTCTTTTCTATTGAGAGGAGGCTAA 600
 DB 581 TGGTTGATGATGAGAACTCATGAAGTCTCTTTTCTATTGAGAGGAGGCTAA 640
 QY 601 TTAGGCTCAGATCTTGTGCAATGTTTACTGTGTGTGAAAGATTTCATGAGAC 660
 DB 641 TTAGGCTCAGATCTTGTGCAATGTTTACTGTGTGTGAAAGATTTCATGAGAC 700
 QY 661 ACAAGTGGCGGGATTTGGCGACAGTAAAGATCATGTGTTCCCGTAAAGAGCGCTTGA 720
 DB 701 ACAAGTGGCGGGATTTGGCGACAGTAAAGATCATGTGTTCCCGTAAAGAGCGCTTGA 760
 QY 721 GGCTCGAAGGATCATCACTCAATTTTGAAGAGTCTGATGAAATCTAGCAGC 780
 DB 761 GGCTCGAAGGATCATCACTCAATTTTGAAGAGTCTGATGAAATCTAGCAGC 820
 QY 781 TGAACCATCCACCATATGTGCAAGAGATCATTTCAAGTTGTCTGAGAGAAAGCGCTT 840
 DB 821 TGAACCATCCACCATATGTGCAAGAGATCATTTCAAGTTGTCTGAGAGAAAGCGCTT 880
 QY 841 CGGACATGCGCGGACAGTGAAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTGAC 900
 DB 881 CGGACATGCGCGGACAGTGAAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTGAC 940
 QY 901 ACTCAATGAAGAGCCCTTTTGTGGAAGACCTTATTAATGCTGTCAGCGGCTATCTT 960
 DB 941 ACTCAATGAAGAGCCCTTTTGTGGAAGATCTTATTAATGCTGTCAGCGGCTATCTT 1000
 QY 961 AAAAGAGTTGGATGAAGAGTGAAGTCAAGGTCAGATGAAGATGAGGCTCTCTTTAT 1020
 DB 1001 AAAAGAGTTGGATGAAGAGTGAAGTCAAGGTCAGATGAAGATGAGGCTCTCTTTAT 1060
 QY 1021 CTCGATTTCTGTCATATCAACACACACACTGTTCTGACGGTTCATCTGGCCATGCG 1080
 DB 1061 CTCGATTTCTGTCATATCAACACACACACTGTTCTGACGGTTCATCTGGCCATGCG 1120
 QY 1081 CCGGATGATCGTTTCTGCTAGCCCTGAGCTCTCTCTGATGATGAGGCGGCTCTG 1140
 DB 1121 CCGGATGATCGTTTCTGCTAGCCCTGAGCTCTCTCTGATGATGAGGCGGCTCTG 1180
 QY 1141 CTGCACTGTGATATCAAGAGGATCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1197

DB 1181 CTGCACTGTGATATCAAGAGGATCCCTCCACCCCTCGAGAGAGTGAAGAA 1237
 RESULT 2
 US-10-750-185-25275/C
 ; Sequence 25275, Application US/10750185
 ; Publication No. US2005026063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MW1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: Patencin version 3.1
 ; SEQ ID NO 25275
 ; LENGTH: 2765
 ; TYPE: DNA
 ; ORGANISM: Bovine 1986881163262
 US-10-750-185-25275
 Query Match 4.3%; Score 61.4; DB 6; Length 2765;
 Best Local Similarity 77.9%; Pred. No. 8,1e-06;
 Matches 74; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 QY 733 CATATCCATCAATTTTGAAGAACTCCGATGCAATTCAGAGAGTGAACCATCCAC 792
 DB 211 CTTCTCCCTAGATATTAAGAAATCTGATGAAATTTCTAGAGAGTGAACCATCCAC 152
 QY 793 CATATGCGAGAGAGTCAATTTCAAGTTGTGCTGA 827
 DB 151 CATATGCGAGAGGTAATTTGAATCTAAGTGTTA 117
 RESULT 3
 US-10-909-125-809
 ; Sequence 809, Application US/10909125
 ; Publication No. US20050261218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Esau, Christine
 ; APPLICANT: Lollo, Bridget
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Freier, Susan M.
 ; APPLICANT: Griefey, Richard H.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Vickers, Timothy
 ; APPLICANT: Marcussen, Eric G.
 ; APPLICANT: Koller, Eric
 ; APPLICANT: Swayze, Eric
 ; APPLICANT: Uain, Ravi
 ; APPLICANT: Bhat, Balkrishen
 ; APPLICANT: Peralta, Egen
 ; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
 ; FILE REFERENCE: ISI50080-100 (CORE0016US)
 ; CURRENT APPLICATION NUMBER: US/10/909,125
 ; PRIOR FILING DATE: 2004-07-30
 ; PRIOR APPLICATION NUMBER: US 60/492,056
 ; PRIOR FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: US 60/516,303
 ; PRIOR FILING DATE: 2003-10-31
 ; PRIOR APPLICATION NUMBER: US 60/531,596
 ; PRIOR FILING DATE: 2003-12-19
 ; PRIOR APPLICATION NUMBER: US 60/562,417

PRIOR FILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 2184
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 809
LENGTH: 2126
TYPE: DNA
ORGANISM: H. sapiens
US-10-909-125-809

Query Match 3.8%; Score 54; DB 6; Length 2126;
Best Local Similarity 68.2%; Pred. No. 0.00054;
Matches 75; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1305 ATCTAGACAGCTCTTTCTCTAGTCCCTGATTCGAATCCGAGTGTCACTTAATTA 1364
DB 2001 ATTTTCAGACACTTTGCTCTAGTGTGTATTTAAATATAAATTAAGAAAAA 2060
QY 1365 AATAGCTATATGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 2061 ATAA 2110

RESULT 4
US-10-689-742-43
Sequence 43, Application US/10689742
Publication No. US20050250180A1
GENERAL INFORMATION:
APPLICANT: Jacoby, Kenneth
APPLICANT: McCoy, John M
APPLICANT: Lavallee, Edward R
APPLICANT: Racie, Lisa A
APPLICANT: Evans, Cheryl
APPLICANT: Weisberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000091.10
CURRENT APPLICATION NUMBER: US/10/689, 742
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 09/746, 783
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn version 3.2
SEQ ID NO 43
LENGTH: 2773
TYPE: DNA
ORGANISM: Homo sapiens
US-10-689-742-43

Query Match 3.5%; Score 49.2; DB 6; Length 2773;
Best Local Similarity 67.6%; Pred. No. 0.01;
Matches 69; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1313 AGTCTTTCTCTGTTCCCTGATTCGAATCCGAGTGTCAATCAATTAATAGCTA 1372
DB 2631 AGTCTTTGCTGTTAGCTCAGTACTCCAGGCACTTAAGTCAAGACTTAAGAC 2650
QY 1373 TATGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 2691 CTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732

RESULT 5
US-10-131-826A-9
Sequence 9, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Aubelin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remainder Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 9
LENGTH: 2276
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-9

Query Match 3.4%; Score 48.6; DB 6; Length 2276;
Best Local Similarity 67.0%; Pred. No. 0.013;
Matches 69; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1312 CAGCTTTCTCTAGTCCCTGATTCGAATCCGAGTGTCAATCAATTAATAGCT 1371
DB 2170 CTGCTTTTATCTCTAGTGAATTAAGTCAAAAGTTATTTATTCCTCAAAAAA 2229
QY 1372 ATATGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 2230 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2272

RESULT 6
US-10-689-742-165
Sequence 165, Application US/10689742
Publication No. US20050250180A1
GENERAL INFORMATION:
APPLICANT: Jacoby, Kenneth
APPLICANT: McCoy, John M
APPLICANT: Lavallee, Edward R
APPLICANT: Racie, Lisa A
APPLICANT: Evans, Cheryl
APPLICANT: Weisberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000091.10
CURRENT APPLICATION NUMBER: US/10/689, 742

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/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 09/746,783
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 165
/ LENGTH: 2487
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-689-742-165

Query Match
Best Local Similarity 58.7%; Pred. No. 0.014;
Matches 84; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1272 ATTTTATCAATGCTGTGAATTCATGCTCAATGCTCTTCCCTAGTCC 1331
DB 2291 ATGTTTAAATGCGCATTAATACTCTGCTGTAATAGTATTGTAATATTGG 2350
QY 1332 CTGTATTCAAATCCAGTGTCTACATTCATTAATAGCTAATGAAATCAAAAAA 1391
DB 2351 CAATATAATCTGCCCCGCAATTAATAAAAAAAAAAAAAAAAAAAAAA 2410
QY 1392 AAAAAAAAAAAAAAAAAAAAAA 1414
DB 2411 AAAAAAAAAAAAAAAAAAAAAA 2433

RESULT 7
US-10-689-742-5
/ Sequence 5, Application US/10689742
/ Publication No. US20050250180A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M
/ APPLICANT: Lavalie, Edward R
/ APPLICANT: Racie, Lisa A
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Spaulding, Vikki
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: 00766.000091.10
/ CURRENT APPLICATION NUMBER: US/10/689,742
/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 09/746,783
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 5
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-689-742-5

Query Match
Best Local Similarity 3.3%; Score 47.2; DB 6; Length 894;
Matches 55; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1347 AGTGTTAATCAATTAATGCTATGAAATCAAAAAAAAAAAAAAAAAA 1406
DB 819 AATCCCTAAATGCAATTAATACTAGTATGTTTCAAAAAAAAAAAAAA 878
QY 1407 AAAAAAA 1414
DB 879 AAAAAAA 886

RESULT 8
US-11-102-240-17
/ Sequence 17, Application US/11102240
/ Publication No. US20050260647A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Wood, William L.
/ TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESSION
/ FILE REFERENCE: P3330R1C106C
/ CURRENT APPLICATION NUMBER: US/11/102,240
/ CURRENT FILING DATE: 2005-04-08
/ PRIOR APPLICATION NUMBER: 10/063662
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 10/006867
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: 60/170262
/ PRIOR FILING DATE: 199-12-09
/ NUMBER OF SEQ ID NOS: 170
/ SEQ ID NO: 17
/ LENGTH: 1672
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-11-102-240-17

Query Match
Best Local Similarity 3.3%; Score 46.8; DB 7; Length 1672;
Matches 54; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1349 TGTCTAATCAATTAATGCTATATGAAATCAAAAAAAAAAAAAAAAAA 1408
DB 1588 TGTCTAATCAATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1647
QY 1409 AAAAAA 1414
DB 1648 AAAAAA 1653

RESULT 9
US-10-689-742-41
/ Sequence 41, Application US/10689742
/ Publication No. US20050250180A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M
/ APPLICANT: Lavalie, Edward R
/ APPLICANT: Racie, Lisa A
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Spaulding, Vikki
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: 00766.000091.10
/ CURRENT APPLICATION NUMBER: US/10/689,742
/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 09/746,783
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 41
/ LENGTH: 588
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-689-742-41

Query Match
Best Local Similarity 3.3%; Score 46.6; DB 6; Length 588;
Matches 112; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1194 AAAATTAATAATTAATCAAGAGAAAGAAAGAAATCCACGAAACAGATTAACCTA 1253
DB 337 AATCTAGTTGACAAAGAAAGAAAGAAAGAAAGGCTTAATCACAAGGTTCTGAAATTA 396
```



```
/ GENERAL INFORMATION:
/ APPLICANT: Esau, Christine
/ APPLICANT: Lollo, Bridget
/ APPLICANT: Bennett, C. Frank
/ APPLICANT: Preleer, Susan M.
/ APPLICANT: Griffey, Richard H.
/ APPLICANT: Baker, Brenda F.
/ APPLICANT: Vickers, Timothy
/ APPLICANT: Marcuseon, Eric G.
/ APPLICANT: Koller, Erich
/ APPLICANT: Swayze, Eric
/ APPLICANT: Jain, Ravi
/ APPLICANT: Bhat, Balkrishen
/ APPLICANT: Peralta, Eizen
/ TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
/ TITLE OF INVENTION: Of Small Non-Coding RNAs
/ FILE REFERENCE: ISIS0080-100 (CORE0016US)
/ CURRENT APPLICATION NUMBER: US/10/909,125
/ PRIOR FILING DATE: 2004-07-30
/ PRIOR APPLICATION NUMBER: US 60/492,056
/ PRIOR FILING DATE: 2003-07-31
/ PRIOR APPLICATION NUMBER: US 60/516,303
/ PRIOR FILING DATE: 2003-10-31
/ PRIOR APPLICATION NUMBER: US 60/531,596
/ PRIOR FILING DATE: 2003-12-19
/ PRIOR APPLICATION NUMBER: US 60/562,417
/ PRIOR FILING DATE: 2004-04-14
/ NUMBER OF SEQ ID NOS: 2184
/ SOFTWARE: PaatSeq for Windows Version 4.0
/ SEQ ID NO 801
/ LENGTH: 4339
/ TYPE: DNA
/ ORGANISM: H. sapiens
US-10-909-125-801
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Query Match          3.2%; Score 45.6; DB 6; Length 4339;
Best Local Similarity 66.0%; Pred. No. 0.11;
Matches 66; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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QY 1315 TCTTCCCTAGTCCGCTGATTCGAATCCAGTGTCTAATCAATTAATAGCTATA 1374
DB 4155 TCTTTACACGTTTAAACCTTCTTAAGCAGCTCTTAATATATATTAATGCTCCC 4214
QY 1375 TGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 4215 TTTTATTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4254
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RESULT 14
US-10-996-217A-8/C
/ Sequence 8, Application US/10996217A
/ Publication No. US2005026651A1
/ GENERAL INFORMATION:
/ APPLICANT: Revivicor, Inc.
/ APPLICANT: Wells, Kevin
/ TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
/ FILE REFERENCE: 10785.105070 REV 1015 US
/ CURRENT APPLICATION NUMBER: US/10/996,217A
/ CURRENT FILING DATE: 2004-11-22
/ PRIOR APPLICATION NUMBER: 60/523,938
/ PRIOR FILING DATE: 2003-11-21
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 2036
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
US-10-996-217A-8
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Query Match          3.2%; Score 45.2; DB 6; Length 2036;
Best Local Similarity 66.3%; Pred. No. 0.093;
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```
Matches 65; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1317 TTTTCCCTAGTCCGCTGATTCGAATCCAGTGTCTAATCAATTAATAGCTATAG 1376
DB 656 TTTTAGATATTTTCTTGTTGTTCCCTTCTCACTGAACCTATTTTAGTAACTAAAA 597
QY 1377 AAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 596 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 559
```

```
RESULT 15
US-11-077-386-7
/ Sequence 7, Application US/11077386
/ Publication No. US20050272067A1
/ GENERAL INFORMATION:
/ APPLICANT: Macina, Roberto
/ APPLICANT: Turner, Leah R.
/ APPLICANT: Chen, Huel-Mei
/ APPLICANT: Rodriguez, Maria
/ APPLICANT: Liu, Shu-Hui
/ TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Cancer Spec
/ TITLE OF INVENTION: Genes and Proteins
/ FILE REFERENCE: DEX-0537
/ CURRENT APPLICATION NUMBER: US/11/077,386
/ CURRENT FILING DATE: 2005-03-10
/ PRIOR APPLICATION NUMBER: US 60/566,706
/ PRIOR FILING DATE: 2004-04-30
/ PRIOR APPLICATION NUMBER: US 60/565,144
/ PRIOR FILING DATE: 2004-04-23
/ PRIOR APPLICATION NUMBER: US 60/551,911
/ PRIOR FILING DATE: 2004-03-10
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 602
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-077-386-7
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Query Match          3.2%; Score 45; DB 7; Length 602;
Best Local Similarity 70.6%; Pred. No. 0.056;
Matches 60; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```
QY 1330 CCTGTATTCGAATCCAGTGTCTAATCAATTAATAGCTATATGAATCAAAAAA 1389
DB 447 CCATGTACTAATTAAGAAAGAGCTTTGAGCTAATAAAAAAAAAAAAAAAAAAAAAA 506
QY 1390 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 507 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 531
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 14, 2005, 11:21:18 ; Search time 46.6092 Seconds
(without alignments)
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Title: US-09-970-076-1

Perfect score: 2540

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-DEF_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOR=6 -DELEXT=7

Database :

Issued Patents AA:*
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6: /cgcn2_6/prodata/1/1aa/backfill1aa.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 965 | 38.0 | 488 | 2 | US-10-104-047-2639 Sequence 2639, Ap |
| 2 | 167 | 6.6 | 1155 | 1 | US-08-286-889-46 Sequence 46, Appl |
| 3 | 167 | 6.6 | 1155 | 1 | US-08-485-618-46 Sequence 46, Appl |
| 4 | 167 | 6.6 | 1155 | 1 | US-08-362-652-46 Sequence 46, Appl |
| 5 | 167 | 6.6 | 1155 | 1 | US-08-605-672-46 Sequence 46, Appl |
| 6 | 167 | 6.6 | 1155 | 1 | US-08-482-293A-46 Sequence 46, Appl |
| 7 | 167 | 6.6 | 1155 | 1 | US-08-943-363-46 Sequence 46, Appl |
| 8 | 167 | 6.6 | 1155 | 2 | US-09-193-043-46 Sequence 46, Appl |
| 9 | 167 | 6.6 | 1155 | 2 | US-09-688-307A-46 Sequence 46, Appl |
| 10 | 167 | 6.6 | 1155 | 2 | US-09-350-259-46 Sequence 46, Appl |
| 11 | 167 | 6.6 | 1161 | 1 | US-08-485-618-53 Sequence 53, Appl |
| 12 | 167 | 6.6 | 1161 | 1 | US-08-362-652-53 Sequence 53, Appl |

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| 13 | 167 | 6.6 | 1161 | 1 | US-08-605-672-53 Sequence 53, Appl |
| 14 | 167 | 6.6 | 1161 | 1 | US-08-482-293A-53 Sequence 53, Appl |
| 15 | 167 | 6.6 | 1161 | 1 | US-08-943-363-53 Sequence 53, Appl |
| 16 | 167 | 6.6 | 1161 | 2 | US-09-193-043-53 Sequence 53, Appl |
| 17 | 167 | 6.6 | 1161 | 2 | US-09-688-307A-53 Sequence 53, Appl |
| 18 | 167 | 6.6 | 1161 | 2 | US-09-350-259-53 Sequence 53, Appl |
| 19 | 163.5 | 6.4 | 1161 | 1 | US-08-173-497-2 Sequence 2, Appl1 |
| 20 | 163.5 | 6.4 | 1161 | 1 | US-08-286-889-2 Sequence 2, Appl1 |
| 21 | 163.5 | 6.4 | 1161 | 1 | US-08-485-618-2 Sequence 2, Appl1 |
| 22 | 163.5 | 6.4 | 1161 | 1 | US-08-485-618-99 Sequence 2, Appl1 |
| 23 | 163.5 | 6.4 | 1161 | 1 | US-08-362-652-2 Sequence 2, Appl1 |
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| 25 | 163.5 | 6.4 | 1161 | 1 | US-08-605-672-99 Sequence 2, Appl1 |
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| 33 | 163.5 | 6.4 | 1161 | 2 | US-09-688-307A-99 Sequence 2, Appl1 |
| 34 | 163.5 | 6.4 | 1161 | 2 | US-09-350-259-2 Sequence 2, Appl1 |
| 35 | 163.5 | 6.4 | 1161 | 2 | US-09-350-259-99 Sequence 2, Appl1 |
| 36 | 162.5 | 6.4 | 1151 | 1 | US-08-286-889-37 Sequence 37, Appl |
| 37 | 162.5 | 6.4 | 1151 | 1 | US-08-485-618-37 Sequence 37, Appl |
| 38 | 162.5 | 6.4 | 1151 | 1 | US-08-362-652-37 Sequence 37, Appl |
| 39 | 162.5 | 6.4 | 1151 | 1 | US-08-605-672-37 Sequence 37, Appl |
| 40 | 162.5 | 6.4 | 1151 | 1 | US-08-482-293A-37 Sequence 37, Appl |
| 41 | 162.5 | 6.4 | 1151 | 1 | US-08-943-363-37 Sequence 37, Appl |
| 42 | 162.5 | 6.4 | 1151 | 2 | US-09-193-043-37 Sequence 37, Appl |
| 43 | 162.5 | 6.4 | 1151 | 2 | US-09-688-307A-37 Sequence 37, Appl |
| 44 | 162.5 | 6.4 | 1151 | 2 | US-09-350-259-37 Sequence 37, Appl |
| 45 | 162.5 | 6.4 | 1161 | 1 | US-08-485-618-55 Sequence 55, Appl |

ALIGNMENTS

RESULT 1
US-10-104-047-2639
; Sequence 2639, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OR INVENTION: No. 6943241el full length CDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2639
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2639

Alignment Scores:

Pred. No.: 2,22e-93 Length: 488
Score: 965.00 Matches: 194
Percent Similarity: 64.34% Conservative: 64
Best Local Similarity: 48.38% Mismatches: 101
Query Match: 37.99% Indels: 42
DB: 2 Gaps: 5

US-09-970-076-1 (1-1414) x US-10-104-047-2639 (1-488)

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QY 68 GAAGAGCGGAGCCCTGCTCTCCCGGCGCTGCGGCGCATGCGCAGCGCGAGAGGCC 127

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QY 305 CAGTTGGCTCACAAATTCATCAGCCCACTGAGATGAGATGCTTTATGTTTCTCCACC 364
Db 68 GlnLeuAlaGlnArgPheValSerProGlnUmetArgLeuSerPheLleValPheSerSer 87
QY 365 CGAGNAACAACCTTAATGAAACTGACAGAAAGACAGAAACMAATCCGTCAAGGCTTAGAA 424
Db 88 GlnAlaThrLlLeuLeuProLeuThrGlyAspArgGlyLysLleSerLysGlyLeuGln 107
QY 425 GAATCTCAAAAAGTTCTGCCAGAGAGACACTTACATGATGAGAAAGATTGAAAGGCC 484
Db 108 AspLeuLysArgValSerProValGlyGlnTyrLleHisGlnGlyLeuLysLeuAla 127
QY 485 AGTGAACAGATTTATATGAAACAGACAAGGGAAGGCAAGCCGTCATCTTGTCT 544
Db 128 AsnGlnGlnLle-----GlnLysAlaGlyGlyLeuLysThrSerLleLleLleAla 145
QY 545 TTGACTGATGAGAACTCCATGAAAGTCTTTTCTTATTCAGAGAGGAGGCTTAATAG 604
Db 146 LeuThrAspGlyLysLeuAspGlyLeuValProSerTyrAlaGlnLysGlnAlaLysLle 165
QY 605 TCTCCAGATCTTGTCATTTGTTACTGTGTGTGTGTAAGATTTCATGAGACAG 664
Db 166 SerArgSerLeuGlyAlaSerValTyrCyValGlyValLeuAspPheGlnGlnAlaGln 185
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Db 186 LeuGlnArgLleAlaAspSerLysGlnGlnValPheProValLysGlyGlyPheGlnAla 205
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Db 226 ProSerSerValCyValGlyGlnGlnPheGlnLleValLeuSerGlyArgGlyPheMet 245
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Db 366 Gln 366

RESULT 2
US-08-286-889-46
; Sequence 46, Application US/0828689
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-889-46

Alignment Scores:
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QY 748 TTGGAAGAGTCTCGATCGAATTTTACGACCTGAACCATCCACCTATGTCAGAGAGA 807
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RESULT 3
US-08-485-618-46
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497

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FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/266,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-46

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Alignment Scores:
Pred. No.: 2,08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 1 Gaps: 14
US-09-970-076-1 (1-1414) x US-08-485-618-46 (1-1155)

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Db 93 GlyLeuSerLeuValAlaAspThrAsnAsnSerGlnLeuLeuAlaCysGlyProThrAla 112
QY 88 CCGCGGGCTGGCGGCG-----CATGGCCAGCGCGAGAGCGGAGACCTCTCGGATCCG 138
Db 113 GlnArgAlaCysAlaLysAsnMetTyrAlaLysGlySerCys-LeuLeuLeuLysSerSe 132
QY 139 CTTCAGATGAGCTCTCTTTGGCCACTGTGCTCATCTGCGCGGCGAAGGGGAGCGAG 198
Db 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
QY 199 GAGAGATGGGGGTCAGACCTGCTACGCGC---GGATTGACCTGATCTTATTTGACAA 255
Db 144 -----ProGluCySProGlyngInGluMeAspIleAlaPheLeuIleAspI1 159
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Db 179 tGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMeGlnTyrSerAsnIleLeuLy 199
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Db 219 aIleValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleG1 234
QY 478 AAGGGCCAGTACAGATTTATTATGAAAACAGACAGAGGTACAGAGACAGC---AGCGT 534
Db 234 nLysValValLysGlnLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLysI1 254
QY 535 CATCATTTGCTTTGACTGATGAGAGAACTCCATGAAGATCTCTTTTCTATTCAAG- 589
Db 254 eLeuIleValIleThrAspGlyGlnLysPheArgAspProLeuGlnLysrArgHisValI1 274

```


CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, 6300 Sear Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/605,672
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/173,497
 FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,889
 FILING DATE: 5-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,652
 FILING DATE: 21-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams Jr., Joseph A.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 27866/32684
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1155 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-605-672-46
 Alignment Scores:
 Pred. No.: 2.08e-08 Length: 1155
 Score: 167.00 Matches: 77
 Percent Similarity: 42.47% Conservative: 50
 Best Local Similarity: 25.75% Mismatches: 125
 Query Match: 6.57% Indels: 47
 DB: 1 Gaps: 14
 US-09-970-076-1 (1-1414) x US-08-605-672-46 (1-1155)
 QY 28 GGCGGTCCTCGTGGAGGTCGCGGAGCTGGAGAGGAGCGGACCTGCTCT 87
 Db 93 GlyleuSerleuValAlaapThrAlaAsnAsnSerGlnleuAlaCysglYProthAla 112
 QY 88 CCCCCGCTCGGCGC-----CATGCCACGCGCGGAGCGGAGAGCCCTCGGCATCGG 138
 Db 113 GlnArgAlaCysAlaIysAsnMetCysAlaIysGlySerCys-LeuLeuGlySerse 132
 QY 139 CTTCCAGTGGCTCTTTGGCCTGCTGCTCATCTGCGCGGCGGAGGAGCGAG 198
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 QY 199 GAGAGATGGGCTCAGCTCTAGCGC---GAGTTTGACCTGTACTTATTTGACAA 255
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 QY 256 ATCAGAAAGTGTG---CTGCACCACTGGAGATGAATCTATTACTTTGTGGAACGTTGGC 312
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 QY 313 TCAGAAATTCATCGCCCAACAGATTGAGAAATGCTTTTATTTTCTCCACCGAGAAC 372
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Db 179 rGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnTySerAsnIleLeu 199
 QY 373 AACCTTAATGAATCTACAGAAAGACAG-----GACAAATCCGTCAAG 417
 Db 199 sThrHisPheThrGlnPheThrGlnPheIysSerLeuSerProGlnSerleuValAspAl 219
 QY 418 CTTAGAAAGAACTCCAGAAAGTTCTCCAGAGAGAGACACTTACATGATGAAATTTGA 477
 Db 219 aIleValGlnLeuGln-----GlyLeuThrTyThrAlaSerGlyIleG1 234
 QY 478 AGGGCCAGTACAGCAATTTATTATGAAAACAGACAGGATACAGACAGCC---AGCGT 534
 Db 234 nIysValIalIysGlnLeuPheHisSerIysAsnGlyAlaArgIysSerAlaIysAs1 254
 QY 535 CATCATTTGCTTTACATGATGAGAACTCCATGAAAGATCTTTTCTTATTCAGAG----- 589
 Db 254 eIeuIleValIleThrAspGlnIysPheArgAspProLeuGlnIysArgHisVal11 274
 QY 590 -AGGAGGCTAATAGCTCTCGAATCTGGTGCATTTGTTACTGTGTGTGTAAGA 648
 Db 274 eProGlnAlaGlnIysAla-----GlyIleIleArgTyAlaIleGlyAlaGlyAs 291
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 Db 291 pAlaPheArgGluProThrAlaLeuGlnGlnIleuAsnThrIleGlySerAlaProSerG1 311
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 Db 311 nAspHisValPheIysValGlyIysn---PheValAlaLeuArgSerIleGlnArgGln1 330
 QY 748 TTTGAAAGAGTCCGTGATGAAATTTCTAGAGCTGAAACATCCACCATATGTCAGAGA 807
 Db 330 eGlnGlnIys-----IlePheAlaIleGlnGlyThrGlnSerArgSerse 346
 QY 808 GTCATTTCAAGTGTCTGTGAGAGAAACGCTTCCGACATGCCCAACGTGAC 862
 Db 346 rSerPheGlnHisGlnMetSerGlnGlnIysPheSerSerAlaLeuSerMetAsp 364
 RESULT 6
 US-08-482-293A-46
 Sequence 46, Application US/08482293A
 Patent No. 5831029
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Van der Vlieten, Monica
 TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
 NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, 6300 Sear Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,293A
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/173,497
 FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,889
 FILING DATE: 5-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,652
 FILING DATE: 21-DEC-1994
 ATTORNEY/AGENT INFORMATION:


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Db      93  G|YLeuSerIeuValAlaAepThrAenSerGlnLeuEulAlaCySgIyProThra1a 112
QY      88  CCCCggGCTGCGGGC-----CATGGCCAGCGCGAGAGAGCCCTCGGCATCGG 138
Db      113  GlnArgAlaCyAlaIyAenMetYrAlaIySgIySerCyS-LeuLeuEugIySerse 132
QY      139  CTTCCAGTGGCTCTCTTTGGCCACTGTGGCTCATCTGGCGCGGCAAGGGAGCGCAG 198
Db      132  rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
QY      199  GAGAGATGGGGGTCCAGCTGTACAGGC---GGATTGACCTGTACTTATTTTGACAA 255
Db      144  -----ProGluCySProGluGlnGluMetAspIleAlaPheLeuIleAspG1 159
QY      256  ATCAGAAAGTGTG---CTGCACCACTGGAATGAATCTATTAATCTTTGGAAACAGTTGC 312
Db      159  ySerGlySerIleAspGlnSerAspPheThrGlnMetIyAspPheValIyAlaLeuMe 179
QY      313  TCACAAATTATCATGCCCACTGAGATGTCTTATTGTCTTCTCCACCGGAGAAC 372
Db      179  rGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnIySerAsnIleLeuIy 199
QY      373  AACCTTAATGAACCTGACAGAAAGACAG-----GAACAAATCCGTCAGAG 417
Db      199  sThrHisPheThrPheThrGluPheIySerSerLeuSerProGlnSerIeuValAspAl 219
QY      418  CCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAAGAGATTGA 477
Db      219  aIleValGlnLeuGln-----GlyLeuThrTyThrAlaSerGlyIleG1 234
QY      478  AAGGGCCAGTGAGACAGATTATTATGAAAACAGACAGAGGTAACAGACAGCC---AGCGT 534
Db      234  nIyValIyAlIySgIyIuLeuPheHisSerIySAsnGlyAlaArgIySerAlaIySyl 254
QY      535  CATCATTTGCTTTGACTGATGAGAAACCTCATGAAGACTCTTTTTCATTTCAGAG----- 589
Db      254  eIeuIleValIleThrAspGlnIyIuPheArgAspProLeuGluTyTrArgHisValI1 274
QY      590  -AGGAGAGCTAATAGTCTCGAAGATCTTGTGCAATTTGTTACTGTGTGGTGAAGA 648
Db      274  eProGluAlIeGluIyAla-----GlyIleIleArgTyAlaIleGlyValG1yAs 291
QY      649  T---TTCAATGAG---ACACAGCTGGCCCGGATT-----GGGACAGTAA 687
Db      291  pAlaPheArgGluProThrAlaLeuGlnGluIuLeuAsnThrIleGlySerAlaProSerG1 311
QY      688  GGATCATGTGTTCCCGGATGATGACGGCTTCAGGCTCTGCAAGGACATTCACCTCAAT 747
Db      311  nAspHisValPheIyValG1yAsn---PheValAlaLeuArgSerIleGlnArgGlnI1 330
QY      748  TTGGAAGAGCTCTGATCTGCAATTTCTAGACAGTGAACCATCCCATATGTGACAGAGA 807
Db      330  eGlnGluIyS-----IlePheAlaIleGluGlyThrGluSerArgSerSerse 346
QY      808  GTCATTTCAAGTTGTCTGTAGAGAGAAACGCTTCGACAGATCCCGCAACGTGCAC 862
Db      346  rSerPheGlnHisIleGluMetSerGlnGluIyPheSerSerAlaLeuSerMetAsp 364

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; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-193-043-46

Alignment Scores:
Pred. No.: 2.08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: Gaps: 14

US-09-970-076-1 (1-1414) x US-09-193-043-46 (1-1155)
QY      28  GGCGCGCTCCCTGAGGGTCTGCGGAGTTCGCGAGCGTGGAGAGAGCGGACCTGCTCT 87
Db      93  G|YLeuSerIeuValAlaAepThrAenSerGlnLeuEulAlaCySgIyProThra1a 112
QY      88  CCCCggGCTGCGGGC-----CATGGCCAGCGCGAGAGAGCCCTCGGCATCGG 138
Db      113  GlnArgAlaCyAlaIyAenMetYrAlaIySgIySerCyS-LeuLeuEugIySerse 132
QY      139  CTTCCAGTGGCTCTCTTTGGCCACTGTGGCTCATCTGGCGCGGCAAGGGAGCGCAG 198
Db      132  rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
QY      199  GAGAGATGGGGGTCCAGCTGTACAGGC---GGATTGACCTGTACTTATTTTGACAA 255
Db      144  -----ProGluCySProGluGlnGluMetAspIleAlaPheLeuIleAspG1 159
QY      256  ATCAGAAAGTGTG---CTGCACCACTGGAATGAATCTATTAATCTTTGGAAACAGTTGC 312
Db      159  ySerGlySerIleAspGlnSerAspPheThrGlnMetIyAspPheValIyAlaLeuMe 179
QY      313  TCACAAATTATCATGCCCACTGAGATGTCTTATTGTCTTCTCCACCGGAGAAC 372
Db      179  rGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnIySerAsnIleLeuIy 199
QY      373  AACCTTAATGAACCTGACAGAAAGACAG-----GAACAAATCCGTCAGAG 417
Db      199  sThrHisPheThrPheThrGluPheIySerSerLeuSerProGlnSerIeuValAspAl 219
QY      418  CCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAAGAGATTGA 477
Db      219  aIleValGlnLeuGln-----GlyLeuThrTyThrAlaSerGlyIleG1 234
QY      478  AAGGGCCAGTGAGACAGATTATTATGAAAACAGACAGAGGTAACAGACAGCC---AGCGT 534
Db      234  nIyValIyAlIySgIyIuLeuPheHisSerIySAsnGlyAlaArgIySerAlaIySyl 254
QY      535  CATCATTTGCTTTGACTGATGAGAAACCTCATGAAGACTCTTTTTCATTTCAGAG----- 589
Db      254  eIeuIleValIleThrAspGlnIyIuPheArgAspProLeuGluTyTrArgHisValI1 274
QY      590  -AGGAGAGCTAATAGTCTCGAAGATCTTGTGCAATTTGTTACTGTGTGGTGAAGA 648
Db      274  eProGluAlIeGluIyAla-----GlyIleIleArgTyAlaIleGlyValG1yAs 291
QY      649  T---TTCAATGAG---ACACAGCTGGCCCGGATT-----GGGACAGTAA 687
Db      291  pAlaPheArgGluProThrAlaLeuGlnGluIuLeuAsnThrIleGlySerAlaProSerG1 311
QY      688  GGATCATGTGTTCCCGGATGATGACGGCTTCAGGCTCTGCAAGGACATTCACCTCAAT 747

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Db      311 naphisValpelysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330
Qy      748 TTGAAGAAGTCTCGATCGAATTCAGAGCTGAGCATCCACATATGTCAGAGAGA 807
Db      330 eGlnGlnLys-----IlePheAlaIleGlnGlyThrGlnLysArgSerIle 346
Qy      808 GTCAATTCAAGTTGCTGTGAGAGAAACGGCTTCGACATGCCCGACAGCTGAC 862
Db      346 rSerPheGlnIleGlnLysMetSerGlnGlnGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 9
US-09-688-307A-46
/ Sequence 46, Application US/09688307A
/ Patent No. 6432404
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6432404el Human Beta-2
/ FILE REFERENCE: 27866/36646
/ CURRENT APPLICATION NUMBER: US/09/688,307A
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/605,672
/ PRIOR FILING DATE: 1996-02-22
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 46
/ LENGTH: 1155
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-688-307A-46

Alignment Scores:
Pred. No.: 2,08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 2 Gaps: 14

US-09-970-076-1 (1-1414) x US-09-688-307A-46 (1-1155)
Qy      28 GGGCGCTCCCTGAGGGTCTGCGGAGTGGCGGAGGCGGAGGAGCCCTGCTCT 87
Db      93 GllYleuSerIleuValAlaaphThraAaenSerGlnleuAlaCySgIlyProthraIa 112
Qy      88 CCCCAGGCTGCGGGC-----CATGGCCAGCGCGAGCGGAGAGCCCTCGGCATCG 138
Db      113 GlnArgAlaCyAlaIalysaenMetYrAlaIySgIySerCyS-LeuLeuIleuIySerSe 132
Qy      139 CTTCCAGTGGCTCTTTGGCCACTCTGGTCTCATCTGCGCGGCGAAGGGGAGCGCAG 198
Db      132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
Qy      199 GGAGATGGGGGTCAGCGCTGCTACGGC---GGATTGACCTGTACTTCATTTTGGACA 255
Db      144 -----ProGlnCySerProGlnGlnGlnMetAspIleAlaPheIleuIleAspG 159
Qy      256 ATCAGAGAGTGTG---CTGCACCACTGATGAATCTATTACTTTGTGAACAGTTGCG 312
Db      159 ySerThrIleAspGlnSerAspPheThrGlnMetClyAspPheValIalysaIleu 179
Qy      313 TCACAAATTCATAGCCCAACGATGAGATGCTCTTATTGTTTCTCCACCCGAGGAA 372
DB: 2 Gaps: 14
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Db      179 rGlnIleuAlaSerThrSerThrSerPheSerLeuMetGlnYrSerAsnIleLeu 199
Qy      373 AACCTTAATGAACATGACAGAGACAGA-----GAACAATCCGTCAGG 417
Db      199 rThrIlePheThrPheThrGlnPheIySerSerIeuserProGlnSerIleuAlaAsp 219
Qy      418 CCTAAGAAATCTCCAGAAAGTTCTCGACAGAGAGACACTTACATGATGAAGATTGA 477
Db      219 alIeValGlnLeuGln-----GlyLeuThrYrThrAlaSerGlyIleG 234
Qy      478 AAGGCCCATGACGACAGATTATTATGAACACAGACAGAGGTACAGACAGCC---AGCG 534
Db      234 nlyeValIalysGlnLeuPheIleSerIySaenGlyAlaArgIySerAlaIySgI 254
Qy      535 CATCATTTGCTTGCATGATGAGAACTCCATGAAGATCTTTTCTATTTCAGAG----- 589
Db      254 eleuIleValIleThrAspGlyGlnIyPheArgAspProIeugIyYrArgHisVal 274
Qy      590 -AGGAGGCTAATAGGCTTCGAGATCTTGTCGAATGTTTACTGTGTGTGTGAAGA 648
Db      274 eProGlnIalGlnYsAla-----GlyIleIleArgYrAlaIleGlyValGlyAs 291
Qy      649 T---TTCAATGAG---ACAACAGTGGCCCGGATT-----GCCGACAGTAA 687
Db      291 palAphArgGlnProThraIalLeuGlnGlnIeuenThrIleGlySerAlaProSer 311
Qy      688 GATCATGTGTTCCCGTGAATGACGGCTTTCAGCTCTGCAAGCATCATCTCAAT 747
Db      311 naphisValpelysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330
Qy      748 TTGAAGAAGTCTCGATCGAATTCAGAGCTGAGCATCCACATATGTCAGAGAGA 807
Db      330 eGlnGlnLys-----IlePheAlaIleGlnGlyThrGlnLysArgSerIle 346
Qy      808 GTCAATTCAAGTTCGTGAGAGAAACGGCTTCGACATGCCCGACAGTGCAC 862
Db      346 rSerPheGlnIleGlnLysMetSerGlnGlnGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 10
US-09-350-259-46
/ Sequence 46, Application US/09350259
/ Patent No. 6620915
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6620915el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/350,259
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 46
/ LENGTH: 1155
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-350-259-46

Alignment Scores:
Pred. No.: 2,08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
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DB: 2 Gaps: 14

US-09-970-076-1 (1-1414) x US-09-350-259-46 (1-1155)

QY 28 GGGCGGCTCTGAGGGTCTGGCGAGTTCCGGAGCGTGGAAAGACCGACCTGCTCT 87
 93 GlyLeuSerLeuValAlaAepThrAenAenSerGlnLeuValaCyGglyProthraAla 112
 QY 88 CCCCCGGCTGGCGGC-----CATGGCCACGGCGGAGAGAGCCCTGGCATCGG 138
 113 GlnArgAlaCyAlaLysAenMetTyraLalysGlySerCys-LeuLeuLeuGlySerse 132
 QY 139 CTTCAGTGGCTCTCTTTGGCCACTCTGCTCATCTGTGGCGGGGAGAGGGAGCGAC 198
 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
 QY 199 GGAGAGATGGGGTTCACGCTGCTACGCGC--GGATTGACCTGTACTTCTTTGGACAA 255
 144 -----ProGlnCysProGlnGlnGlnMetAAspIleAlaPheLeuIleAAspG1 159
 QY 256 ATCAGAGAGTGTG---CTGCACCACTGGAAATGAAATCTATTACTTTGTGGAACGTTGGC 312
 159 ySerGlySerIleAAspGlnSerAAspPheThrGlnMetLysAAspPheValLysAlaLeuMe 179
 QY 313 TCACAAATTTCATCAGCCACAGTTGAGAAATGCTCTTATTGTTTCTCCACCGGAGAAC 372
 179 rGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnTySerAenIleLeuLy 199
 QY 373 AACCTTAATGAATCAGACAGAGACAGACAG-----GAACAAATCCGTCMAAG 417
 199 eThrIlePheThrPheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAAspAl 219
 QY 418 CCTAGAAAGAACTCCAGAAAGTTTGCAGAGAGACACTTACATGATGAAGATTGA 477
 219 aIleValGlnLeuGln-----GlyLeuThrTyThrAlaSerGlyIleG1 234
 QY 478 AAGGGCAGTGGAGAGATTATTATGAAGCAAGCAAGGTACAGACAGC---AGCCT 534
 234 nLysValValLysLeuLeuPheHleSerLysAenGlyAlaArgLysSerAlaLysLysB1 254
 QY 535 CATCATTTGCTTGTACTGATGAGAGAACTCCATGAAGATCTCTTTTCTATTCCAGAG--- 589
 254 eLeuIleValIleIleThrAAspGlyGlnLysPheArgAAspProLeuGlnLysrghIshVal11 274
 QY 590 -AGGAGAGCTTAATAGTCTCGAGATCTTGTGCAATGTTACTGTGTTGGTGTGAAGA 648
 274 eProGlnAlaGlnLysAla-----GlyIleIleArgTyraIleGlyValGlyAs 291
 QY 649 T---TTCAATGAG---ACACAGCTGGCCCGGATT-----CGGACACTGA 687
 291 palAphArgGlnProThrAlaLeuGlnGlnLeuAenThrIleGlySerAlaProSerG1 311
 QY 688 GGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTTGCAGAGCACTCACTCAAT 747
 311 nAepHleValAlaPheLysValGlyAen---PheValAlaLeuArgSerIleGlnArgGlnI1 330
 QY 748 TTTCAGAAAGTCTCGATCGAATTTCTAGCAGCTGAACCATCCACCATATGTGAGAGAGA 807
 330 eGlnGlnLys-----IlePheAlaIleGlnGlyThrGlnSerAAspSerse 346
 QY 808 GTCAATTTCAGAGTTTCGTGAGAGAGAAAGGCTTCCGACATGCCCGCAACGTGGAC 862
 346 rSerPheGlnHleGlnLysMetSerGlnGlnGlyPheSerSerAlaLeuSerMetAep 364

DB

RESULT 11

US-08-485-618-53

Sequence 53: Application US/08485618

Patent No. 5728533

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vlieten, Monica

TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 1161 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-618-53

Alignment Scores:

Pred. No.: 2,08e-08 Length: 1161

Score: 167.00 Matches: 77

Percent Similarity: 42.47% Conservative: 50

Best Local Similarity: 25.75% Mismatches: 125

Query Match: 6.57% Indels: 47

DB: 1 Gaps: 14

US-09-970-076-1 (1-1414) x US-08-485-618-53 (1-1161)

QY 28 GGGCGGCTCTGAGGGTCTGGCGAGTTCCGGAGCGTGGAAAGACCGACCTGCTCT 87
 93 GlyLeuSerLeuValAlaAepThrAenAenSerGlnLeuValaCyGglyProthraAla 112
 QY 88 CCCCCGGCTGGCGGC-----CATGGCCACGGCGGAGAGAGCCCTGGCATCGG 138
 113 GlnArgAlaCyAlaLysAenMetTyraLalysGlySerCys-LeuLeuLeuGlySerse 132
 QY 139 CTTCAGTGGCTCTCTTTGGCCACTCTGCTCATCTGTGGCGGGGAGAGGGAGCGAC 198
 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
 QY 199 GGAGAGATGGGGTTCACGCTGCTACGCGC--GGATTGACCTGTACTTCTTTGGACAA 255
 144 -----ProGlnCysProGlnGlnGlnMetAAspIleAlaPheLeuIleAAspG1 159
 QY 256 ATCAGAGAGTGTG---CTGCACCACTGGAAATGAAATCTATTACTTTGTGGAACGTTGGC 312
 159 ySerGlySerIleAAspGlnSerAAspPheThrGlnMetLysAAspPheValLysAlaLeuMe 179
 QY 313 TCACAAATTTCATCAGCCACAGTTGAGAAATGCTCTTATTGTTTCTCCACCGGAGAAC 372
 179 rGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnTySerAenIleLeuLy

Db 179 tclglnleuAlaSerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeu 199
Qy 373 AACCTTAATGAAGTACAGAGACAGA-----GAACAAAATCCGTCAAG 417
Db 199 eThrlshpethrPhethrGluPheIysSerSerLeuSerProGlnSerLeuValAspAl 219
Qy 418 CCTAGAAAGACTCCAGAAAGTTCTGCGACAGAGAGACACTTACATGATGAAGATTGA 477
Db 219 alIeValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleG 234
Qy 478 AAGGCCAGTACAGACAGATTATTATGAAAACAGACAGAGGTACAGACAGCC---AGCCT 534
Db 234 nlysvAlValIlybGluLeuPheIleSerIlysaGlnIyAlaArgIySerAlaIlybAl 254
Qy 535 CATCATGCTTGTGATGATGAGAGAACTCCATGAAATCTCTTTTCTATTATTCAGAG--- 589
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Qy 590 -AGGAGGCTAATAGCTCTCGAGATCTTGTCATTTGTTTACTGTGTGTGAAGA 648
Db 274 eProGluAlaGluIyAla-----GlyIleIleArgIyAlaIleGlyValGlyb 291
Qy 649 T---TTCAATGAG---ACAACAGCTGCGCGGAT-----GCGACAGTAA 687
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Qy 748 TTGGAAGAAGCTCGATGAAATTTAGACAGCTGACCATCATATGTGCAGAGA 807
Db 330 eGlnGlnIyys-----IlePheAlaIleGlnGlnIyThrGlnIySerArgSerSer 346
Qy 808 GTCATTTCAAGTTGTGTCGAGAGAGAAACGGCTTCCAGCATGCCCGCAAGCTGAC 862
Db 346 rSerPheGlnIlybGlnMetSerGlnGlnIyPheSerSerAlaLeuSerMetAsp 364

RESULT 12
US-08-362-652-53
Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-53

Alignment Scores:
Pred. No.: 2,08e-08 Length: 1161
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: Gaps: 14

US-09-970-076-1 (1-1414) x US-08-362-652-53 (1-1161)

Qy 28 GCGCGGCTCCGAGGCTGTCGCGAGTTCGCGAGCGTGGAGAAGCGGACCTGCTCT 87
Db 93 GlyLeuSerLeuValAlaAspThrAsnSerGlnLeuAlaCysGlyProThrAla 112
Qy 88 CCGCGGCTGCGGCG-----CATGGCCACGGCGGAGCGGAGAGCCCTCGCATCGG 138
Db 113 GlnArgAlaCysAlaIlybAsnMetCyrAlaIyGlySerCys-LeuLeuLeuGlyIySer 132
Qy 139 CTTCAAGTGGCTCTCTTGGCCACTGTGCTCATCTGCGCGGCAAGGGGAGCGAG 198
Db 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
Qy 139 GGAGATGGGGGTCCAGCGCTGTAAGCG---GATTGACCTGTAATTTGGAGCA 255
Db 144 -----ProGluCysProGlyGlnGlnIyMetAspIleAlaPheLeuIleAspG 159
Qy 256 ATCAGAAAGTGTG---CTGCACCACTGGAATGAATCTATTCTTTGTGAACAGTTGCG 312
Db 159 ySerGlySerIleAspGlnSerAspPheThrGlnMetIyAspPheValIyAlaLeu 179
Qy 313 TCACAAATTCATCAGCCCAAGTTGAAATGCTTTATTGTTTCTCCACCCGAGAAC 372
Db 179 tclglnleuAlaSerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeu 199
Qy 373 AACCTTAATGAAGTACAGAGACAGA-----GAACAAAATCCGTCAAG 417
Db 199 eThrlshpethrPhethrGluPheIysSerSerLeuSerProGlnSerLeuValAspAl 219
Qy 418 CCTAGAAAGACTCCAGAAAGTTCTGCGACAGAGACACTTACATGATGAAGATTGA 477
Db 219 alIeValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleG 234
Qy 478 AAGGCCAGTACAGACAGATTATTATGAAAACAGACAGAGGTACAGACAGCC---AGCCT 534
Db 234 nlysvAlValIlybGluLeuPheIleSerIlysaGlnIyAlaArgIySerAlaIlybAl 254
Qy 535 CATCATGCTTGTGATGATGAGAGAACTCCATGAAATCTCTTTCTATTATTCAGAG--- 589
Db 254 eleuIleValIleThrAspGlyGlnIlybPheArgAspProLeuGluTyrArgHisValI 274
Qy 590 -AGGAGGCTAATAGCTCTCGAGATCTTGTCATTTGTTTACTGTGTGTGAAGA 648
Db 274 eProGluAlaGluIyAla-----GlyIleIleArgIyAlaIleGlyValGlyb 291
Qy 649 T---TTCAATGAG---ACAACAGCTGCGCGGAT-----GCGACAGTAA 687
Db 291 palapPheArgGluProThrAlaLeuGlnGlnIleuAsnThrIleGlySerAlaProSerG 311
Qy 688 GATCATGCTTCCCGTGAATGACGGCTTTCAGGCTTGCAGAGCATCATCATCAT 747
Db 311 nAspHisValIlePheIyValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330


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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-482-293A-53
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Alignment Scores:
Pred. No.: 2,086-08 Length: 1161
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 1 Gaps: 14
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US-09-970-076-1 (1-1414) x US-08-482-293A-53 (1-1161)

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QY 28 GGCGCGTCCCTGAGGGTCGTGGCGAGTTCGCGAGCGGAGGACCGACCTGCTCT 87
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DB 93 GlyLeuSerLeuValAlaIaAspThrAsnAnSerGlnLeuLeuAlaCysGlyProThrAla 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 88 CCCCAGGCTGCGGGC-----CATGGCCACGGCGGAGCGGAGAGCCCTGGCATCGG 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 GlnArgAlaCysAlaLeuAsnMetTyrAlaLysGlySerCys-LeuLeuLeuGlySerSe 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 139 CTTCCAGTGGCTCTCTTGGCCACTGTGGTGCATCTGCGCGGCGGAGGAGGAGCGAG 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 199 GGAGGATGGGGGTCCAGCCTGCTACCGC--GGATTGACCTGTACTTCATTGGAACAA 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 -----ProGluCysProGlnGlnMetAspIleAlaPheLeuIleAsp 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 ATCAGGAATGTG--CTGCACACCTGGAATGAAATCTTACTTTGTTGGAACAGTTGGC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 159 ySerGlySerIleAspGlnSerAspPheThrGlnMetLysAspPheValLysAlaLeuMe 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 313 TCACAAATTCATCAGCCCAACAGTTCAGAAATGTCCTTATGTTTCTCCACCGGAGAAC 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 179 cGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeu 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 373 AACCTTAATGAACCTGACAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 eThrHisPheThrPheThrGlnPheLysSerLeuSerProGlnSerLeuValAspAl 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 CCTAGAGAACTTCAGAGAAATGTTCTGCGAGGAGAGAGACTTTCATCATGAAAGATTGA 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
DB 219 aIleValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleG 234
QY 478 AAGGCCCATGACAGATTATTTATGAAAACAGAACAGGGTACAGGACAGCC--AGCGT 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 234 nLysValValLysGlnLeuPheHisSerLysAsnGlnAlaArgLysSerAlaLysVal 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 535 CATCATTCCTTTGACTGATGAGAAATCCACATGAAGATCTTTTCTTATTCACAG-- 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 254 eLeuIleValIleThrAspGlnLysPheArgAspProLeuGlnTyrArgHisValI 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 590 -AGGAGGCTAATAGTCTCCGAGATCTTGTCATATGTTTACTGTTGTTGTTGTTGTTG 648
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 274 eProGlnAlaGlnLysAla-----GlyIleIleArgTyrAlaIleGlyValGly 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 649 T--TTCAATGAG--ACACAGCTGCGCCGAGTT-----GCCGACAGTAA 687
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 291 palAheArgGlnProThrAlaLeuGlnGlnLeuAsnThrIleGlySerAlaProSerG 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 688 GGATCATGTGTTCCCGTGATGATGACGGCTTCAGACTTCGACAGGCATCATCCACTCA 747
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 nAspHisValPheLysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGln 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 748 TTTGAAAGAACTCTGCATCGAAATTTCTAGCAGCTGAACCATCCACCATTTGCGAGAA 807
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 eGlnGlnLys-----IlePheAlaIleGlnGlnThrGlnLysSerArgSerSe 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 808 GTCATTTCAAGTTGTCGTAGAGAGAAACGGCTTCGACATGCCCGCAACGTGAC 862
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 rSerPheGlnHisGlnMetSerGlnGlnLysPheSerSerAlaLeuSerMetAsp 364
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-08-943-363-53
/ Sequence 53, Application US/08943363
/ Patent No. 5837478
/
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/
/ INFORMATION FOR SEQ ID NO: 53:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Alignment Scores:
Pred. No.: 2.08e-08 Length: 1161
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 1 Gaps: 14

US-09-970-076-1 (1-1414) x US-08-943-363-53 (1-1161)

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QY 28 GGGCGCTCCTGAGGGCTGTGCGAGTTCCGGAGCGTGGAAAGACGGACCTGCTCT 87
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DB 93 GlyLeuSerLeuValAlaIaepThrIaenAsnSerGlnLeuLeuAlaCysGlyProThrAla 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 88 CCCCAGGCTGCGGGC-----CATGGCCAGCGCGAGCGGAGAGCCCTCGCATCGG 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 GlnArgAlaCysAlaIysAsnMetTyrAlaIysGlySerCys-LeuLeuLeuGlySerSe 132
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QY 139 CTTCCAGTGGCTCTCTTTGGCCACTGTGTCTCATCTGCGCGGCGAAGGGGACGACG 198
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DB 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 199 GAGAGATGGGGGTCCAGCTGTACGGC---GGATTGACCTGTAATTGTTGACAA 255
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DB 144 -----ProGlyCysProGlyGlnGluMetAspIleAlaPheLeuIleAspG1 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 ATCAGAGAAGTGTG---CTGCACCACTGGAATGAATCTATTACTTTGGAACAGTTGGC 312
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DB 159 ySerGlySerIleAspGlnSerAspPheThrGlnMetIysAspPheValIysAlaLeuMe 179
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QY 313 TCACAAATTATCATCAGCCCAAGTGAAGATGCTTATTGTTTCTCCACCGAGAAC 372
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DB 179 rGlyGlnLeuAlaSerThrSerPheSerLeuMetGlnTrpSerAsnIleLeuLy 199
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QY 373 AACCTTAATGAACCTGACAGAACAGACAG-----GAACAAATCCGTCMAAG 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 eThrIlePheThrPheThrGlnPheIysSerSerLeuSerProGlnSerLeuValaIaepAl 219
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QY 418 CTTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACATTACATGATGAAGGATTGA 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 219 aIleValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleG1 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 478 AAGGGCCAGTGAAGCAGATTATTATGAAAACAGCAAGGTACAGACAGC---AGCGT 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 234 nIysValIysAlaIysGlnLeuPheIleSerIysAsnGlyAlaArgIysSerAlaIysIy 254
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QY 535 CATGATTGCTTTGACTGATGAGAACCTCATGAAGATCTCTTTCTATTACAGAG----- 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 254 eIeuIleValIleThrAspGlyGlnIysPheAspAspProLeuGlnIyTrArgIleVal111 274
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QY 590 -AGGAGGCTTAATAGTCTCGAGATCTTGTCATTTGTTACTGTGTGTGAAAGA 648
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DB 274 eProGlnIleGlnIysAla-----GlyIleIleArgTyrAlaIleGlyValIys 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 649 T---TTCAATGAG---ACACAGCTGGCCCGGATT-----GGGACAGTAA 687
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 291 pAlaPheArgGlnProThrAlaIleGlnIleuAsnThrIleGlySerAlaProSerG1 311
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QY 688 GGATCATGTGTTTCCGGAATGACGGGTTTCAAGCTCTGCAAGCATCATCCATCAAT 747
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 nAspIleValaIysPheIysValIysAsn---PheValaIleuArgSerIleGlnArgGlnI1 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 748 TTGGAAGAAGTCTGATCGAATTTCAAGAGCTGAACCATCAATATGTGACAGAGA 807
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DB 330 eGlnGlnIys-----IlePheAlaIleGlnGlyThrGlnSerArgSerSerSe 346
```

```
QY 808 GTGATTTCAGTTGTCTGTAGAGAGAAACGAGCTTCCGACATGCCCGCAAGTGGAC 862
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 rSerPheGlnIleGlnMetSerGlnIleGlyPheSerSerAlaLeuSerMetAsp 364
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: December 14, 2005, 12:02:33
Job time : 63.1092 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 14, 2005, 11:59:14 ; Search time 212.268 Seconds

(Without alignments)
5566.636 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 2540

Sequence: 1 aggaccgcggaggagggcc.....aaaaaaaaaaaaaaaaaaaa 1414

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p.model -DEV=xlp
-Q/cgnt2_1/USPTO.spool_P/US09970076/runat_14122005_110511_26579/app.query.fasta_1.2894
-DB=Published Applications_AA_Main -OPMT=faetan -SUFFIX=rapbm -MINMATCH=0.1
-LOORCL=0 -LOOEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cgi -LIST=45 -DLOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFM=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076@CGN_1_1_604@runat_14122005_110511_26579
-NCPU=6 -ICPU=3 -NO_MMAP -LARGECUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_AA_Main:
1: /cgnt2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgnt2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgnt2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgnt2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
5: /cgnt2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgnt2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1914 | 75.4 | 368 | 6 | US-11-047-278-2 |
| 2 | 1894 | 74.6 | 564 | 3 | US-09-918-715-187 |
| 3 | 1894 | 74.6 | 564 | 3 | US-09-918-715-187 |
| 4 | 1894 | 74.6 | 564 | 3 | US-09-918-715-187 |
| 5 | 1894 | 74.6 | 564 | 4 | US-10-301-822-199 |
| 6 | 1894 | 74.6 | 564 | 4 | US-10-408-765A-1823 |
| 7 | 1894 | 74.6 | 564 | 4 | US-10-474-794-187 |
| 8 | 1894 | 74.6 | 564 | 4 | US-10-474-794-232 |
| 9 | 1894 | 74.6 | 564 | 5 | US-10-979-159-187 |
| 10 | 1894 | 74.6 | 564 | 5 | US-10-979-159-232 |
| 11 | 1889 | 74.4 | 403 | 3 | US-11-047-278-6 |
| 12 | 1870 | 73.6 | 403 | 3 | US-09-833-245-620 |

| | | | | | | |
|----|--------|------|-----|---|-------------------|-------------------|
| 13 | 1793 | 70.6 | 562 | 3 | US-09-918-715-194 | Sequence 194, App |
| 14 | 1793 | 70.6 | 562 | 3 | US-09-918-715-301 | Sequence 301, App |
| 15 | 1793 | 70.6 | 562 | 4 | US-10-474-794-194 | Sequence 194, App |
| 16 | 1793 | 70.6 | 562 | 4 | US-10-474-794-301 | Sequence 301, App |
| 17 | 1793 | 70.6 | 562 | 5 | US-10-979-159-194 | Sequence 194, App |
| 18 | 1793 | 70.6 | 562 | 5 | US-10-979-159-301 | Sequence 301, App |
| 19 | 1670 | 65.7 | 551 | 4 | US-10-038-307-18 | Sequence 18, App |
| 20 | 1670 | 65.7 | 551 | 4 | US-10-038-307-18 | Sequence 18, App |
| 21 | 1654.5 | 65.1 | 564 | 4 | US-10-038-307-20 | Sequence 20, App |
| 22 | 1654.5 | 65.1 | 564 | 4 | US-10-201-292-20 | Sequence 20, App |
| 23 | 1649 | 64.9 | 333 | 3 | US-09-796-753-12 | Sequence 12, App |
| 24 | 1649 | 64.9 | 333 | 4 | US-10-038-307-2 | Sequence 2, App |
| 25 | 1649 | 64.9 | 333 | 4 | US-10-038-307-2 | Sequence 2, App |
| 26 | 1649 | 64.9 | 333 | 6 | US-11-047-278-2 | Sequence 8, App |
| 27 | 1649 | 64.9 | 345 | 4 | US-10-038-307-24 | Sequence 24, App |
| 28 | 1649 | 64.9 | 345 | 4 | US-10-201-292-24 | Sequence 24, App |
| 29 | 1636 | 64.4 | 328 | 4 | US-10-038-307-26 | Sequence 26, App |
| 30 | 1636 | 64.4 | 328 | 4 | US-10-201-292-26 | Sequence 26, App |
| 31 | 1636 | 64.4 | 543 | 4 | US-10-038-307-14 | Sequence 14, App |
| 32 | 1636 | 64.4 | 543 | 4 | US-10-201-292-14 | Sequence 14, App |
| 33 | 1634.5 | 64.4 | 342 | 4 | US-10-038-307-22 | Sequence 22, App |
| 34 | 1634.5 | 64.4 | 342 | 4 | US-10-201-292-22 | Sequence 22, App |
| 35 | 1633 | 64.3 | 543 | 4 | US-10-038-307-16 | Sequence 16, App |
| 36 | 1633 | 64.3 | 543 | 4 | US-10-201-292-16 | Sequence 16, App |
| 37 | 1626 | 64.0 | 543 | 4 | US-10-038-307-10 | Sequence 10, App |
| 38 | 1626 | 64.0 | 543 | 4 | US-10-201-292-10 | Sequence 10, App |
| 39 | 1555 | 61.2 | 534 | 4 | US-10-038-307-12 | Sequence 12, App |
| 40 | 1495 | 58.9 | 534 | 4 | US-10-201-292-12 | Sequence 12, App |
| 41 | 1495 | 58.9 | 534 | 4 | US-10-201-292-34 | Sequence 34, App |
| 42 | 1434.5 | 51.5 | 479 | 4 | US-10-201-292-32 | Sequence 32, App |
| 43 | 1307 | 47.0 | 460 | 4 | US-10-201-292-28 | Sequence 28, App |
| 44 | 1193 | 46.6 | 460 | 4 | US-10-201-292-30 | Sequence 30, App |
| 45 | 1183 | 46.6 | 460 | 4 | US-10-201-292-30 | Sequence 30, App |

ALIGNMENTS

RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Alignment Scores:

Pred. No.: 1.46e-170
Score: 1914.00
Percent Similarity: 100.00%
Best local Similarity: 100.00%
Query Match: 75.35%
DB: 6
Gaps: 0

US-09-970-076-1 (1-1414) x US-11-047-278-2 (1-368)
QY 104 ATGGCAGCGGAGGAGCGGAGCCCTCGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 163

Db 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
QY 164 CTGGTCTCATCTGCGCCCGGCAAGGGGAGACGAGGAGAGATGGGGGTCCAGCTGCTAC 223
Db 21 LeuValLeuIleCysValIleGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTrp 40
QY 224 GCGGATTTGACCTGACTTCAATTTTGGACAATTCAGAAAGTGTGTGACCACTGAGAT 283
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn 60
QY 284 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGATG 343
Db 61 GluIleTrpTrpPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTATTGTTTTTCCCAACCGAGAAACACTTAAATGAAATGACAGAAACAGAA 403
Db 81 SerPheIleValPheSerThrArgGlyThrTrpLeuMetLysLeuThrGlnAspArgGlu 100
QY 404 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATG 463
Db 101 GlnIleArgGlnGlnLeuGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 464 CATGAAGATTTGAAAAGGCGCAGTGAAGATTTATTATGAAAACAGACAAAGGTAACAG 523
Db 121 HisGlnGlyPheGlnLysArgLysSerGlnIleTrpTrpGlnAsnArgGlnGlyArg 140
QY 524 ACAGCCAGGCTCATCTTGTGACTGATGAGAACTCCAGAAATCTCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160
QY 584 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGAGTGAATTTGTTACTGTGTGTGTG 643
Db 161 SerGluArgGlnLysAsnArgSerArgAspLeuGlyAlaIleValTrpCysValGlyVal 180
QY 644 AAGATTTCAATGAGACACAGCTGGCCGAGATTTGCGAGACAGTAAGATCATGTGTTCC 703
Db 181 LysAspPheAsnGlnTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 704 GTGAATGAGGCTTTTNAAGCTCTGCAAGGACATCATCTCAATTTTGAAGAAGTCTTCC 763
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 764 ATCGAAATTTAGACAGCTGAACCATCACTATGTGACAGAGATCATTTCAAGTTTGC 823
Db 221 IleGlnIleLeuAlaIleGlnProSerThrIleCysAlaGlyGlnSerPheGlnValVal 240
QY 824 GTGAGAGAAACGCTTCCGACATGCCCGCAACGTGACAGAGGCTCTGACAGTTTCAAG 883
Db 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGATCTGGTCACTCAATGAGAAAGCTTTTGTGGAACAACCTTATTATACG 943
Db 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGlnAspThrTrpLeuLeu 280
QY 944 TGTCCAGGCTTAATCTTAAAGAAAGTTGGATGAAGAGTGAAGTCACTCCAGGTCAGTGAAC 1003
Db 281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaIleLeuGlnValSerMetAsn 300
QY 1004 GATGGCTCTTTTATTTCTCAGATTGTGCATCATCAACCAACACACTGTTTGAAGGT 1063
Db 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCysSerAspGly 320
QY 1064 TCCATCTTGGCCATGGCCCTGCTGATCCCTGTTCTCTCTTACGCTTGGCTCTCTG 1123
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTTTGGCCCTCTGTGCTGACATGTGATTAATCAAGAGAGTCCCTCCAGCCCTGCGAG 1183
Db 341 TrpPheTrpProLeuCysCysThrValIleIleIleLysGlnValProProProAlaGln 360
QY 1184 GAGAGTGAAGAAATTAATAA 1207

Db 361 GluSerGlnGluAsnLysIleLys 368
RESULT 2
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOGENOUS CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-918-715-187
Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
Gaps: 0
DB: 3
US-09-970-076-1 (1-1414) x US-09-918-715-187 (1-564)
QY 104 ATGGCAGAGGAGGAGGAGGAGGAGCCCTCGGCATCGGCTTCAGAGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGlnArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
QY 164 CTGGTCTCATCTGCGCCCGGCAAGGGGAGACGAGGAGAGATGGGGGTCCAGCTGCTAC 223
Db 21 LeuValLeuIleCysValIleGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTrp 40
QY 224 GCGGATTTGACCTGACTTCAATTTTGGACAATTCAGAAAGTGTGTGACCACTGAGAT 283
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn 60
QY 284 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGATG 343
Db 61 GluIleTrpTrpPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTATTGTTTTTCCCAACCGAGAAACACTTAAATGAAATGACAGAAACAGAA 403
Db 81 SerPheIleValPheSerThrArgGlyThrTrpLeuMetLysLeuThrGlnAspArgGlu 100
QY 404 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATG 463
Db 101 GlnIleArgGlnGlnLeuGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 464 CATGAAGATTTGAAAAGGCGCAGTGAAGATTTATTATGAAAACAGACAAAGGTAACAG 523
Db 121 HisGlnGlyPheGlnLysArgLysSerGlnIleTrpTrpGlnAsnArgGlnGlyArg 140
QY 524 ACAGCCAGGCTCATCTTGTGACTGATGAGAACTCCAGAAATCTCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160
QY 584 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGAGTGAATTTGTTACTGTGTGTGTG 643
Db 161 SerGluArgGlnLysAsnArgSerArgAspLeuGlyAlaIleValTrpCysValGlyVal 180

QY 644 AAAGATTTCATGAGACACAGCTGGCCCGGATTCCGACAGTAAGATCATGTGTTTCCC 703
DB 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 704 GTGAATGACGGCTTTGAGGCTGTGCAAGGATCATCCACTCAATTGGAAGAAGTCTGCG 763
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
QY 764 ATCGAAATTGTAGACAGTGAACCATCCACATATGTGCAGAGAGATTCATTCAAGTTGTC 823
DB 221 IleGlnIleLeuAlaIleGlnProSerThrIleCysAlaGlyGlnSerPheGlnValVal 240
QY 824 GTGAGAGGAAACGGCTTCCGACATGCCCCGACCAAGTGAAGAGGCTCTGTGACGTTCAAG 883
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGACTCGGCACTCAATGAGAGGCCCTTTCTGTGGAAGACACTTATTACTG 943
DB 261 IleAsnAspSerValThrLeuAsnGlnLysPheProPheSerValGlnAspThrTyrLeuLeu 280
QY 944 TGTCACAGCGCTATTCTTAAAGAGTGGACATGAAGCTGCACCTCCAGGTCAAGCATGAAC 1003
DB 281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaIleGlnValIleSerMetAsn 300
QY 1004 GATGGCCTCTTTTATCTCCAGTTCGTGATCATCATCACACACACACTGTTCTGACGGT 1063
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 1064 TCCATCTGGCGCATCGGCTGTGATCTGTCTGTCTGCTGAGGCTGAGCTCTGCTCTG 1123
DB 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
QY 1124 TGGTTCTGGCCCTCTGCTGCTGCATGTGATTAACAAGAGGTCCCTCCACCCCTGCGAG 1183
DB 341 TrpPheThrProLeuLysCysThrValIleIleLysGlnValIleProProProAlaGln 360
QY 1184 GAGAGTAGGAA 1195
DB 361 GluSerGlnGln 364

RESULT 3
US-09-918-715-232
Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRF
ORGANISM: Homo sapiens
US-09-918-715-232

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0

DB: 3 Gaps: 0
US-09-970-076-1 (1-1414) x US-09-918-715-232 (1-564)
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DB 1 MetAlaThrAlaGlnArgAlaLeuGlyIleGlyPheGlnThrLeuSerLeuAlaThr 20
QY 164 CTGTGCTCATCTGCGCGGGGCAAGGGGAGCGAGGAGAGATGGGGTCCAGCTGTGAC 223
DB 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGlnAspGlyGlyProAlaCysTyr 40
QY 224 GCGGATTTGACCGTCACTTTCATTGGAACAATTCAGGAAGTGTGTCACCACTGGAAT 283
DB 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisSerTrpAsn 60
QY 284 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGATG 343
DB 61 GluIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTTATGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAA 403
DB 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnAspArgGln 100
QY 404 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCAGAGAGGACACTTACATG 463
DB 101 GlnIleArgGlnGlyLeuGlnGlnGlnLysValLeuProGlyGlyAspThrTyrMet 120
QY 464 CATGAAGATTGAAAGGCGCAGTAGACAGATTATTAATAAACAAGACAGAGGTACAG 523
DB 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGlnLysArgGlnGlyTyrArg 140
QY 524 ACAGCCGCTCATCATCTGCTTTCAGTGAAGAGAACTCCATGAAGATCTCTTTCTAT 583
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnLysLeuPhePheTyr 160
QY 584 TCAGAGAGGAGGCTAATAGATCTCGAGACTTGTGTCATATGTTACTGTGTGTGTG 643
DB 161 SerGlnArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
QY 644 AAAGATTTCATGAGACACAGCTGGCCCGGATTCCGACAGTAAGATCATGTGTTTCCC 703
DB 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 704 GTGAATGACGGCTTTGAGGCTGTGCAAGGATCATCCACTCAATTGGAAGAAGTCTGCG 763
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
QY 764 ATCGAAATTGTAGACAGTGAACCATCCACATATGTGCAGAGAGATTCATTCAAGTTGTC 823
DB 221 IleGlnIleLeuAlaIleGlnProSerThrIleCysAlaGlyGlnSerPheGlnValVal 240
QY 824 GTGAGAGGAAACGGCTTCCGACATGCCCCGACCAAGTGAAGAGGCTCTGTGACGTTCAAG 883
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGACTCGGCACTCAATGAGAGGCCCTTTCTGTGGAAGACACTTATTACTG 943
DB 261 IleAsnAspSerValThrLeuAsnGlnLysPheProPheSerValGlnAspThrTyrLeuLeu 280
QY 944 TGTCACAGCGCTATTCTTAAAGAGTGGACATGAAGCTGCACCTCCAGGTCAAGCATGAAC 1003
DB 281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaIleGlnValIleSerMetAsn 300
QY 1004 GATGGCCTCTTTTATCTCCAGTTCGTGATCATCATCACACACACTGTTCTGACGGT 1063
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 1064 TCCATCTGGCGCATCGGCTGTGATCTGTCTGTCTGCTGAGGCTGAGCTCTGCTCTG 1123
DB 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
QY 1124 TGGTTCTGGCCCTCTGCTGCTGCATGTGATTAACAAGAGGTCCCTCCACCCCTGCGAG 1183

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Db 341 TtphetpProleucyScyThrValIleIleIyGluValProProProProIaGlu 360
Qy 1184 GAGAGTGAGGAA 1195
Db 361 GluserGluGlu 364

RESULT 4
US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamelkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-301-822-199

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-301-822-199 (1-564)
Qy 104 ATGGCCAGCGGCGGAGGAGAGCCCTCGGCGATCGGCTTCAGTGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGluIuArgAlaGluIleGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Qy 164 CTGGTGTCTATCTGCGCCGCGGAGGAGGAGCGGAGGAGGATGGGGGTCCAGCCTGCTAC 223
Db 21 LeuValIleuIleCysAlaGluIleGlyIleGlyAlaArgGluIuAspGlyGlyProAlaCysTy 40
Qy 224 GGGGAGTTTGACCTGTACTTCACTTTTGGACAAATTCAGAAAGTGTCTGCACCCCTGGAA 283
Db 41 GlyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerValIleuHisIleTrpAsn 60
Qy 284 GAAATCTATTAATCTTTGGGAAAGTGGCTCACAATTCATCGCCCAAGTTGAGAGATG 343
Db 61 GluIleTyrrTyrrPheValGluGluIleuAlaHisLysPheIleSerProGlnLeuArgMet 80
Qy 344 TCTTTATTTGTTTCTCCACCAGGAAACACCTTAATGAAATGACAGAAAGACAGAGAA 403
Db 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Qy 404 CAAATCCGTCAGGCGCTAGAGAAATCCAGAAAGTTTGGCAGAGAGACACTTACATG 463
Db 101 GlnIleArgGlnIleGluGluGluIleuGlnLysValLeuProGlyGlyAspThrTyrrMet 120
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Qy 464 CATGAAGATTGAAAGGCCAGTGAAGACATTTATTAATGAAACAGACAGGTTACAGG 523
Db 121 HisGluGlyPheGluIuArgAlaSerGluGlnIleTyrrTyrrGluAsnArgGlnGlyTyrrArg 140
Qy 524 ACAGCCAGCGGTATCATCTTGTGACTGTAGAGAACTTCAGAAAGATCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleIleIleuThrAspGlyGluLeuHisGluAspLeuPhePheTy 160
Qy 584 TCAGAGAGGAGGAGCTAATAGTGTGAGATCTTGGGCAATTTGATCTGTGTGTG 643
Db 161 SerGluValGluAlaAsnArgSerThrGAspLeuGlyAlaIleValTyrrCysValGlyVal 180
Qy 644 AAAGATTTCAATGAGACACAGCTGGCCCGGATGGCGAGACAGTAAAGATCATGTGTTCC 703
Db 181 LysAspPheAsnGluThrGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Qy 704 GTGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCTCAATTTTGAAGAGTCTGC 763
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysLysSerCys 220
Qy 764 ATCGAAATCTAGCAGCTGAACCATCCACATATGTCAGAGAGATTCATTAAGTTGTC 823
Db 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Qy 824 GTGAGAGGAAACGGCTTCGACATGCGCCGCAACGTGACAGGAGTCTCTGACGTTCAAG 883
Db 241 ValArgGlyAsnGlyPheArgHisAlaIArgAsnValAspArgValLeuCysSerPheLys 260
Qy 884 ATCAATGACTCGGTCACTCACTCAATGAAAGCCCTTTCTGTGGAGACATTTATTCAG 943
Db 261 IleAsnAspSerValThrIleuAsnGluLysProPheSerValGluAspThrTyrrIleuLeu 280
Qy 944 TGTCCAGCGCTATCTTAATAAGAGTGGCATGAAGAGTCACTCCAGGTCAGCATGAAC 1003
Db 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIleuGlnValSerMetAsn 300
Qy 1004 GATGGCTCTCTTTATCTTCAGTTCGATTCATCATCCACACACAGACTGTTCGACG 1063
Db 301 AspGlyLeuSerPheIleSerSerValIleIleIleThrThrThrIleCysSerAspGly 320
Qy 1064 TCCATCTCTGGCATGCGCTGCTGATCCGTGTTCTCTGCTCTGAGCCCTGCTCTCTGG 1123
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Qy 1124 TGGTTCGGCCCTCGCTGCTGCACTGATTAATCAAGAGAGTCCCTCCACCCCTGCCAG 1183
Db 341 TtphetpProleucyScyThrValIleIleIyGluValProProProProIaGlu 360

Qy 1184 GAGAGTGAGGAA 1195
Db 361 GluserGluGlu 364

RESULT 5
US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Boi D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
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; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-408-765A-1823 (1-564)

QY 104 ATGGCCAGCGGAGCGGAGAGCCCTGCGCATCGGCTTCAGTGGCTCTCTTGGCCACT 163
DB 1 MetAlaThrAlaGluArgAlaGluAlaGluAlaGluAlaGluAlaGluAlaThr 20

QY 164 CTGGTGTCTATCTGCGCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTAC 223
DB 21 LeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40

QY 224 GGGGAGTTTGACCTGTACTTCAATTTGGACAAATCAGAAATGCTGTGACCACTGGAAT 283
DB 41 GlyGlyPheAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60

QY 284 GAATCTATTACTTTGTGAAACAGTTGGCTCACAATTCATCAGCCCACTTGAGATG 343
DB 61 GluIleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80

QY 344 TCTCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAATCTGAACAAAGACAGAA 403
DB 81 SerPheIleValPheSerThrArgGlyThrThiLeuMetLeuLeuLeuLeuLeuLeu 100

QY 404 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCGAGGAGGACCTTAATG 463
DB 101 GlnIleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120

QY 464 CATGAAGATTGTGAAGGCGCAGTGCAGACATTTATTATGAACAAGAGGTACAGG 523
DB 121 HisGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140

QY 524 ACAGCCAGCGTCATCTGCTTGTGATGAGGAACTCCATGAAGATCTTTTCTAT 583
DB 141 ThrLeuSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheLeu 160

QY 584 TCAGAGAGGAGGCTAATAGGCTCGAGACTTGTGTCATTTGTTTCTGTGAGGTG 643
DB 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180

QY 644 AAGATTTCATATGACAGACAGCTGGCCGAGATTGCGGACAGTAAGATCAATGTGTTCC 703
DB 181 LeuAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLeuValPhePro 200

QY 704 GTGAATACGCGCTTTCAGGCTCTGCAAGGACATCATCACTCAATTTGAAAGATCTCC 763
DB 201 ValAsnAspArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValLeuSerCys 220

QY 764 ATGCAATTTCTAGAGAGTGAACATTCACCAATATGTGAGAGAGATGATTTCAAGTTGTC 823
DB 221 IleGluIleLeuAlaAlaGluPheSerThrIleCysAlaGlyGluSerPheGlnValVal 240

QY 824 GTGAGAGAAACGCGCTTCGACATGCCGCAACGTGACAGAGGTCTCTGACGCTTCAAG 883
DB 241 ValArgGlyAsnGlnPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLeu 260

QY 884 ATCAATGACTGGTGCACACTCAATGAGAACCTTTTCTGTGAAAGACCTTAATTTACTG 943
DB 261 IleAsnAspSerValThrLeuAsnGlnLeuArgProPheSerValGluAspThrTyrLeuLeu 280

QY 944 TGTCAGGCGCTAATCTTAAAGAAAGTTGGCAAGGTGACCTCCAGGTCAAGATGAC 1003
DB 944 TGTCAGGCGCTAATCTTAAAGAAAGTTGGCAAGGTGACCTCCAGGTCAAGATGAC 1003
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DB 281 CysProAlaProIleLeuLeuGluValGlyMetLeuAlaAlaLeuGlnValSerMetAsn 300
QY 1004 GATGGCCTCTCTTTTATCTCCAGTTCTGTGCATATACACCAACACACTGTTGACGGT 1063
DB 301 AspGlyLeuSerPheIleSerPheSerValIleIleThrThrThiCysSerAspGly 320
QY 1064 TCCATCTGGCCATCCGCGCTGATCTGTTCTCTGCTCTGACCCCTGGCTCTCTGG 1123
DB 321 SerIleLeuAlaIleAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 340
QY 1124 TGGTGTGCGCCCTGTCTGTGCACCTGATATATCAAGAGAGTCCCTCAACCCCTGCCAG 1183
DB 341 ThrPheThrProLeuLeuCysThrValIleIleLeuGluValProProProAlaGlu 360
QY 1184 GAGAGTGAGGAA 1195
DB 361 GluSerGluGlu 364

RESULT 6
US-10-474-794-187
; Sequence 187, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-187

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-474-794-187 (1-564)

QY 104 ATGGCCAGCGGAGCGGAGAGCCCTGCGCATCGGCTTCAGTGGCTCTCTTGGCCACT 163
DB 1 MetAlaThrAlaGluArgAlaGluAlaGluAlaGluAlaGluAlaGluAlaThr 20

QY 164 CTGGTGTCTATCTGCGCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTAC 223
DB 21 LeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40

QY 224 GGGGAGTTTGACCTGTACTTCAATTTGGACAAATCAGAAATGCTGTGACCACTGGAAT 283
DB 41 GlyGlyPheAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60

QY 284 GAATCTATTACTTTGTGAAACAGTTGGCTCACAATTCATCAGCCCACTTGAGATG 343
DB 61 GluIleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80

QY 344 TCTCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAATCTGAACAAAGACAGAA 403
DB 81 SerPheIleValPheSerThrArgGlyThrThiLeuMetLeuLeuLeuLeuLeuLeu 100
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QY 404 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACATTACATG 463
| | | | |
DB 101 GlnIleArgGlnGlnIleuGlnIleuGlnIleuValIleuProGlyGlyAspThrTyrMet 120
QY 464 CATGAAGATTGAAAAGGCGCAGTGCAGATTTATTATGAAAACAGACAGAGGTACAG 523
| | | | |
DB 121 HIsGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGlnAsnArgGlnGlyTyrAsp 140
QY 524 ACAGCCAGGCTCATCTGCTTGTGATGATGAGAACTCCATGAAGATCCTTTTCTAT 583
| | | | |
DB 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGlnLeuHisGlnAsnLeuPhePheTyr 160
QY 584 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCGCAATTGTTTACTGTGTGTGTG 643
| | | | |
DB 161 SerGlnArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValIleGlyVal 180
QY 644 AAAAGATTCAATGAGACACAGCTGGCCCGATTTGGCGACAGTAAAGATCATGTGTTCCC 703
| | | | |
DB 181 LysAspPheAsnGlnIleuArgIleuAlaArgIleAlaAspSerLysAspHisValIlePhePro 200
QY 704 GTGAATGAGCGGCTTTCAGGCTCGCAAGGCATCATCAATTTTGAAGAAGCTCTCG 763
| | | | |
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysSerCys 220
QY 764 ATCGAAATTTCTAGCAGCTGAAACCATCCACATATGTGCAAGAGATCATTTCAAGTTGATC 823
| | | | |
DB 221 IleguIleuAlaIleuAlaIleuProSerThrIleCysAlaGlyGlnSerPheGlnValVal 240
QY 824 GTGAGAGAAAACGGCTTCCGACATGCCCCGCAACGTGACAGAGGTCTCTGACGTTCAAG 883
| | | | |
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGAGCTCGGTGCACACTCAATGAGAAAGCCCTTTCTGTGAGAGACATTTTAACTG 943
| | | | |
DB 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGlnAspThrTyrLeuLeu 280
QY 944 TGTCACCGCCTATCTTAAAGAGTTGGCATGAAAGCTGACATCCAGGTCAAGTCAAGTAAAC 1003
| | | | |
DB 281 CysProAlaProIleuLysGlnValGlyMetLysAlaIleuGlnValIleSerMetAsn 300
QY 1004 GATGGCTCTCTTTTATCTTCCAGTCTGTGCATATATACCCACACACATGTTTGAACGT 1063
| | | | |
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrIleCysSerAspGly 320
QY 1064 TCCATCTGGCCATCGCCCTGATCGTCTGCTCTGCTCTGACCTGAGTCTCTCTGAG 1123
| | | | |
DB 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
QY 1124 TGGTCTGGCCCTCTGTGCTGCACTGTGATTATCAGAGAGGTCCCTCCACCCCTGCGCAG 1183
| | | | |
DB 341 TrpPheTrpProLeuCysCysThrValIleIleIleLysGlnValProProProProAlaGln 360
QY 1184 GAGAGTGAGGAA 1195
| | | | |
DB 361 GluSerGlnGln 364
| | | | |
RESULT 7
US-10-474-794-232
; Sequence 232, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107,00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
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; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-474-794-232

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-474-794-232 (1-564)
QY 104 ATGGCCACGCGGAGCGAGAGAGCCCTCGGATCGGCTTCAGTGCTCTTTGGCCACT 163
| | | | |
DB 1 MetAlaThrAlaGlnArgArgAlaLeuGlyIleGlyPheGlnThrLeuSerLeuAlaThr 20
QY 164 CTGTCCTCATCTGCGCCGCGGCAAGGGGAGCCGAGGAGAGATGGGGGTCCAGCTTCTAC 223
| | | | |
DB 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGlnAspGlyGlyProAlaCysTyr 40
QY 224 GCGGATTTGACCTGATCTTCAATTTTGGACAATCAGAAAGTGTGTCGACCACTGGAAT 283
| | | | |
DB 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisStrPheAsn 60
QY 284 GAAATCTATTACTTTGTGGAAAGTTGGCTCACAATTCATACGCCACAGTTGAGAAATG 343
| | | | |
DB 61 GluIleTyrTyrPheValGlnGlnIleuAlaHisLysPheIleSerProGlnLeuAlaGmet 80
QY 344 TCTTTATTTGTTTCTCCACCCGAGGAAACAACCTTAATGAATCTGACAGAGACAGAGA 403
| | | | |
DB 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnAspArgGln 100
QY 404 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACATTACATG 463
| | | | |
DB 101 GlnIleArgGlnGlnIleuGlnIleuGlnIleuValIleuProGlyGlyAspThrTyrMet 120
QY 464 CATGAAGATTGAAAAGGCGCAGTGCAGATTTATTATGAAAACAGACAGAGGTACAG 523
| | | | |
DB 121 HIsGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGlnAsnArgGlnGlyTyrAsp 140
QY 524 ACAGCCAGGCTCATCTGCTTGTGATGATGAGAACTCCATGAAGATCCTTTTCTAT 583
| | | | |
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnAsnLeuPhePheTyr 160
QY 584 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCGCAATTGTTTACTGTGTGTGTG 643
| | | | |
DB 161 SerGlnArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValIleGlyVal 180
QY 644 AAAAGATTCAATGAGACACAGCTGGCCCGATTTGGCGACAGTAAAGATCATGTGTTCCC 703
| | | | |
DB 181 LysAspPheAsnGlnIleuArgIleuAlaArgIleAlaAspSerLysAspHisValIlePhePro 200
QY 704 GTGAATGAGCGGCTTTCAGGCTCGCAAGGCATCATCAATTTTGAAGAAGCTCTCG 763
| | | | |
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysSerCys 220
QY 764 ATCGAAATTTCTAGCAGCTGAAACCATCCACATATGTGCAAGAGATCATTTCAAGTTGATC 823
| | | | |
DB 221 IleguIleuAlaIleuAlaIleuProSerThrIleCysAlaGlyGlnSerPheGlnValVal 240
QY 824 GTGAGAGAAAACGGCTTCCGACATGCCCCGCAACGTGACAGAGGTCTCTGACGTTCAAG 883
| | | | |
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGAGCTCGGTGCACACTCAATGAGAAAGCCCTTTCTGTGAGAGACATTTTAACTG 943
| | | | |
DB 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGlnAspThrTyrLeuLeu 280
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/ CURRENT FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US/09/918,715
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FastSeq for windows Version 3.0
/ SEQ ID NO 232
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-970-159-232

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 5 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-979-159-232 (1-564)

QY 104 ATGGCCAGCGGCGAGGAGAGAGCCCTCGGCATCGCTTCAGAGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGluArgAlaGluAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20

QY 164 CTGTGCTCATCTGCGCCGCGGCAAGCGGAGACGCGAGGAGAGATGGGGCTCGACTAC 223
Db 21 LeuValLeuIleIleCyAlaGlyGlnGlyArgArgGluAspGlyIleProAlaCysTrp 40

QY 224 GGGCGATTGACCTGACTTCACTTTCATTTGGACAAATTCAGAAAGTGCTGTCACCACTGGAA 283
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60

QY 284 GAAATCTATTACTTTGTGGAACAGTGGGCTCAAAATTCATATCAGCCACAGTTTGAGAATG 343
Db 61 GluIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80

QY 344 TCCCTTATTTGTTTCTCCACCCGAGGAGAACACCTTATGAACTGACAGAGACAGAGA 403
Db 81 SerPheIleValPheSerThrArgGlyTrpThrLeuMetLysLeuThrGluAspArgGlu 100

QY 404 CAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGGAGAGACACTTACATG 463
Db 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120

QY 464 CATGAGAGATTGAAAGGCGCAGTGAAGCATTTATGAAAGACAGACAGGCTCAGG 523
Db 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTrpTrpGlnAsnArgGlnGlyTrpAsn 140

QY 524 ACAGCAGGCTCATCTGCTTTCATGCTGATGAGAACTCCATGAGATCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160

QY 584 TCAGAGAGGAGGCTTAATAGGTTTCGAGATCTTGGTGAATTTGTTACTGTGTGGTGG 643
Db 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValGlyVal 180

QY 644 AAAAGATTTCAATGAGACAGAGCTGGCCCGGATGGCGGACAGTGAAGATCATGTGTTCC 703
Db 181 LysAspPheAsnGlnIleThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200

QY 704 GTGAATGAGCGCTTTCAGGCTTCGACAGGATCATCATTTTGAAGAAGTCTGCG 763
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220

QY 764 ATCGAAATTTCTAGCAGCTGAACCATCCACCAATATGTGACAGAGAGTTCATTTCAAGTTGTC 823
Db 764 ATCGAAATTTCTAGCAGCTGAACCATCCACCAATATGTGACAGAGAGTTCATTTCAAGTTGTC 823
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Db 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY 824 GTGAGAGAAAAGCGTTCCGACATGCGCCGCAACGTGACAGGGTCTCTGACGTTCAAG 883
Db 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerThrLys 260
QY 884 ATCAATGACTCGGTGACACTCAATGAGAGAGCCCTTTCTGTGGAAAGACATTATTACTG 943
Db 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTrpLeuLeu 280
QY 944 TGTCCAGGCGCTTATTTAAAGAAAGTGGCAATGGAAGCTGCAGCTCAGTCAAGTGAAC 1003
Db 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
QY 1004 GATGCGCTCTCTTTATCTCCAGTTCTGTTCATCATCACCCACACACTGTTCTGACGCT 1063
Db 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrThiIleCysSerAspGly 320
QY 1064 TCCATCTGGCCATGCGCTGCTGATCTGTTCTGCTTCCTAGCCCTGGCTCTCTGCG 1123
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTCTGGCCCTCTGCTGCTGCACTGTGATTATCAGAGAGTCCCTCCAGCCCTGCGAG 1183
Db 341 TrpPheTrpProLeuCysCysThrValIleIleIleLysGluValProProProAlaGlu 360
QY 1184 GAGAGTGAAGAA 1195
Db 361 GluSerGlnGlu 364

RESULT 10
US-11-047-278-6
/ Sequence 6, Application US/11047278
/ Publication No. US20050196407A1
/ GENERAL INFORMATION:
/ APPLICANT: Young, John A.T.
/ APPLICANT: Bradley, Kenneth A.
/ APPLICANT: Collier, Robert J.
/ APPLICANT: Mogridge, Jeremy S.
/ TITLE OF INVENTION: Anthrax Toxin Receptor
/ FILE REFERENCE: 960296, 97745
/ CURRENT APPLICATION NUMBER: US/11/047,278
/ PRIOR FILING DATE: 2005-01-31
/ PRIOR APPLICATION NUMBER: US/09/970,076
/ PRIOR FILING DATE: 2001-10-03
/ PRIOR APPLICATION NUMBER: 60/251,481
/ PRIOR FILING DATE: 2000-12-05
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-047-278-6

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-1 (1-1414) x US-11-047-278-6 (1-564)

QY 104 ATGGCCAGCGGCGAGGAGAGCCCTCGGCATCGGCTTCAGAGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGluArgAlaGluAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20

QY 164 CTGTGCTCATCTGCGCCGCGGCAAGCGGAGACGCGAGGAGAGATGGGGCTCGACTAC 223
Db 21 LeuValLeuIleIleCyAlaGlyGlnGlyArgArgGluAspGlyIleProAlaCysTrp 40
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QY 224 GGGGATTTGACCTGATCTCATTTTGGACAATTCAGAAAGTGCTGACACAGTGAAT 283
DB 41 G1yG1yPheAspLeuYrPheI1eLeuAspLysSerG1ySerValLeuH1sh1StrPha 60
QY 284 GAAATCTATTACTTTGTGAAACAGTTGGCTCCACAATTCATCAGCCACAGTTGAGAATG 343
DB 61 G1u1leTyTyRrPheValG1uG1nLeuAlaH1sh1bYrPheH1leSerProG1nLeuA1gMet 80
QY 344 TCTTTATTGTTTCTCCACCCGAGAAACCTTAATGAATCTGACAGAAAGACAGAA 403
DB 81 SerPheH1leValPheSerThrArgG1yThrTh1eUmetLysLeuThrG1uAspArgG1u 100
QY 404 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGACAGAGGACCTTCATG 463
DB 101 G1n1leArgG1nG1yLeuG1uG1nLeuG1nLysValLeuProG1yG1yAspTr1yRmet 120
QY 464 CATGAAGATTTGAAAGGCGCAGTGAAGACAGATTTATTATGAAAACAGACAGGCTACAG 523
DB 121 H1eG1uG1yPheG1uArgAlaSerG1uG1n1leTyTyRrG1uAsnArgG1nG1yTyArg 140
QY 524 ACAGCCAGCTCATCATGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 583
DB 141 ThrAlaSerVal1le1leAlaLeuThrAspG1yG1uLeuH1eG1uAspLeuPhePheTyR 160
QY 584 TCAGAGAGGAGGCTAATAGCTCTCGAATCTTGTCGATTTGTTTACTGTTGGTGTG 643
DB 161 SerG1uArgG1uAlaAsnArgSerArgAspLeuG1yAla1leValTyRysValG1yVal 180
QY 644 AAAGATTTCAATGAGACACAGCTGGCCGAGATTGGCGACAGTAAAGATCATGTGTTTCCC 703
DB 181 LysAspPheAsnG1uThrG1nLeuAlaArg1leAlaAspSerTyAspH1sh1StrPha 200
QY 704 GTGAATGACGGCTTTCAGGCTCTGCAAGGACATCATCTCAATTTTGAAGAGTCTGTC 763
DB 201 ValAsnAspG1yPheG1nAlaLeuG1nG1y1le1leH1Ser1leLeuLysSerCys 220
QY 764 ATCGAATTTCTAGAGCTGAACCATTCACATATGTCAGAGAGTCAATTTCAAGTTGTC 823
DB 221 1leG1u1leLeuAlaAlaG1uProSerThr1leCysAlaG1yG1uSerPheG1nVal 240
QY 824 GTGAGAGAAACGGCTTCCGACATGCCCGCAACGTGACAGAGGCTCTGACAGCTTCAAG 883
DB 241 ValArgG1yAsnG1yPheAlaArgH1sh1AlaArgAsnValAspArgValLeuCySerPheLys 260
QY 884 ATCAATGACTCGGTACACTCAATGAGAAAGCTTTTCTGTGAAGACACTTATTATCTG 943
DB 261 1leAsnAspSerVal1ThrLeuAsnG1uLysPhePheSerValG1uAspTr1yRLeu 280
QY 944 TGTCACAGCGCTATCTTAAAGAAAGTTGGCATGAAGCTGACCTCCAGGTCAGATGAAC 1003
DB 281 CysProAlaPro1leLeuLysG1uValG1yMetLysAla1leLeuG1nVal1SerMetAsn 300
QY 1004 GATGCGCTCTCTTTATCTCCAGTTCTGTGATCATCAACACACACACTGTTTCAAGCT 1063
DB 301 AspG1yLeuSerPheH1leSerSerVal1le1leH1ThrTr1sh1eCySerAspG1y 320
QY 1064 TCCATCTCTGGCATCGCCCTGCTGATCTGTCTCTGCTCTGAGCTGCTCTCTG 1123
DB 321 Ser1leLeuAla1leAlaLeuLeu1leLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTTCTGGCCCTCTGCTGACATGTGATTATCAAGAGGTCCTCCACCCCTGCCGAG 1183
DB 341 TrpPheTrpProLeuCySerThrVal1le1leLysG1uValProProProAlaG1u 360
QY 1184 GAGAGTGAGAA 1195
DB 361 G1uSerG1uG1u 364

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RESULT 11
 US-09-833-245-621
 ; Sequence 621, Application US/09833245
 ; Publication No. US20040010134A1
 ; GENERAL INFORMATION:

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; APPLICATION: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albinin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-833-245-621

Alignment Scores:
pred. No.: 3 39e-168 length: 403
Score: 1889.00 Matches: 363
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.37% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-1 (1-1414) x US-09-833-245-621 (1-403)

QY 104 ATGGCCAGCGGCGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 163
DB 1 MetAlaThrAlaG1uArgArgAlaLeuG1y1leG1yPheG1nTrpLeuSer1eAlaThr 20
QY 164 CTGGTCTCATCTGCGCCGCGGCAAGGGGACGACGAGAGAGTGGGGCTCCAGCTCTGAC 223
DB 21 LeuValLeu1leCysAlaG1yG1nG1yArgArgG1uAspG1yG1yProAlaCyTyR 40
QY 224 GGGGATTTGACCTGATCTCATTTTGGACAATTCAGAAAGTGCTGACACAGTGAAT 283
DB 41 G1yG1yPheAspLeuYrPheI1eLeuAspLysSerG1ySerValLeuH1sh1StrPha 60
QY 284 GAAATCTATTACTTTGTGAAACAGTTGGCTCCACAATTCATCAGCCACAGTTGAGAATG 343
DB 61 G1u1leTyTyRrPheValG1uG1nLeuAlaH1sh1bYrPheH1leSerProG1nLeuA1gMet 80
QY 344 TCTTTATTGTTTCTCCACCCGAGAAACCTTAATGAATCTGACAGAAAGACAGAA 403
DB 81 SerPheH1leValPheSerThrArgG1yThrTh1eUmetLysLeuThrG1uAspArgG1u 100
QY 404 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGACAGAGGACCTTCATG 463
DB 101 G1n1leArgG1nG1yLeuG1uG1nLeuG1nLysValLeuProG1yG1yAspTr1yRmet 120
QY 464 CATGAAGATTTGAAAGGCGCAGTGAAGACAGATTTATTATGAAAACAGACAGGCTACAG 523
DB 121 H1eG1uG1yPheG1uArgAlaSerG1uG1n1leTyTyRrG1uAsnArgG1nG1yTyArg 140
QY 524 ACAGCCAGCTCATCATGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 583
DB 141 ThrAlaSerVal1le1leAlaLeuThrAspG1yG1uLeuH1eG1uAspLeuPhePheTyR 160
QY 584 TCAGAGAGGAGGCTAATAGCTCTCGAATCTTGTCGATTTGTTTACTGTTGGTGTG 643
DB 161 SerG1uArgG1uAlaAsnArgSerArgAspLeuG1yAla1leValTyRysValG1yVal 180
QY 644 AAAGATTTCAATGAGACACAGCTGGCCGAGATTGGCGACAGTAAAGATCATGTGTTTCCC 703
DB 181 LysAspPheAsnG1uThrG1nLeuAlaArg1leAlaAspSerTyAspH1sh1StrPha 200
QY 704 GTGAATGACGGCTTTCAGGCTCTGCAAGGACATCATCTCAATTTTGAAGAGTCTGTC 763
DB 201 ValAsnAspG1yPheG1nAlaLeuG1nG1y1le1leH1Ser1leLeuLysSerCys 220

```


QY 1124 TGGTTCGCGCCCTCTGCTGCACTGTATTTATCAAGAGGTCCTCCATCCAGCCCTCCGAG 1183
| | | | |
DB 341 TTPPhetPrProLeuCyCySthValIleIleYsgluValProProProAlaGlu 360
| | | | |
QY 1184 GAGAGTGAG 1192
| | | | |
DB 361 GluSerGlu 363
| | | | |
RESULT 13
US-09-918-715-194
; Sequence 194, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-194
Alignment Scores:
Pred. No.: 4.05e-159 Length: 562
Score: 1793.00 Matches: 342
Percent Similarity: 97.75% Conservative: 6
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 70.59% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-1 (1-1414) x US-09-918-715-194 (1-562)
QY 128 CTCGCAATCGGCTTCAGTGGCTCTCTTTGGCCACTGTGCTCATCTGCGCGGCA 187
| | | | | : : : | | | | | : : : | | | | |
DB 7 LeuclYlaagLYleuAagLYleuCyvalAlaIleValIleValIleValIleGlyHis 26
| | | | |
QY 188 GGGGAGCGAGGAGGATGGGGGTCAGCCCTGCTACGGCGGATTTGACTGTACTTCA 247
| | | | |
DB 27 GYlYlYatrgatrgLYuaprgLYglYProAlaCystrYrgLYglYpheaSpleuTYrPheIle 46
| | | | |
QY 248 TTGACAAATCAGAAAGTGTCTGACCACTGGAATGAATCTTCTTGTGGAACAG 307
| | | | |
DB 47 LeuApySserGlySerValIleuHisIstrPaangluIleTYrTYrPheValGluGln 66
| | | | |
QY 308 TTGGCTCACAATTCATCAGCCCAAGTTCGAAATGTCCTTATGTTTCTCCACCGA 367
| | | | | : : : | | | | | : : : | | | | |
DB 67 LeuAlaHisArgPheIleSerProGlnIleuArgMetSerPheIleValPheSerThrArg 86
| | | | |
QY 368 GGAACAACTTAATGAATCTGACAGAGAGACAGAAACAATCCGTCAGAGCCTTGAAGAA 427
| | | | |
DB 87 GYlYrThrLeuMetLYleuThrGluuaprgGluGlnIleArgGlnIleuGluGln 106
| | | | |
QY 428 CTCGAGAAAGTTCGCGGAGGAGGAGACCTTAACATGATGAAGATTTGAAGGCGCAGT 487
| | | | |
DB 107 LeuGlnLYvalLeuProGlyGlyAapThrTYrMetHisGluGlyPheGluArgAlaSer 126
| | | | |
QY 488 GAGCAGATTTATTAAGAAACAGACAGAGGTAACAGAGCAGGCGTCAATGCTTGG 547
| | | | |
DB 127 GluGlnIleTYrTYrGluuAensSerGlnIleTYrArgThrAlaSerValIleIleIleu 146
| | | | |

QY 548 ACTGATGAGAACTCCATGAAGATCTTTTCTATTCAGAGAGGAGCTAATAGCTCT 607
| | | | |
DB 147 ThrAapGlyGluuIleuHisGluuAapLeuPhePheTYrSerGluuArgGluuAlaAenArgSer 166
| | | | |
QY 608 CGAGATCTTGGTGCATTTGTTACTGTGTGGTGCAGAAAGATTTCAATGACAGACAGCTG 667
| | | | |
DB 167 ArgAapLeuGlyAlaIleValTYrCySValGlyValIleAapPheAenGluThrGlnLeu 186
| | | | |
QY 668 GCCCGGATTCGGAGACAGTAAGATCAATGTGTTTCCCGTGAATGACGGCTTTCAGGCTG 727
| | | | |
DB 187 AlaArgIleAlaAapSerLYsaPheHisValPheProValAaAapSilyPheGlnAlaLeu 206
| | | | |
QY 728 CAAGCATCATCCATCAATTTGAAGAAGTCTGATGAGAAATTTAGACAGCTGAACCA 787
| | | | |
DB 207 GlnGlyIleIleHisSerIleLeuYsLYSerCYsIleGluIleuAlaIleGluPro 226
| | | | |
QY 788 TCCACATATGTGACAGAGAGTCAATTCAGTTGTGTGAGAGAGAAACGGCTTCCGACAT 847
| | | | |
DB 227 SerThrIleCYsaIleGlyuSerPheGlnValIleValArgGlyAangIYPheArgHis 246
| | | | |
QY 848 GCCCGCAAGCTGACAGAGGGTCTCTGCAAGTCAAGATCAATGACTCCGTCACACTCAAT 907
| | | | |
DB 247 AlaArgAaValAaAapArgValIleuCySerPheLYsIleAaAapSerValIthrLeuAen 266
| | | | |
QY 908 GAGAGCCCTTTCTGTGGAAGACACTTATTTACTGTGTCCAGCGCTATCTTAAAGAA 967
| | | | |
DB 267 GluLYaPhePheAlaValGluAapThrTYrLeuLeuCYeProAlaProIleLeuLYsGlu 286
| | | | |
QY 968 GTTGGCATGAAGCTGCACTCCAGGTCAAGCATGAGATGAGCCTCTCTTTATCTCCAGT 1027
| | | | |
DB 287 ValGlyMetLYsaIleAlaIleuGlnValSerMetAaAapSilyuSerPheIleSerSer 306
| | | | |
QY 1028 TCTGTATCATCAACCAACACACTGTTGACAGGTTCCATCCTGGCAATCGGCGCTGCTG 1087
| | | | |
DB 307 SerValIleIleThrThrThrHisCySerAapSilySerIleuAlaIleAlaLeuLeu 326
| | | | |
QY 1088 ATCCTGTCTCTGCTCTAGCGCTGCTCTCTCTGTGATGTTCTGAGCCCTCTGCTGCACT 1147
| | | | | : : : | | | | | : : : | | | | |
DB 327 ValIleuPheLeuLeuAlaLeuAlaLeuIleThrIleThrPheTrpProLeuCYeSth 346
| | | | |
QY 1148 GTGATTAATCAAGAGGTCCTCCACCCCTCCGAGAGAGTAGAGAA 1195
| | | | |
DB 347 ValIleIleLYsgluValIleProProProValIleGluSerGluGln 362
| | | | |
RESULT 14
US-09-918-715-301
; Sequence 301, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-301
Alignment Scores:
Pred. No.: 4.05e-159 Length: 562
Score: 1793.00 Matches: 342

Percent Similarity: 97.75% Conservative: 6
 Best Local Similarity: 96.07% Mismatches: 8
 Query Match: 70.59% Indels: 0
 DB: 3 Gaps: 0

US-09-970-076-1 (1-1414) x US-09-918-715-301 (1-562)

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128 CTCGGATCGGCTTCAGATGGCTCTCTTTGGCCACTGTGGTCACTTCGCCGGGCAA 187
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  LeuGlyAlaGlyLeuArgGlyLeuCySValAlaAlaLeuValLeuValCySAlaGlyHis 26

QY 188 GGGGGACGAGAGGAGATGGGGCTCCAGCCCTGTACGCGGATTTGACCTGTACTT 247
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  27 GlyGlyArgArgGlyLeuArgGlyGlyProAlaCySValGlyGlyPheAspLeuTyrPheIle 46

QY 248 TTGGCAAAATTCAGAGTGTGTCGACCACTGGAATGAATCATCTTGGAGACAG 307
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  47 LeuAspLysSerGlySerValLeuHisStrPaSngInIleTyrTyrPheValGluGln 66

QY 308 TTGGCTCACAAATTCATCAGCCACAGTTGAGAATGCTCTTATGTTTTCACCCGA 367
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  67 LeuAlaHisArgPheIleSerProGlnLeuArgMetSerPheIleValIleSerThrArg 86

QY 368 GGAACAACCTTAAATGAAGTGAACAAGACAGAACAAAATCCGTCAAGGCTTAGAAG 427
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  87 GlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGluGln 106

QY 428 CTCGCAAAAGTTCTGCGAGAGAGACACTTACATGAGAAAGATTTGAAAGGCGCAGT 487
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  107 LeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGlnIlyPheGlnArgAlaSer 126

QY 488 GAGCAGATTATATGAAAAACAGACAGGATACAGACAGCCGCTCATCTTGGCTTGG 547
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  127 GluGlnIleTyrTyrGluAsnSerGlnGlyTyrArgThrIleSerValIleIleAlaLeu 146

QY 548 ACTGATGGAAGTCCATGAGAAATCTCTTTTCTTATTCAGAGGAGGCTAATAGTCT 607
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  147 ThrAspGlyGluLeuHisGlnAspLeuPhePheTyrSerGlnArgGlnAlaAsnArgSer 166

QY 608 CGAGATCTTGGTGCATTTGTTTACTGTGTTGGTGAAGATTTCAATGAGACAGCGTG 667
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  167 ArgAspLeuGlyAlaIleValTyrCySValGlyValLysAspPheAsnGlnThrGlnLeu 186

QY 668 GCCCGGATTCGCGACAGTAAAGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTGTG 727
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  187 AlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeu 206

QY 728 CAAGCATCATCTCAATTTTGAAGAAGTCTGTGATCGAAATTTTGAAGCTTGAACA 787
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  207 GlnGlyIleIleHisSerIleLeuLysLysSerCySIlleGlnIleLeuAlaIleGlnPro 226

QY 788 TCCACATATGTCAGAGAGTGCATTTCAAGTGTGTGAGAGAAACGGCTTCCGACAT 847
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  227 SerThrIleCySValGlyGlnSerPheGlnValValAlaArgIlyAsnGlyPheAlaGlyHis 246

QY 848 GCCCGCAACGTGACAGAGGCTCTGTGACGCTTCAAGATCATGATCGGTCAACCTCAAT 907
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  247 AlaArgAsnValAspArgValLeuCySAspPheLysIleAsnAspSerValIleThrLeuAsn 266

QY 908 GAGAGACCTTTTCTGTGAAAGACCTTATTTACTGTGTCCAGCGCTTATCTTAAAGAA 967
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  267 GluLysProPheAlaValGluAspThrTyrLeuLeuCySProAlaProIleLeuLysGln 286

QY 968 GTTGGATGAAGAACTGTCACCTCCAGGTCAAGATGAAGATGAGCTCTTTTATCTCAAT 1027
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  287 ValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSerSer 306

QY 1028 TCTGTATCATCACCAACACACACTGTTTGAAGGTTTCACTCTGGCCATCGGCTGTG 1087
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  307 SerValIleIleThrThrThrHisCySAspArgGlySerIleLeuAlaIleAlaLeuLeu 326

QY 1088 ATCTGTCTCTGCTCTTACGCGCTGTCTCTGTGTGTTGTGGCCCTGTGCTGCACT 1147
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```

```

Db 327 ValLeuPheLeuLeuAlaLeuAlaLeuLeuTyrTrpTrpProLeuCySValThr 346
QY 1148 GTGATTATCAAGAGAGTCCCTCCACCCCTGCGGAGAGATGAGAGAA 1195
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 347 ValIleIleLysGlnValProProProProValGlnGlnSerGlnGln 362

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RESULT 15

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US-10-474-794-194
; Sequence 194, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 562
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-474-794-194

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Alignment Scores:

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Pred. No.: 4,05e-159 Length: 562
Score: 1793.00 Matches: 342
Percent Similarity: 97.75% Conservative: 6
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 70.59% Indels: 0
DB: 4 Gaps: 0

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US-09-970-076-1 (1-1414) x US-10-474-794-194 (1-562)

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QY 128 CTCGGATCGGCTTCAGATGGCTCTCTTTGGCCACTGTGGTCACTTCGCCGGGCAA 187
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  7 LeuGlyAlaGlyLeuArgGlyLeuCySValAlaAlaLeuValLeuValCySAlaGlyHis 26

QY 188 GGGGGACGAGAGGAGATGGGGCTCCAGCCCTGTACGCGGATTTGACCTGTACTT 247
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  27 GlyGlyArgArgGlyLeuArgGlyGlyProAlaCySValGlyGlyPheAspLeuTyrPheIle 46

QY 248 TTGGCAAAATTCAGAGTGTGTCGACCACTGGAATGAATCTTATCTTGTGGAACAG 307
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  47 LeuAspLysSerGlySerValLeuHisStrPaSngInIleTyrTyrPheValGluGln 66

QY 428 CTCGCAAAAGTTCTGCGAGAGAGACACTTACATGAGAAAGATTTGAAAGGCGCAGT 487
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  107 LeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGlnIlyPheGlnArgAlaSer 126

QY 488 GAGCAGATTATATGAAAAACAGACAGGATACAGACAGCCGCTCATCTTGGCTTGG 547
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  127 GluGlnIleTyrTyrGluAsnSerGlnGlyTyrArgThrIleSerValIleIleAlaLeu 146

QY 548 ACTGATGGAAGTCCATGAGAAATCTCTTTTCTTATTCAGAGGAGGCTAATAGTCT 607
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  147 ThrAspGlyGluLeuHisGlnAspLeuPhePheTyrSerGlnArgGlnAlaAsnArgSer 166

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 14, 2005, 11:59:39 ; Search time 7.30024 Seconds
(without alignments)
2608.649 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 2540
Sequence: 1 agagaccgcgaggaagggcc.....aaaaaaaaaaaaaaaa 1414

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Egapop 6.0 , Egapext 7.0
Delop 6.0 , Delext 7.0

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 102882

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xip
-Q=/cgn2_1/USPTO.spool.p/US09970076/runat_14122005_110512_26598/app.query.fasta_1.2894
-DB=Published Applications AA New -QOPT=faster -SUFFIX=rapbn -MINMATCH=0.1
-LOOPC=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdt -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 @CGN 1 1 1 @runat_14122005_110512_26598
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1894 | 74.6 | 564 | 7 | US-11-186-284-199 |
| 2 | 145.5 | 5.7 | 1152 | 7 | US-11-080-026-4 |
| 3 | 134.5 | 5.3 | 3063 | 7 | US-11-186-284-26 |
| 4 | 126.5 | 5.0 | 739 | 7 | US-11-057-047-2 |
| 5 | 126.5 | 5.0 | 764 | 7 | US-11-057-047-1 |
| 6 | 126.5 | 5.0 | 798 | 6 | US-10-821-234-1034 |
| 7 | 119.5 | 4.7 | 761 | 7 | US-11-057-047-6 |
| 8 | 113.5 | 4.5 | 915 | 6 | US-10-131-826A-294 |
| 9 | 113.5 | 4.5 | 956 | 7 | US-11-113-424-39 |
| 10 | 111 | 4.4 | 1141 | 6 | US-10-601-368-24 |

| | | | | | | |
|----|-------|-----|------|---|--------------------|---------------------|
| 11 | 111 | 4.4 | 1166 | 6 | US-10-601-368-22 | Sequence 22, Appl |
| 12 | 111 | 4.4 | 1188 | 6 | US-10-601-368-21 | Sequence 21, Appl |
| 13 | 107 | 4.2 | 1141 | 6 | US-10-601-368-6 | Sequence 6, Appl |
| 14 | 107 | 4.2 | 1166 | 6 | US-10-601-368-4 | Sequence 4, Appl |
| 15 | 107 | 4.2 | 1188 | 6 | US-11-000-463-338 | Sequence 338, Appl |
| 16 | 107 | 4.2 | 1188 | 7 | US-11-000-463-810 | Sequence 810, Appl |
| 17 | 107 | 4.2 | 1188 | 7 | US-10-995-561-983 | Sequence 983, Appl |
| 18 | 104.5 | 4.1 | 918 | 6 | US-10-995-561-982 | Sequence 981, Appl |
| 19 | 104.5 | 4.1 | 1019 | 6 | US-10-995-561-982 | Sequence 982, Appl |
| 20 | 104.5 | 4.1 | 182 | 6 | US-10-601-368-25 | Sequence 25, Appl |
| 21 | 103.5 | 3.9 | 678 | 7 | US-11-102-240-34 | Sequence 34, Appl |
| 22 | 100 | 3.9 | 182 | 6 | US-10-601-368-7 | Sequence 7, Appl |
| 23 | 99.5 | 3.8 | 1379 | 7 | US-11-097-125-1 | Sequence 158, Appl |
| 24 | 97 | 3.8 | 184 | 6 | US-10-510-368-158 | Sequence 1, Appl |
| 25 | 95.5 | 3.8 | 1196 | 6 | US-10-995-561-921 | Sequence 521, Appl |
| 26 | 95.5 | 3.8 | 1196 | 6 | US-11-097-125-2 | Sequence 2, Appl |
| 27 | 95 | 3.7 | 1167 | 7 | US-10-467-657-5432 | Sequence 5432, Appl |
| 28 | 94.5 | 3.7 | 353 | 7 | US-11-137-465-44 | Sequence 44, Appl |
| 29 | 94 | 3.7 | 448 | 7 | US-11-137-465-45 | Sequence 45, Appl |
| 30 | 94 | 3.7 | 619 | 6 | US-10-999-886-3 | Sequence 3, Appl |
| 31 | 93.5 | 3.7 | 640 | 6 | US-10-999-886-4 | Sequence 4, Appl |
| 32 | 93.5 | 3.7 | 1167 | 6 | US-10-467-657-5670 | Sequence 5670, Appl |
| 33 | 91 | 3.6 | 184 | 6 | US-10-601-368-18 | Sequence 18, Appl |
| 34 | 91 | 3.6 | 436 | 7 | US-11-116-939-9 | Sequence 9, Appl |
| 35 | 90.5 | 3.6 | 1062 | 7 | US-11-137-465-43 | Sequence 43, Appl |
| 36 | 88 | 3.5 | 1467 | 6 | US-10-821-234-1688 | Sequence 1688, Appl |
| 37 | 87 | 3.4 | 1798 | 6 | US-10-995-561-1033 | Sequence 1033, Appl |
| 38 | 85.5 | 3.4 | 1798 | 6 | US-10-995-561-1034 | Sequence 1034, Appl |
| 39 | 85.5 | 3.4 | 494 | 6 | US-10-467-657-592 | Sequence 592, Appl |
| 40 | 85 | 3.3 | 948 | 6 | US-10-523-477-14 | Sequence 14, Appl |
| 41 | 84.5 | 3.3 | 495 | 6 | US-10-770-726-81 | Sequence 81, Appl |
| 42 | 83.5 | 3.3 | 513 | 7 | US-11-000-463-458 | Sequence 458, Appl |
| 43 | 83.5 | 3.3 | 730 | 7 | US-11-082-389-358 | Sequence 358, Appl |
| 44 | 83.5 | 3.3 | 432 | 7 | US-11-084-624-20 | Sequence 20, Appl |
| 45 | 83 | 3.3 | | | | |

ALIGNMENTS

RESULT 1
US-11-186-284-199
; Sequence 199, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Kametkar, Shubangi
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEMO1-02922RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-199

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 1,24e-162 | Length: | 564 |
| Score: | 1894.00 | Matches: | 36 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 74.57% | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |

US-09-970-076-1 (1-1414) X US-11-186-284-199 (1-564)

| | | | |
|----|------|--|------|
| QY | 104 | ATGGCCAGCGGGAGCGGAGGAGCCCTGGCATCGGCTTCAGTGGCTCTCTTTGGCACT | 163 |
| Db | 1 | MetAatntrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAtr | 20 |
| QY | 164 | CTGGTGTCAATCTGCGCCGGGCGAGGGGACCGCAGAGAGATGGGGGTCCAGCTGTAC | 223 |
| Db | 21 | LeuValLeuIleCysAlaGlyIleGlnGlyAlaArgArgGluAspGlyGlyProIlaCysTrp | 40 |
| QY | 224 | GGCGGATTTGACCTGTATCTTCAATTTTGGACAAATCAGGAAGTGTGTGCAACATCGAAT | 283 |
| Db | 41 | GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn | 60 |
| QY | 284 | GAATCTATTACTTTGTGGAAACAGTGTGCTCAAAATTCATCAGCCCAAGTTGGAAATG | 343 |
| Db | 61 | GluIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgIleC | 80 |
| QY | 344 | TCCTTTATTTGTTTCTCCACCCGAGAACACCTTATGAACTGAACAGAACAGAA | 403 |
| Db | 81 | SerPheIleValPheSerThrArgGlyThrTrpLeuMetLysLeuThrClnAspArgGln | 100 |
| QY | 404 | CAATCCGTCAGGCTGAGAAACCTCCAGAAAGTTCTGCCAGGAGGAGCACTTAACATG | 463 |
| Db | 101 | GlnIleArgGlnGlyLeuGlnGluGlnLeuGlnLysValLeuProGlyLysAspTrpTrpIleC | 120 |
| QY | 464 | CATGAAGGATTTGAAAGGGCCAGTAGGAGCATTTTATGAAACAGACAGAGGTACAG | 523 |
| Db | 121 | HisGluGlyPheGluLysArgAlaSerGluGlnIleTrpTrpGluAsnArgGlnIleLysArg | 140 |
| QY | 524 | ACAGCCAGGCTATCATCTTGTCTTGAAGTGAAGAACTCATGAAGATCTCTTTTCTAT | 583 |
| Db | 141 | ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluLysPheLeuPheTrp | 160 |
| QY | 584 | TCAGAGAGGAGGCTAATAGTCTCGAAGTCTTGGGCAATGTGTTACTGTGTGGTGG | 643 |
| Db | 161 | SerGluArgGlnAlaAsnArgSerHisArgPheGlyAlaIleValTrpCysValGlyAla | 180 |
| QY | 644 | AAAGATTTCAATGAGACACAGCTGGCCGCGATGTGGGACAGTAAGATCATGTGTTTCC | 703 |
| Db | 181 | LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro | 200 |
| QY | 704 | GTGAATGACGGGTTTCAGGCTGTGCAAGGATCATCACTCAATTTTGAAGAAGCTGCG | 763 |
| Db | 201 | ValAlaAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys | 220 |
| QY | 764 | ATGGAATTTCTAGAGCTGAAACCATCAACATATGTGACGAGAGATCATTTCAATGTGC | 823 |
| Db | 221 | IleGlnIleLeuAlaAlaGluProSerTrpIleCysAlaGlyGlnSerPheGlnVal | 240 |
| QY | 824 | GTGAAGGAACGGCTTCCGACATGCGCCGAACTGGAACAGGCTCTCTGCAGCTTCAAG | 883 |
| Db | 241 | ValArgGlyAsnGlyPheArgHisAlaAspAsnValAspArgValLeuLysSerPheLys | 260 |
| QY | 884 | ATCAATGACTGGGTACACTCAATGAGAGCCCTTTCTGTGGAAGACCTTATTTACTCG | 943 |
| Db | 261 | IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspTrpTrpLeuLeu | 280 |
| QY | 944 | TGTCAGCGCTTATCTTAAAGAAGTTGGCATGAAGTGCATCTCCAGGTGACATGAAC | 1003 |
| Db | 281 | CysProAlaProIleLeuLysGluValGlyMetLysAlaIleGlnIleValSerMetAsn | 300 |
| QY | 1004 | GATGGCTCTCTTTTATCTCCAGTTCTGTCAATCATGACACACACACTGTTTCTGACGT | 1063 |

Db 301 AsgIyLeuSerPheIleSerSerSerValIleIleIleThrThrThiLeuSerLeuAsgIy 320

QY 1064 TCCATCCTGCSCCAGTCGCCCTGTGTATCTGTCTCTCTACGCCCTGTGCTCTGTGG 112

Db 321 SerIleLeuAlaIleAlaIleuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340

QY 1124 TGGTTCGAGCCCTCTGTGTCACATGTATATCAAGAGAGTCCCTCCACCCCTGGCCGAG 118

Db 341 TrpPheTrpProLeuCySCysThrValIleIleLeuGluValProProProAlaIleGlu 360

QY 1184 GAGAGTGAAGAA 1195

Db 361 GluSerGluGlu 364

```

RESULT 2
US-11-080-026-4
/ Sequence 4, Application US/11080026
/ Publication No. US20050280192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shimaoka, Motomu
/ APPLICANT: Lu, Chafan
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR
/ FILE REFERENCE: CFBF-P02-021
/ CURRENT APPLICATION NUMBER: US/11/080,026
/ CURRENT FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: 09/945,265
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1152
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-080-026-4

```

| | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No.: | 1,3e+05 |
| Score: | 145.50 |
| Percent Similarity: | 45.85% |
| Best Local Similarity: | 26.20% |
| Query Match: | 5.73% |
| DB: | 7 |
| Gaps: | 12 |
| Length: | 1152 |
| Matches: | 60 |
| Conservative: | 45 |
| Mismatch: | 81 |
| Indels: | 43 |
| Gaps: | 12 |

US-09-970-076-1 (1-1414) X US-11-080-026-4 (1-1152)

```

QY      233  AACCTGTACTTCATTTTGGACAAATCAGAAATGTCGCTG---CACCACTGGAAATGAATAC 283
Db      150  AspIleAlaPheLeuIleIleAspIlySerGlySerIleIleProHisIaspHeArgAlaMet 169
QY      290  TATTACTTTGGGAACAGCTTGCGCTCAAAATTCATCAGCCCAAGTTGGAATGTCCTTT 349
Db      170  LysGluPheValSerThr-----ValMetGluGlnLeuIlylSerIlyl 184
QY      350  ATTGTTTCTCCACCCGAGAAACAACCTTAATGAAGAACTGACGAAGAC----- 397
Db      185  ThrLeuPheSer-----LeuMetGlnTyrSerGluGlnIleuHeArgIleHis 199
QY      398  -----AGAAACAACATCCGTCGAAGGCGCTTAAGACAACTCCAG 433
Db      200  PheThrPheIlyGluPheGlnAsnAsnProAnProArgSerLeuValIlyProIleThr 219
QY      434  AAAGTCTGCCAGAGAGACACTTAATCATGTGAAGATTGAAAGGCCCACTGACGAG 493
Db      220  GlnLeuLeu-----GlyArgThrHisEthAlaThrGlyIleArgIlyValAlaArgGlu 237
QY      494  ATTTATTATGAAAAACAGACAAGGTAACAGGACAGCG---AGCGTCATCAATGGCTTGAT 550
Db      238  LeuPheAsnIleThrAsnGlyAlaIleArgIlyAsnAlaPheIlyIleLeuValIleThr 257

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QY 551 GATGGAACTCCATGAGATCTTTTCTATTACAG-----AGGAGGCTAATAGG 604
DB 258 AAGGlyGluLysPheGlyAspProLeuGlyTyrGluAspValIleProGluAlaAspArg 277
QY 605 TCTCGAGATCTTGTCACATTTGTTTACTGTGTGTGTGTAAGATTTCAATGACAGAC 664
DB 278 Glu-----GlyValIleArgTyrValIleGlyValGlyAspAlaPheArgSerGlu 294
QY 665 CTGGCCCGG-----ATTGGGACAGT-----AAGATCATGTGTTTCCC 703
DB 295 LysSerArgGlnGluLeuAsnThrIleAlaSerLysProProArgAspHisValPheGln 314
QY 704 GTGAATGACGGCTTACAGCTTCGACAGCATCATCATCATTTTGAAGAGTCTCTGC 763
DB 315 ValAsnAsn---PheGluAlaLeuLysThrIleGlnAsnGlnLeuArgGluLys----- 331
QY 764 ATCGAATTCTACAGCTGACGTAACCATCCACCATATGTGACAGAGATCATTTCAAGTTGTC 823
DB 332 -----IlePheAlaIleGlnGlyThrGlnThrGlySerSerSerSerPheGlnHisGlu 349
QY 824 GTGAGAGAAACGGCTTCCGACATGCC 850
DB 350 MetSerGlnGluGlyPheSerAlaAla 358

RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, ShubhangI.
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186, 284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301, 822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339, 971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361, 978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381, 988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Alignment Scores:
Pred. No.: 0.000164 Length: 3063
Score: 134.50 Matches: 81
Percent Similarity: 43.10% Conservative: 44
Best Local Similarity: 27.93% Mismatches: 123
Query Match: 5.30% Indels: 42
DB: 7 Gaps: 17

US-09-970-076-1 (1-1114) x US-11-186-284-26 (1-3063)
QY 233 GACCTGACTTCATTTTGGACAAATCAGAGAGTGTG---CTGACACCTGGAAATGATC 289
DB 440 AspIleValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheValIleVal 459
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QY 290 TATTACTTTGTGAACAGTTGGCTCCCAATTC---ATCAGCCCA---CAGTTGAGATG 343
DB 460 ArgAlaPheLeuGluValIleValLysSerPheGlnIleSerProAsnArgValGlnIle 479
QY 344 TCTTTTATGTTTCTTCACC-----CGAGAACACCTTAAATGAATGACAGAA 394
DB 480 SerLeuValGlnTyrSerArgAspProHisThrGlnPheThrLeuLysPheThrLys 499
QY 395 GACAGAGAACAAATCCGTCAAGCCCTAGAAAGCTCCAGAAAGTTCTGCA-----GGA 448
DB 500 ValGluAspIleIle-----GluAlaIleAsnThrPheProTyrArgGly 514
QY 449 GGAGACACTTATCATGATGAGATTTGAAGGGCCAGACAGATTTATTATGAAAC 508
DB 515 GlySerThrAsnThrGlyValAlaMetThrTyrValArgGlnLysIlePheValProSer 534
QY 509 AGACAAAGGTATACAGACA-----GCCAGCTCATCATTTGCTTTCAGTGTGAGAACTC 562
DB 535 Lys---GlySerArgSerAsnValProLysValIleLeuIleThrAspGlyLys--- 552
QY 563 CATGAAGATCTCTTTTCTATTACAGAGAGGAGGCTAATAGCTTCAGATCTGTGCA 622
DB 553 SerSerAspAlaPhe-----ArgAspProAlaIleLysLeuArgAsnSerAspVal 569
QY 623 ATGTCTTACTGTGTGTGTAAGATTTCAATGACACACAGCTGCCCGATTCGGCAG 682
DB 570 GluIlePheAlaValGlyValLysAspAlaValArgSerGlnLeuGlnAlaIleAlaSer 589
QY 683 -----AGTAAGCATGATGTTTCCGTGAATGACGGCTTTCAGGCTTCGCAAGCATC 736
DB 590 ProProAlaGlnThrHisValPheThrValGluAsp---PheAspAlaPheGlnArgIle 608
QY 737 ATCCACTCAATTTGGAAGAGTCTGCATCGAAATCTTGACAGCTCAACCATCCACAT 796
DB 609 SerPheGlnLeuThrXinSerIleCysLeuArgIle-----GlnGlnGluLeuAla 625
QY 797 TGTGACAGAGATCATTTCAAGTTGCTGACAGAGAAAGGCTCCGACATGCCCCCAAC 856
DB 626 AlaIleLysLysValAlaTyrValProProLysAspLeuSerPheSerGluValThrSer 645
QY 857 GTGACAGAGGCTCTGTCAGCTTCAGATCATGACTCGTCACTCAATGAGAAAGCC 916
DB 646 Tyr-----GlyPheLysThrAsnTyrSer---ProAlaGlyGluAsnVal 659
QY 917 TTTTCTGTGGAAGACATTTACTGTGTGCCAGCCCATATCTTAAAGAGTTGGCAG 976
DB 660 PheSerTyrHisIleThrTyr-----LysGluAlaAlaGly 671
QY 977 AAGCTGACCTCCAGGTGACATGAGATGAGCGCTCTTTTATCTTCAGTTCTGTATC 1036
DB 672 AspAspGluValThrVal---ValGluPro-AlaSerSerThrSerValValLeuSerSe 650
QY 1037 ATCACCAACACACACTGTTCGACGGTT 1064
DB 690 IleuLysProGluThrLeuTyrIleuVal 699

RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Raube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilleson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057, 047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543, 594
; PRIOR FILING DATE: 2004-02-10
```


PRIOR APPLICATION NUMBER: 60/288,153
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 956
TYPE: PR
ORGANISM: Homo sapiens
US-11-113-424-39

Alignment Scores:
Pred. No.: 0.00922 Length: 956
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 4.47% Indels: 35
DB: Gaps: 13

US-09-970-076-1 (1-1414) x US-11-113-424-39 (1-956)

QY 233 GACCTGACTTCTATTTGGCAAAATCGGAAGTGTG---CTGCACCACTGGAATGAATC 289
DB 57 AepLelValPheLleIleAspSerArgSerValAsnThrHisAspTyrAlaLysVal 76
QY 290 TATTACTTT---GTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTG--AGAAATG 343
DB 77 LysGluPheLeValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal 96
QY 344 TCCTTATTGTTTCTCCACCCGAGAACACCTTA-----ATGAAACTG 388
DB 97 GlyLeuGlnTyr-----GlySerThrValLysAsnGluPheSerLeuLysThr 113
QY 389 ACGAAGACAGACAAATCCGTCAGGCGCTGAAGTCCAGAAAGTTCGCCAGG 448
DB 114 PheLysArgLysSerGluValGluArgAlaValLysArgWetArgHisLeuSerThrGly 133
QY 449 GGAGACACTTACATGATGATGAGATTTGAAAGGCCAGTGCAGACATTTATGAAAC 508
DB 134 ThrMetThrGlyLeuAlaIleGlnTyr-----AlaLeuAsnIleAlaPheSerGlu 150
QY 509 AGAAGAGGTACAGG-----ACAGCCAGCTCATCTGTTGACTGAT 553
DB 151 AlaGluGlyAlaArgProLeuArgLysAsnValProArgValIleMetIleValThrAsp 170
QY 554 GGAGAACTCCATGAATCTCTTTTCTATTACAGAGGAGGCTAATAGGCTCGAGAT 613
DB 171 GlyArgProGlnAspSerVal-----AlaGluValAlaAlaLysAlaArgAsp 186
QY 614 CTGGTGCATTTGTTACTGTGTGTGTG-----AAAGATTTCAATGACACAGCTG 667
DB 187 ThrGlyIleLeuIlePheAlaIleGlyValGlyLysValAspPheAsnThrLeuLysSer 206
QY 668 GCCCGAGTTGCGGACAGTAAGATCATGTGTTCCCGTCATAGAGGCTTACAGGCTG 727
DB 207 IleGlySerGluProHisGluAspHisValPheLeuValAlaAsn--PheSerGlnIle 225
QY 728 CAAGGATCATCACTCAATTTTGAAGAGTCCGATCGAATTCGATGAGACCA 787
DB 226 GlnThrLeuThrSerValPheGlnLysLysLeuLysCysThrAlaHisMetCysSerThrLeu 245
QY 788 TCCACCATATGTCAGAGAGATGATTTCAAGTTGTCTGAGAGAAACGGCTTCCGACAT 847
DB 246 GlnHisAsnCysAla-----HisPheCysIleAsnIleProGlySerTyrValCysAsp 263
QY 848 GCCCGC-----AACGTGACACAGGCTCTGCAAGCTTCAAGATCAATGAC 892
DB 264 CysLysGlnGlnGlyTyrIleLeuAsnSerAspGlnThrCys-----ArgIleGlnAsp 281
QY 893 TCGGTCACTCAATGAG 910
DB 282 LeuCysAlaMetGluAsp 287

RESULT 10

US-10-601-368-24
Sequence 24, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 0734-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1141
TYPE: PR
ORGANISM: Mus musculus
US-10-601-368-24

US-10-601-368-24

Alignment Scores:
Pred. No.: 0.0162 Length: 1141
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.37% Indels: 38
DB: Gaps: 9
US-09-970-076-1 (1-1414) x US-10-601-368-24 (1-1141)
QY 218 TGCCTAGCGGATTTGACCTGTACTTATTTGCAAAATCAGAAAGTGTGCACAC 277
DB 159 CysGlnThrTyrMetAspIleValIleValLeuAspGlySerAsnSerIle---TyrPro 177
QY 278 TCGAATGAATATTACTTGTGGAACAGTTGGCTCACAATTC--ATCAGCCCA--- 331
DB 178 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 197
QY 332 CAGTTGAGATGCTCTTATTTGTTTCTCCACCCGAGAAACCACTTAATGAACTGACA 391
DB 198 GlnIleGlnValGlyIleValGlnTyrGlyLysAspAlaValHisGluPheHisLeu--- 216
QY 392 GAAACAGACAGACAAATCCGTCAGGCGCTGAAGAACTCAGAAAGTTCGCCAGAGGA 451
DB 217 AsnAspTyrArgSerValLysAspValValGluAlaAlaSerHisIleGluGlnArgGly 236
QY 452 GACACTTACATCATGAAAGATTTGAA-----AGGCGCAGTGCAGATTTATAT 502
DB 237 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 256
QY 503 GAAACAGACAGGTTACAGACAGACAGCCGCTCATGTTGCTTGAAGAGAACTC 562
DB 257 GlyGlyArgLysGlyAlaLys-----LysValMetIleValIleThrAspGlyGluSer 274
QY 563 CATGAAGAT----- 571
DB 275 HisAspSerProAspLeuGlnLysValIleArgGlnSerGlnLysAsnValThrArg 294
QY 572 -----CTCTTTTCTATTGACAGAGGAGGCTAATAGTCTCGAGATCTT 616
DB 295 TyrAlaValAlaValLeuGlnLysTyrTyrAsnArgAspGlyIleAsnProGluThrPheLeu 314
QY 617 GGTGCATTTGTTACTGTGTGTGTGGAAGAT-----TTCAATGACACAG 664
DB 315 AsnGlnLysLysTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 334
QY 665 CTGGCCCGAGTTGCGGACAGTAAGATCATGTGTTCCCGTCATGACGAGCTTACAGGCT 724
DB 335 GluAlaAlaLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 351
QY 725 CTGCAAGGC 733

Db 352 LeuGluGly 354

RESULT 11
US-10-601-368-22
Sequence 22, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lore, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
PRIORITY FILING DATE: 2003-06-23
PRIORITY FILING DATE: 2000-04-27
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 1999-05-28
NUMBER OF SEQ. ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 1166
TYPE: PRT
ORGANISM: Mus musculus
US-10-601-368-22

Alignment Scores:
Pred. No.: 0.0163 Length: 1166
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.37% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1 (1-1414) x US-10-601-368-22 (1-1166)

QY 218 TGCTACGGCGGATTTGACCTGCTACTTTCATTTGGACAATTCAGAGAGTGTGTCACAC 277
DB 137 CysGlnThrTyrMetAspIleValIleValIleuAspGlySerAsnSerIle--TyrPro 155
QY 278 TGGAAATGAATCTATTTACTTTGTGGAACAGTTGGCTCACAATAATC--ATCAGCCCA 331
DB 156 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 175
QY 332 CAGTTGAGAAATGTCCTTATTTGTTTCTCCACCCGAGAAACACCTTAATGAAATGACA 391
DB 176 GlnIleGlnValGlyIleValGlnTyrGlyGluAspAlaValHisGluPheHisLeu--- 194
QY 392 GAAGACAGAGAAACAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTTCCGACAGGA 451
DB 195 AsnAspTyrArgSerValLysAspValValGluAlaAlaSerHisIleGluGlnArgGly 214
QY 452 GACACTTAACATGATGATGAAGATTGAA-----AGGCGCAGTGACAGATTATATAT 502
DB 215 GlyThrGluThrArgHisAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 234
QY 503 GAAAAACAGACAGAGGTACAGACAGCCGTCATCATTTGCTTGAAGTGAAGAACTC 562
DB 235 GlyGlyArgGlyAlaLys-----LysValMetIleValIleThrAspGlyGluSer 252
QY 563 CATGAAGAT----- 571
DB 253 HisAspSerProAspLeuGluLysValIleArgGlnSerGluLysAspAsnValThrArg 272
QY 572 -----CTCTTTTCTATTCAGAGAGGCTAATAGGCTCGAGATCTT 616
DB 273 TyrAlaValAlaValIleuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 292
QY 617 GGTGCAATTTGTTACTGTGTGGTGTGAAGAT-----TTCAATGACACACAG 664
DB 293 AsnGluIleLysTyrIleAlaSerAspProAspAspLysHisPheAsnValThrAsp 312
QY 665 CTGCGCCGCGATTTGGGACAGTAAAGATCATGTGTTCCCGTAATGACGCTTCAGAGCT 724

Db 313 GluAlaAlaLeu-----LysAspIleValAlaAspAlaLeuGlyAspArgIlePheSer 329

QY 725 CTGCAAGGC 733

Db 330 LeuGluGly 332

RESULT 12
US-10-601-368-21
Sequence 21, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lore, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
PRIORITY FILING DATE: 2003-06-23
PRIORITY FILING DATE: 2000-04-27
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 1999-05-28
NUMBER OF SEQ. ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 1188
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-21

Alignment Scores:
Pred. No.: 0.0164 Length: 1188
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.37% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1 (1-1414) x US-10-601-368-21 (1-1188)

QY 218 TGCTACGGCGGATTTGACCTGCTACTTTCATTTGGACAATTCAGAGAGTGTGTCACAC 277
DB 159 CysGlnThrTyrMetAspIleValIleValIleuAspGlySerAsnSerIle--TyrPro 177
QY 278 TGGAAATGAATCTATTTACTTTGTGGAACAGTTGGCTCACAATAATC--ATCAGCCCA 331
DB 178 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 197
QY 332 CAGTTGAGAAATGTCCTTATTTGTTTCTCCACCCGAGAAACACCTTAATGAAATGACA 391
DB 198 GlnIleGlnValGlyIleValGlnTyrGlyGluAspAlaValHisGluPheHisLeu--- 216
QY 392 GAAGACAGAGAAACAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTTCCGACAGGA 451
DB 217 AsnAspTyrArgSerValLysAspValValGluAlaAlaSerHisIleGluGlnArgGly 236
QY 452 GACACTTAACATGATGATGAAGATTGAA-----AGGCGCAGTGACAGATTATATAT 502
DB 237 GlyThrGluThrArgHisAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 256
QY 503 GAAAAACAGACAGAGGTACAGACAGCCGTCATCATTTGCTTGAAGTGAAGAACTC 562
DB 257 GlyGlyArgGlyAlaLys-----LysValMetIleValIleThrAspGlyGluSer 274
QY 563 CATGAAGAT----- 571
DB 275 HisAspSerProAspLeuGluLysValIleArgGlnSerGluLysAspAsnValThrArg 294
QY 572 -----CTCTTTTCTATTCAGAGAGGCTAATAGGCTCGAGATCTT 616

Db 295 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 314
QY 617 GGTCATTTGTTTACTGTGTGGTGTGAAGAT-----TTCAATGAGACACAG 664
Db 315 AengluilelyTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 334
QY 665 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTCAGGCT 724
Db 335 GluAlaIleLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 351
QY 725 CTGCAGGC 733
Db 352 LeuGluGly 354
RESULT 13
US-10-601-368-6
Sequence 6, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 0734-275001
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1141
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-6
Alignment Scores:
Pred. No.: 0.037 Length: 1141
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.21% Indels: 38
Gaps: 9
US-09-970-076-1 (1-1414) x US-10-601-368-6 (1-1141)
QY 218 TGCTACGGCGGATTTGACCTGTACTTATTTGACAATAATCAGAGAAGTGTGCACAC 277
Db 159 CysGlnThrTyrMetCAspIleValIleValLeuAspGlySerAsnSerIle---TyrPro 177
QY 278 TGGATGAATATCTATTACTTTGTGGAACGTTGGCTCACAATTC---ATCAGCCCA--- 331
Db 178 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 197
QY 332 CAGTTAGAAATGCTCTTATTTGTTTCTCCACCCGAGAACCAACTTAATGAACCTGACA 391
Db 198 GlnIleGlnValGlyValGlnTyrGlyGluAspValValHisGluPheHisLeu--- 216
QY 392 GAAGACAGAGAACAAATCCGTCAAGGCTGAGAGAACTCCAGAAAGTTGCGCAGAGGA 451
Db 217 AsnAspTyrArgSerValLysAspValValGluAlaIleAsnHisIleGluGlnArgGly 236
QY 452 GACACTTACATGCATGAGAGATTGAA-----AGGCCAGTGCAGCAGATTATTAT 502
Db 237 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 256
QY 503 GAAACAGACAGAGGTTGACAGACAGCAGCAGCTATCTGCTTGACTGTAGGAACCTC 562
Db 257 GlyGlyArgLysGlyValLys-----LysValMetIleValIleThrAspGlyGluSer 274

QY 563 CATGAAGAT----- 571
Db 275 HisAspSerProAspLeuGluLysValIleGlnGlnSerGluArgAspAsnValThrArg 294
QY 572 -----CTCTTTTCTATTTCAGAGAGGAGGCTAATNAGCTCTGCAATCTT 616
Db 295 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 314
QY 617 GGTCATTTGTTTACTGTGTGGTGTGAAGAT-----TTCAATGAGACACAG 664
Db 315 AengluilelyTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 334
QY 665 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTCAGGCT 724
Db 335 GluAlaIleLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 351
QY 725 CTGCAGGC 733
Db 352 LeuGluGly 354
RESULT 14
US-10-601-368-4
Sequence 4, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 0734-275001
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-601-368-4
Alignment Scores:
Pred. No.: 0.0373 Length: 1166
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.21% Indels: 38
Gaps: 9
US-09-970-076-1 (1-1414) x US-10-601-368-4 (1-1166)
QY 218 TGCTACGGCGGATTTGACCTGTACTTATTTGACAATAATCAGAGAAGTGTGCACAC 277
Db 137 CysGlnThrTyrMetCAspIleValIleValLeuAspGlySerAsnSerIle---TyrPro 155
QY 278 TGGATGAATATCTATTACTTTGTGGAACGTTGGCTCACAATTC---ATCAGCCCA--- 331
Db 156 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 175
QY 332 CAGTTAGAAATGCTCTTATTTGTTTCTCCACCCGAGAGAACCAACTTAATGAACCTGACA 391
Db 176 GlnIleGlnValGlyValGlnTyrGlyGluAspValValHisGluPheHisLeu--- 194
QY 392 GAAGACAGAGAACAAATCCGTCAAGGCTGAGAGAACTCCAGAAAGTTGCGCAGAGGA 451
Db 195 AsnAspTyrArgSerValLysAspValValGluAlaIleAsnHisIleGluGlnArgGly 214
QY 452 GACACTTACATGCATGAGAGATTGAA-----AGGCCAGTGCAGCAGATTATTAT 502
Db 215 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 234

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QY 503 GAAACAGACAAAGGCTACAGACAGCCAGCTCATCTTGTGACTGATGAGAACTC 562
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Db 235 GlyGlyArgGlySerGlyAlaLys-----LysValMetIleValIleThrAspGlyGluSer 252
QY 563 CATGAAGAT----- 571
    |||:::
Db 253 HisAspSerProAspLeuGlyLysValIleGlnGlnSerGluArgAspAsnValThrArg 272
QY 572 -----CTCTTTTCTATTTCAGAGAGGAGCTTAATAGCTCTCGAGATCTT 616
    |||:::|||||
Db 273 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrProLeu 292
QY 617 GGTGCATTGTTTACTGTCTGTGGTGTGAAGAT-----TTCAATGAGACACAG 664
    |||:::|||||
Db 293 AsnGluIleLysTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 312
QY 665 CTGCCCCGATTGCGGACAGTAAGATCATGTGTTTCCCGTAATGACGCGCTTTCAGAGCT 724
    |||:::|||||
Db 313 GluAlaAlaLeu-----LysAspIleValAlaAspAlaLeuGlyAspArgIlePheSer 329
QY 725 CTGCAAGGC 733
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Db 330 LeuGluGly 332

RESULT 15
US-10-601-368-3
/ Sequence 3, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Par. Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 1188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(122)
US-10-601-368-3

Alignment Scores:
Pred. No.: 0.0374 Length: 1188
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.21% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1 (1-1414) x US-10-601-368-3 (1-1188)

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Db 159 CysGlnThrTyrMetAspIleValIleValLeuAspGlySerAsnSerIle--TyrPro 177
QY 278 TGGAAATGAAATCTTATCTTGTGTAAGACAGTGGCTCAAAATC--ATCAGCCCA 331
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Db 178 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 197
QY 332 CAGTTGGAATGCTTATGTTTCTTSCACCCGAGAACAACTTAATGAACTGACA 391
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QY 452 GACACTTACATGCATGACAGATTTTGA-----AGGCGCAGTACGACAGATTATTAT 502
    |||:::|||||
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QY 503 GAAACAGACAAAGGCTACAGACAGCCAGCTCATCTTGTGACTGATGAGAACTC 562
    |||:::|||||
Db 257 GlyGlyArgGlySerGlyAlaLys-----LysValMetIleValIleThrAspGlyGluSer 274
QY 563 CATGAAGAT----- 571
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Db 275 HisAspSerProAspLeuGlyLysValIleGlnGlnSerGluArgAspAsnValThrArg 294
QY 572 -----CTCTTTTCTATTTCAGAGAGGAGCTTAATAGCTCTCGAGATCTT 616
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QY 617 GGTGCATTGTTTACTGTCTGTGGTGTGAAGAT-----TTCAATGAGACACAG 664
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QY 665 CTGCCCCGATTGCGGACAGTAAGATCATGTGTTTCCCGTAATGACGCGCTTTCAGAGCT 724
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Db 352 LeuGluGly 354
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Search completed: December 14, 2005, 12:55:25
Job time : 26.3002 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:01:38 ; Search time 5918.11 Seconds
(without alignments)
10603.927 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207

Perfect score: 1104
1 atggcaccagcgagcgagcgag.....gtgaggaataataataaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5083141 seqs, 2842125653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_to: *
10: gb_str: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_ncg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1104 | 100.0 | 1414 | 6 | AX458366 Sequence |
| 2 | 1104 | 100.0 | 1414 | 6 | AF421380 Homo sapi |
| 3 | 1090.8 | 98.8 | 5540 | 6 | AX393246 Sequence |
| 4 | 1090.8 | 98.8 | 5540 | 6 | AX393301 Sequence |
| 5 | 1090.8 | 98.8 | 5540 | 6 | AX458370 Sequence |
| 6 | 1090.8 | 98.8 | 5540 | 8 | AF279145 Homo sapi |
| 7 | 1090.4 | 98.8 | 1576 | 8 | AY928975 Homo sapi |
| 8 | 1090.4 | 98.8 | 1658 | 8 | AY928977 Homo sapi |
| 9 | 1089.4 | 98.7 | 1496 | 8 | AY928974 Homo sapi |
| 10 | 1089.4 | 98.7 | 1578 | 8 | AY928976 Homo sapi |
| 11 | 949.4 | 86.0 | 2112 | 6 | AX458372 Sequence |
| 12 | 949.4 | 86.0 | 2112 | 8 | BC012074 Homo sapi |
| 13 | 949.2 | 86.0 | 2052 | 8 | AK223273 Homo sapi |
| 14 | 853.4 | 77.3 | 5220 | 6 | AX393256 Sequence |
| 15 | 853.4 | 77.3 | 5220 | 6 | AX393370 Sequence |
| 16 | 853.4 | 77.3 | 5220 | 9 | AF378762 Mus muscu |
| 17 | 853.4 | 77.3 | 5225 | 9 | BC094544 Mus muscu |
| 18 | 803.8 | 72.8 | 1609 | 6 | AR338517 Sequence |

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|----|-------|------|------|---|--------------------|
| 19 | 802.2 | 72.7 | 1718 | 6 | CQ498433 Sequence |
| 20 | 787 | 71.3 | 1436 | 6 | BD156323 Primer fo |
| 21 | 787 | 71.3 | 1436 | 6 | AX458374 Sequence |
| 22 | 787 | 71.3 | 1436 | 6 | AX876800 Sequence |
| 23 | 787 | 71.3 | 1436 | 6 | AK001463 Homo sapi |
| 24 | 667.8 | 60.5 | 4739 | 9 | BC057043 Homo sapi |
| 25 | 573.4 | 51.9 | 736 | 9 | AY754025 Ratius no |
| 26 | 542.8 | 49.2 | 4007 | 8 | AK025429 Homo sapi |
| 27 | 516.8 | 46.8 | 3981 | 6 | AR578074 Sequence |
| 28 | 349 | 31.6 | 336 | 6 | CQ426476 Sequence |
| 29 | 348 | 31.5 | 355 | 6 | CQ415556 Sequence |
| 30 | 346.2 | 31.4 | 2234 | 6 | AX747144 Sequence |
| 31 | 346.2 | 31.4 | 2234 | 6 | AK091721 Homo sapi |
| 32 | 346 | 31.3 | 1464 | 6 | CQ433315 Sequence |
| 33 | 344.6 | 31.2 | 1464 | 6 | BD272493 Secreted |
| 34 | 344.6 | 31.2 | 1467 | 6 | BD272541 Secreted |
| 35 | 344.6 | 31.2 | 1470 | 8 | AY233452 Homo sapi |
| 36 | 344.6 | 31.2 | 3676 | 8 | AB209913 Homo sapi |
| 37 | 344.6 | 31.2 | 3677 | 6 | BD272492 Secreted |
| 38 | 344.6 | 31.2 | 4348 | 6 | CQ414929 Sequence |
| 39 | 344.6 | 31.2 | 4350 | 6 | BD272540 Secreted |
| 40 | 343 | 31.1 | 3677 | 6 | BD272508 Secreted |
| 41 | 343 | 31.1 | 3677 | 6 | BD272509 Secreted |
| 42 | 342.8 | 31.1 | 3677 | 6 | BD272510 Secreted |
| 43 | 342.8 | 31.1 | 1461 | 6 | BD272532 Secreted |
| 44 | 341.8 | 31.0 | 3501 | 6 | BD272513 Secreted |
| 45 | 340.2 | 30.8 | 1458 | 6 | BD272533 Secreted |

ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
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104..1210
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SERBANKSRDLGAIVYCVGKRDRENOALAIADSKHVPFVNGFALDGLHEDLFY
SCIEILAEPSITCAGSFQVVGNGFARVARDVLCFKINDSVTLNEKPSVSD
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ORIGIN

Query Match 100.0%; Score 1104; DB 6; Length 1414;
Best Local Similarity 100.0%; Pred. No. 1e-311;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 224 GCGGATTTGACCTGACTTCAATTTTGGACAAATCAGAAAGTGTGTCGACCACTGGAAAT 283
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Qy 361 CATGAAGATTGAAAAGGCGCAGTGAAGCAATTTATGAAAACAGACAAGGATACAG 420
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Qy 421 AAGAGCAGGCTCATCTTGTGACTGATGAGAACTCAGAGAACTCATGAGATCTCTTTTCTAT 480
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Qy 841 TGTCCAGCCCTATCTTAAAGAGTGGCATGAAGTGAAGTCACTCCAGGTCAAGATGAAC 900
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Db 944 TGTCCAGCCCTATCTTAAAGAGTGGCATGAAGTGAAGTCACTCCAGGTCAAGATGAAC 1003
|||
Qy 901 GATGGCTCTCTTTATCTCCAGTTGTCTATCATACCAACACACACTGTTCTGACGAT 960
|||
Db 1004 GATGGCTCTCTTTATCTCCAGTTGTCTATCATACCAACACACACTGTTCTGACGAT 1063
|||
Qy 961 TCCATCTTGGCCATTCGCGCTGCTGATTCCTGCTCTCTGCTCTGCTCTCTCTCTG 1020
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Db 1064 TCCATCTTGGCCATTCGCGCTGCTGATTCCTGCTCTCTGCTCTCTCTCTCTCTCTG 1123
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Qy 1021 TGGTTTGGGCCCCCTGTGTCACATGATTAATCAAGAGAGTCCCTCAACCCCTGCGAG 1080
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Db 1124 TGGTTTGGGCCCCCTGTGTCACATGATTAATCAAGAGAGTCCCTCAACCCCTGCGAG 1183
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Qy 1081 GAGAGTGAAGAAATTAATAA 1104
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Db 1184 GAGAGTGAAGAAATTAATAA 1207
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LOCUS Homo sapiens anthrax toxin receptor mRNA, complete cds.
DEFINITION
AF421380
ACCESSION
AF421380.1 GI:16566412
VERSION
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 1414)
Bradley,K.A., Morige,J., Mourez,M., Collier,R.J. and Young,J.A.
Identification of the cellular receptor for anthrax toxin
JOURNAL
Nature 414 (6860), 225-229 (2001)
PUBMED
11700562
REMARK
http://www.nature.com
2 (bases 1 to 1414)
Bradley,K.A., Morige,J., Mourez,M., Collier,R.J. and Young,J.A.T.
Direct Submision
Submitted (19-SEP-2001) Department of Oncology, University of
Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA
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LOCUS-
DEFINITION Sequence 176 from Patent WO0210217.
ACCESSION AX393246
VERSION AX393246.1 GI:19701296
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.

REFERENCE
1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 176 07-FEB-2002;

FEATURES The Johns Hopkins University (US)
Location/Qualifiers
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Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS AX393301 5540 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 231 from Patent WO0210217.
ACCESSION AX393301
VERSION AX393301.1 GI:19701322
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Homnidae; Homo.
REFERENCE
1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
AUTHORS Endothelial cell expression patterns
TITLE Patent: WO 0210217-A 231 07-FEB-2002;
JOURNAL The Johns Hopkins University (US)
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ORIGIN
Query Match 98.8%; Score 1090.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 9.3e-308;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 60
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LOCUS AX458370 5540 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 5 from Patent WO0246228.
ACCESSION AX458370
VERSION AX458370.1 GI:21725040
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Young, J.A., Bradley, K.A., Collier, R.J. and Mowridge, J.S.
AUTHORS Receptor for b. Anthracis toxin
TITLE Patent: WO 0246228-A 5 13-JUN-2002;
JOURNAL WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
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AY28977 1658 bp mRNA linear PRI 10-MAY-2005
LOCUS Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
DEFINITION Homo sapiens variant 4 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY28977
VERSION AY28977.1 GI:62870690
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1658)
Oberthuer, A., Kahler, Y., Splitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F., and Fischer, M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
JOURNAL 2 (bases 1 to 1658)
REFERENCE Oberthuer, A., Kahler, Y., Splitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F., and Fischer, M.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
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Best Local Similarity 99.5%; Pred. No. 1e-307;
Matches 1094; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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LOCUS AY928974
DEFINITION Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
transcript variant 1 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY928974
VERSION AY928974.1 GI:62870684
KEYWORDS
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Hominoidea; Homo.
REFERENCE
1 (bases 1 to 1496)
Oberthuer A., Kahler Y., Spitz R., Skowron M., Westermann F.,
Mehler K., Berthold F. and Fischer M.,
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
2 (bases 1 to 1496)
Oberthuer A., Kahler Y., Spitz R., Skowron M., Westermann F.,
Mehler K., Berthold F. and Fischer M.,
Direct Submission
Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
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LOCUS AY28976
DEFINITION Homo sapiens anthrax toxin receptor/neutroblastoma fusion protein
transcript variant 3 (ANTXR1/NNGI fusion) mRNA, complete cds.
ACCESSION AY28976
VERSION AY28976.1 GI:62870688
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Homidae; Homo.
REFERENCE 1 (bases 1 to 1578)
AUTHORS Oberthuer A., Kahler Y., Spitz R., Skowron M., Westermann F.,
Mehler K., Berthold F. and Fischer M.
SNGB-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1578)
AUTHORS Oberthuer A., Kahler Y., Spitz R., Skowron M., Westermann F.,
Mehler K., Berthold F. and Fischer M.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
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ACCESSION      AX458372
VERSION      AX458372.1
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              Homnidae; Homo.
REFERENCE      1
AUTHORS      Young,J.A., Bradley,K.A., Collier,R.J. and Mogridge,J.S.
TITLE      Receptor for b. anthracis toxin
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LOCUS
DEFINITION Homo sapiens anchirax toxin receptor 1, transcript variant 3, mRNA

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| SOURCE | Homo sapiens (human) | |
| ORGANISM | Homo sapiens | |
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| AUTHORS | Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, I., Wang, J., Heist, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Ioshizuka, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalins, D.E., Scherch, A., Schen, J.E., Jones, S.J., and Marra, M.A. | |
| TITLE | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences | |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) | |
| REFERENCE | 2 (bases 1 to 2112) | |
| AUTHORS | Strausberg, R. | |
| TITLE | Direct Submission | |
| JOURNAL | Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA | |
| REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov | |
| COMMENT | Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@cgsc.bc.ca | |
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Series: IRAL Plate: 29 Row: 9 Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16933552.

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Query Match 86.0%; Score 949.4; DB 8; Length 2112;
 Best Local Similarity 99.9%; Pred. No. 2.3e-266;
 Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 13

AK223273

LOCUS

AK223273

DEFINITION

Homo sapiens mRNA for tumor endothelial marker 8 isoform 3 precursor variant, clone: STM07451.

ACCESSION

AK223273.1 GI:62898106

VERSION

FLI_CDNA; oligo capping.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1

Maruyama, K. and Sugano, S.

Oligo-capping: a simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides

Gene 138 (1-2), 171-174 (1994)

JOURNAL

8125298

PUBMED

2

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.

Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library

Gene 200 (1-2), 149-156 (1997)

JOURNAL

9373149

PUBMED

3

(bases 1 to 2052)

Suzuki, Y., Sugano, S., Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A. and Yokoyama, S.

Direct Submision

Submitted (22-APR-2005) Akiko Tanaka, RIKEN Yokohama Institute, Protein Research Group, 1-7-22 Suehito, Tsurumi, Yokohama, Kanagawa, 230-0045, Japan (E-mail: akitanaka@riken.jp, URL: http://protein.gsc.riken.jp/, Tel: 81-45-503-9452, Fax: 81-45-503-9450)

COMMENT

This work was supported in part by the National Project on Protein Structural and Functional Analysis, Ministry of Education, Culture, Sports, Science and Technology of Japan.

Sumio Sugano, Yutaka Suzuki

Laboratory of Functional Genomics Department of Medical Genome Sciences Graduate School of Frontier Sciences The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639 Japan email: sugano@u-tokyo.ac.jp

URL: http://www.k.u-tokyo.ac.jp/index.html.en.

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Query Match 86.0%; Score 949.2; DB 8; Length 2052;
Best Local Similarity 99.7%; Pred. No. 2,66-266;
Matches 951; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 14

AX393256
LOCUS AX393256
DEFINITION Sequence 186 from Patent WO0210217.
ACCESSION AX393256
VERSION AX393256.1 GI:19701303
KEYWORDS
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Mammalia; Eutelestia; Chordata; Vertebrata; Eutelestia;
Mammalia; Eutelestia; Chordata; Vertebrata; Eutelestia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
Endothelial cell expression patterns
Patent: WO 0210217-A 186 07-FEB-2002;
The Johns Hopkins University (US)
Location/Qualifiers

FEATURES

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Best Local Similarity 87.3%; Pred. No. 3,66-238;
Matches 935; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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RESULT 15
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LOCUS AX393370 5220 bp DNA linear PART 23-MAR-2002
DEFINITION Sequence 300 from Patent WO0210217.
ACCESSION AX393370
VERSION AX393370.1 GI:19701356
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
AUTHORS
TITLE
JOURNAL
Patent: WO 0210217-A 300 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
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Best Local Similarity 87.3%; Pred. No. 3,6e-238;
Matches 935; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 24 CCTGGCATCGGCTTCAGTGTCTCTTTGGCCACTGTGGTCTCATCTGCGCGGACA 83
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DB 1311 AGTGATCATCAAGAGAGTCCCTCCACCCCTGTTGAGAGAGTGAAGAAA 1361
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Search completed: December 18, 2005, 11:23:36
Job time : 5922.11 secs

PS Claim 7, Page 27-29; 45pp; English.
 CC The present sequence is that of cDNA encoding a human surface-bound
 CC anthrax toxin receptor (ATR). The cDNA is a PCR amplification product
 CC from HeLa cells and human placenta cDNA libraries. Anthrax toxin
 CC protective antigen (PA) binds to the ATR at a von Willebrand factor A
 CC domain located in the extracellular domain of ATR. The invention provides
 CC ATR polypeptides and polynucleotides, vectors, host cells, and transgenic
 CC and knock-out animals. The invention also provides methods for
 CC identifying molecules that bind the ATR and which reduce the toxicity of
 CC anthrax toxin. A claimed method for treating anthrax in a human or animal
 CC involves administering an agent that inhibits binding between PA and ATR
 CC at a level effective to reduce the severity of anthrax. Suitable agents
 CC include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at
 CC least 80% identical to these, a fusion protein, a monoclonal or
 CC polyclonal antibody, a polysaccharide, a lipid or a nucleic acid. ATR
 CC polynucleotides can also be used in the recombinant production of ATR
 CC polypeptides, and as molecular probes

Sequence 1414 BP; 394 A; 344 C; 344 G; 332 T; 0 U; 0 Other;

Query Match 100.0%; Score 1104; DB 6; Length 1414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 824 GTGAGAGAAAACGGCTTCCGACATCCCGCAACGTGACAGGGTCTCTGACGTTCAAG 883
 QY 781 ATCAATGATCGGTGTACACTGAATGAAGCCCTTTCTGTGGAAGACACTTATTACG 840
 DB 884 ATCAATGATCGGTGTACACTGAATGAAGCCCTTTCTGTGGAAGACACTTATTACG 943
 QY 841 TGTCCAGGCGCTATCTTAAAAGAAATGGGATGAAGGTGACATCCAGGTGACATGAAAC 900
 DB 944 TGTCCAGGCGCTATCTTAAAAGAAATGGGATGAAGGTGACATCCAGGTGACATGAAAC 1003
 QY 901 GATGCGCTCTCTTTTATCTCCAGTTCGTATCATATCACCACACACACTGTCTGACGCT 960
 DB 1004 GATGCGCTCTCTTTTATCTCCAGTTCGTATCATATCACCACACACACTGTCTGACGCT 1063
 QY 961 TCCATCTGGCCATGCGCCCTGCTGATCCCTGCTTCCCTGCTGCTGCTGCTGCTGCTG 1020
 DB 1064 TCCATCTGGCCATGCGCCCTGCTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
 QY 1021 TGGTCTGGCCCTCTGCTGCACTGTGATTAATCAAGAGGTCCCTCCACCCCTGCGAG 1080
 DB 1124 TGGTCTGGCCCTCTGCTGCACTGTGATTAATCAAGAGGTCCCTCCACCCCTGCGAG 1183
 QY 1081 GAGAGTGAAGAAATTAATAATAA 1104
 DB 1184 GAGAGTGAAGAAATTAATAATAA 1207

RESULT 2
 ABL92078 standard; cDNA; 5540 BP.
 ID ABL92078

XX ABL92078;
 AC 30-MAY-2002 (first entry)
 XX DT

DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 176.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neovascularization; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.

XX Homo sapiens.

XX WO200210217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US024031.

XX 02-AUG-2000; 2000US-0222599P.

XX 11-AUG-2000; 2000US-0224360P.

XX 11-APR-2001; 2001US-0282850P.

XX (Uydo) UNIV JOHNS HOPKINS.

XX St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291856/33.

XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth.

XX Disclosure; Page 121-123; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM

CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
Query Match 98.8%; Score 1090.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCCACGCGGAGGAGGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTGGCCACT 60
DB 144 ATGCCACGCGGAGGAGGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTGGCCACT 203
QY 61 CTGTGCTCATCTGCGCGGCGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGTAC 120
DB 204 CTGTGCTCATCTGCGCGGCGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGTAC 263
QY 121 GGGGAGTTGACCTGTACTCATTTTGGACAATCAGGAGTGTGTCGACCACTGGAA 180
DB 264 GGGGAGTTGACCTGTACTCATTTTGGACAATCAGGAGTGTGTCGACCACTGGAA 323
QY 181 GAATCTATCTACTTTGTGGAACAGTTGGCTCACAAATTCAGCCCAAGTTGAGATG 240
DB 324 GAATCTATCTACTTTGTGGAACAGTTGGCTCACAAATTCAGCCCAAGTTGAGATG 383
QY 241 TCGTTATTTGTTTCTCCACCCGAGGAACACTTAAATGAACTGACAGAAACAGAA 300
DB 384 TCGTTATTTGTTTCTCCACCCGAGGAACACTTAAATGAACTGACAGAAACAGAA 443
QY 301 CAATCCGTCAAGGCGCTGAGAACTCCAGAAATTCGCGAGGAGGACCTTACATG 360
DB 444 CAATCCGTCAAGGCGCTGAGAACTCCAGAAATTCGCGAGGAGGACCTTACATG 503
QY 361 CATGAAGATTTGAAAGGCGCAGTGAAGCAATTTATTAATGAAACAGACAGGTA 420
DB 504 CATGAAGATTTGAAAGGCGCAGTGAAGCAATTTATTAATGAAACAGACAGGTA 563
QY 421 ACAAGCAGCGTCATCTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTCTAT 480
DB 564 ACAAGCAGCGTCATCTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTCTAT 623
QY 481 TCGAGAGGAGGCTAATAGTCTCCGAGATCTTGTCATTTGTTA CTGTGAGTG 540
DB 624 TCGAGAGGAGGCTAATAGTCTCCGAGATCTTGTCATTTGTTA CTGTGAGTG 683
QY 541 AAAGATTTCAATGAGACACAGCTGGCCGAGTTGCGAGACATGAAGATCAATGTTCC 600
DB 684 AAAGATTTCAATGAGACACAGCTGGCCGAGTTGCGAGACATGAAGATCAATGTTCC 743
QY 601 GTGAATGACGCGCTTTCAGGCTTGCAAGGCAATCACTCAATTTTGAAGACTCTGC 660
DB 744 GTGAATGACGCGCTTTCAGGCTTGCAAGGCAATCACTCAATTTTGAAGACTCTGC 803
QY 661 ATGGAATTTCTAGAGCTGAACCATCCACCATATGTGCAAGAGTCAATTTCAAGTGT 720
DB 804 ATGGAATTTCTAGAGCTGAACCATCCACCATATGTGCAAGAGTCAATTTCAAGTGT 863
QY 721 GTGAGAGAAACGCGCTTCCGACATGCCGCAAGCTGACAGGGTCTCTGAGCTTCAAG 780
DB 864 GTGAGAGAAACGCGCTTCCGACATGCCGCAAGCTGACAGGGTCTCTGAGCTTCAAG 923
QY 781 ATCAATGACTGTGTCACACTCAATGAGAAAGCCCTTTTCTGTGGAAGCACTTATTA 840
DB 924 ATCAATGACTGTGTCACACTCAATGAGAAAGCCCTTTTCTGTGGAAGCACTTATTA 983
QY 841 TGTCCACGCGCTATCTTAAAGAAAGTTGGCATGAAGCTGCATCCAGGTCAGATGAC 900

DB 984 TGTCCAGCGCCTATCTTAAAGAAAGTTGGCATGAAGCTGCACTCAGGTCAGCATGAAC 1043
QY 901 GATGCGCTCTCTTTATCTCCAGTTGTGCATCATACCAACACACACATGTTCTGACGG 960
DB 1044 GATGCGCTCTCTTTATCTCCAGTTGTGCATCATACCAACACACACATGTTCTGACGG 1103
QY 961 TCCATCTGCGCATGCGCCCTGCTGATCTGTTCTCTGCTCTGACCTGCTCTCTG 1020
DB 1104 TCCATCTGCGCATGCGCCCTGCTGATCTGTTCTCTGCTCTGACCTGCTCTCTG 1163
QY 1021 TGGTTTGGCCCTCTGCTGCACTGATTAATCAAGAGATCCCTCACCCCTGCGAG 1080
DB 1164 TGGTTTGGCCCTCTGCTGCACTGATTAATCAAGAGATCCCTCACCCCTGCGAG 1223
QY 1081 GAGAGTGAGGAAA 1094
DB 1224 GAGAGTGAGGAAA 1237
RESULT 3
ABL92104
ID ABL92104 standard; cDNA; 5540 BP.
XX ABL92104;
AC 30-MAY-2002 (first entry)
XX
DT Human Tumour Endothelial Marker polynucleotide SEQ ID NO 231.
XX
DE Human
XX Human: mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001MO-US024031.
XX
PR 02-AUG-2000; 2000US-0222599P.
PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
XX (U9J0) UNIV JOHNS HOPKINS.
PA
XX St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2002-291856/33.
XX P-PSDB; ABB90750.
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS Claim 30; Page 207-209; 331pp; English.
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers

```

CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
Query Match 98.8%; Score 1090.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGCGGAGAGAGCCCTCGGCATCGGCTCCAGTGGGCTCTTTGGCCACT 60
   |||
DB 144 ATGGCCACGCGGAGAGAGCCCTCGGCATCGGCTCCAGTGGGCTCTTTGGCCACT 203

QY 61 CTGGTCTCATCTGCGCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTTGAC 120
   |||
DB 204 CTGGTCTCATCTGCGCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTTGAC 263

QY 121 GGGGATTTGACCTGTACTTCACTTTTGGACAAATCGAGAAAGTGTCTGCACCACTGGAA 180
   |||
DB 264 GGGGATTTGACCTGTACTTCACTTTTGGACAAATCGAGAAAGTGTCTGCACCACTGGAA 323

QY 181 GAAATCTATTACTTTGAGAACAGTTGGCTCAAAATTCAGCCACAGTTGAGAAATG 240
   |||
DB 324 GAAATCTATTACTTTGAGAACAGTTGGCTCAAAATTCAGCCACAGTTGAGAAATG 383

QY 241 TCTTTATTGTTTCTCAACCCGAGAACAACTTAATGAACTGACAGAAAGACAGAGAA 300
   |||
DB 384 TCTTTATTGTTTCTCAACCCGAGAACAACTTAATGAACTGACAGAAAGACAGAGAA 443

QY 301 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACAG 360
   |||
DB 444 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACAG 503

QY 361 CATGAGAGATTTGAAAGGGCCAGTAGAGAGATTTATGAAACAGACAAAGGTTACAG 420
   |||
DB 504 CATGAGAGATTTGAAAGGGCCAGTAGAGAGATTTATGAAACAGACAAAGGTTACAG 563

QY 421 ACAGCCAGGCTCATCTGCTTGTGATGATGAGAACTCCATGAGATCTTTTCTAT 480
   |||
DB 564 ACAGCCAGGCTCATCTGCTTGTGATGATGAGAACTCCATGAGATCTTTTCTAT 623

QY 481 TCAGAGAGGAGGCTTAATAGGCTTCGAGATCTTGGTGCAATTGTTAACTGTGTGGTG 540
   |||
DB 624 TCAGAGAGGAGGCTTAATAGGCTTCGAGATCTTGGTGCAATTGTTAACTGTGTGGTG 683

QY 541 AAAAGATTTCAATAGACACAGCTGCGCCGAGATTCGAGACGTAAGATCATGTGTTCC 600
   |||
DB 684 AAAAGATTTCAATAGACACAGCTGCGCCGAGATTCGAGACGTAAGATCATGTGTTCC 743

QY 601 GTGAAATGACGGCTTTGAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTGC 660
   |||
DB 744 GTGAAATGACGGCTTTGAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTGC 803

QY 661 ATGGAATTTAGACAGTGAACCATTCACATATGTGCGAGAGAGATCATTTCAAGTTGC 720
   |||
DB 804 ATGGAATTTAGACAGTGAACCATTCACATATGTGCGAGAGAGATCATTTCAAGTTGC 863

QY 721 GTGAGAGAAAGGCTTCGACATGCGCCGACAGCTGAGAGAGGTTCCCTGACACTTCAAG 780
   |||
DB 864 GTGAGAGAAAGGCTTCGACATGCGCCGACAGCTGAGAGAGGTTCCCTGACACTTCAAG 923

QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACACTTAATTTACTG 840
   |||
DB 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGTAATTTAATTTACTG 983

QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACCTCCAGCTCAGCATGAA 900
   |||
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACCTCCAGCTCAGCATGAA 1043

QY 901 GATGGGCTCTTTTATCTCAATTCGATCATATACACACACACACTGTTGACGGT 960
   |||
DB 1044 GATGGGCTCTTTTATCTCAATTCGATCATATACACACACACACTGTTGACGGT 1103

QY 961 TCAATCTGAGCATGCGCTGTGATCTGTCTCTGCTCTAGCCCTGAGCTCTCTCTGAG 1020

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DB 1104 TCCATCTGGGCGCATGCGCCCTGCTGATCCCTGCTCTAGCCCTGCTCTCCCTCG 1163
QY 1021 TGGTTCGGCCCTCTGCTGCACTGATTAATCAAGAGAGTCCCTACACCCCTGCGAG 1080
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTAATCAAGAGAGTCCCTACACCCCTGCGAG 1223
QY 1081 GAGAGTGAGGAAAA 1094
DB 1224 GAGAGTGAGGAAAA 1237

RESULT 4
ABV73882
ID ABV73882 standard; cDNA; 5540 BP.
XX
AC ABV73882;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human anthrax toxin receptor cDNA.
XX
KW Anthrax; toxin; receptor; human; TEM8; antibacterial; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 144..1838
   /tag= 8
   /product= "anthrax toxin receptor"
FT sig_peptide 144..224
   /tag= b
FT mat_peptide 225..1838
   /tag= c
FT
XX
PN W0200246228-A2.
XX
PD 13-JUN-2002.
XX
PF 03-OCT-2001; 2001WO-US030941.
XX
PR 05-DEC-2000; 2000US-0251481P.
XX
PA (WISC ) WISCONSIN ALUMNI RES FOUNDD.
XX
PI Young JAT, Bradley KA, COLLIER RJ, Mogridge JS;
XX
DR WPI; 2002-713235/77.
XX
DR P-PSDB; ABP54904.
XX
PT Novel isolated polypeptide useful for identifying agent that prevents or
PT reduces effect of anthrax toxin on host cell, for treating human or non-
PT human animal suffering from anthrax.
XX
PS Disclosure; Page 32-37; 45pp; English.
XX
CC The present sequence is that of cDNA encoding a human anthrax toxin
CC receptor (ATR). The cDNA, previously designated TEM8, was originally
CC isolated by PCR from HeLa cell and human placenta cDNA libraries. It was
CC identified in a database screening using a newly isolated human cDNA (see
CC ABV73881) which encodes an ATR (see ABP54903) that is identical to the
CC TEM8 polypeptide except in the cytoplasmic tail, suggesting differential
CC splicing of a primary mRNA transcript. TEM8 was not previously identified
CC as an ATR. The invention provides ATR polypeptides and polynucleotides,
CC host cells, vectors, and transgenic and knock-out animals. It also
CC provides methods for identifying molecules that bind the ATR and which
CC reduce the toxicity of anthrax toxin. A claimed method for treating
CC anthrax in a human or animal involves administering an agent that
CC inhibits binding between anthrax toxin protective antigen (PA) and ATR at
CC a level effective to reduce the severity of anthrax. Suitable agents
CC include the TEM8 polypeptide or a PA-binding fragment of it, a PA-binding
CC polypeptide at least 80% identical to these, a fusion protein, a
CC monoclonal or polyclonal antibody, a polysaccharide, a lipid or a nucleic

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CC acid. ATR polynucleotides can also be used in the recombinant production
 CC of ATR polypeptides, and as molecular probes

XX Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

Query Match 98.8%; Score 1090.8; DB 6; Length 5540;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 ATGGCCAGCGCGAGAGAGCCCTGGAGATCGGCTTCAGTGGCTCTCTTGGCCACT 60
DB 144 ATGGCCAGCGCGAGAGAGCCCTGGAGATCGGCTTCAGTGGCTCTCTTGGCCACT 203
QY 61 CTGCTGCTCATCTGCGCGCGGCAAGGGGAGAGCGAGAGATGGGGGTCCAGCTGTCTAC 120
DB 204 CTGCTGCTCATCTGCGCGCGGCAAGGGGAGAGCGAGAGATGGGGGTCCAGCTGTCTAC 263
QY 121 GGGGATTTGACCTGTACTTCAATTTTGAACAAATCAGGAAGTGTGCACTGGAAT 180
DB 264 GGGGATTTGACCTGTACTTCAATTTTGAACAAATCAGGAAGTGTGCACTGGAAT 323
QY 181 GAAATCTATTACTTTGTGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATG 240
DB 324 GAAATCTATTACTTTGTGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATG 383
QY 241 TCCTTTATTTGTTTCTCCACCCGAGAAACACCTTAATGAACTGACAGAAAGAGAA 300
DB 384 TCCTTTATTTGTTTCTCCACCCGAGAAACACCTTAATGAACTGACAGAAAGAGAA 443
QY 301 CAATCGGTCAAGGCTGAGAAACCTCAGAAAGTTGCGAGAGAGACACTTACATG 360
DB 444 CAATCGGTCAAGGCTGAGAAACCTCAGAAAGTTGCGAGAGAGACACTTACATG 503
QY 361 CATGAAGATTTGAAAGGCGCAGTGAAGATTTATGAAACAGACAAAGGTACAGG 420
DB 504 CATGAAGATTTGAAAGGCGCAGTGAAGATTTATGAAACAGACAAAGGTACAGG 563
QY 421 ACAGCCAGCGCTCATCTGCTTTGACGTGAGAAATCCATGAAGATCTCTTTTCTAT 480
DB 564 ACAGCCAGCGCTCATCTGCTTTGACGTGAGAAATCCATGAAGATCTCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTAATAGGCTCGAATCTTGATGCAATTTGTTTCTGTTGTTG 540
DB 624 TCAGAGAGGAGGCTAATAGGCTCGAATCTTGATGCAATTTGTTTCTGTTGTTG 683
QY 541 AAGATTTCAATGAGACACAGCTGGCCCGAATTCGAGCAAGTAAGATCAATGTTTCCC 600
DB 684 AAGATTTCAATGAGACACAGCTGGCCCGAATTCGAGCAAGTAAGATCAATGTTTCCC 743
QY 601 GTGAATACGCGCTTTCAGGCTTCGAAAGGCTATCCATCTCAATTTGAAAGATCCTG 660
DB 744 GTGAATACGCGCTTTCAGGCTTCGAAAGGCTATCCATCTCAATTTGAAAGATCCTG 803
QY 661 ATGGAATTTGAGAGCTGAACCATCCACATATGTGAGAGAGTCAATTTCAAGTTGTC 720
DB 804 ATGGAATTTGAGAGCTGAACCATCCACATATGTGAGAGAGTCAATTTCAAGTTGTC 863
QY 721 GTGAGAGAAACGCGCTTCGACATGCCCGCAACGTGACAGAGGCTCTCTGAGCTTCAAG 780
DB 864 GTGAGAGAAACGCGCTTCGACATGCCCGCAACGTGACAGAGGCTCTCTGAGCTTCAAG 923
QY 781 ATCAATACCTGCTGACATCAATGAGAGGCTTTTCTGTGAAAGACCTTAATTTACTG 840
DB 924 ATCAATACCTGCTGACATCAATGAGAGGCTTTTCTGTGAAAGATTAATTTACTG 983
QY 841 TGTCAGAGCGCTATCTTAAGAAAGTGGCATGAAAGTGACCTCCAGGTGAGATGAAAC 900
DB 984 TGTCAGAGCGCTATCTTAAGAAAGTGGCATGAAAGTGACCTCCAGGTGAGATGAAAC 1043
QY 901 GATGAGCTCTCTTTATCTCCAGTTCTGTCAATCAACACACACACTGTTCTGACGGT 960
DB 1044 GATGAGCTCTCTTTATCTCCAGTTCTGTCAATCAACACACACACTGTTCTGACGGT 1103

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QY 961 TCCATCTGAGCATGCGCCCTGCTGATCTGCTCTGCTCTAGACCTGAGCTCTCTG 1020
DB 1104 TCCATCTGAGCATGCGCCCTGCTGATCTGCTCTGCTCTAGACCTGAGCTCTCTG 1163
QY 1021 TGGTTCTGCGCCCTGCTGCTGCTGCTGATTAATGAGAGGTTCCCTCCACCTCTGCGAG 1080
DB 1164 TGGTTCTGCGCCCTGCTGCTGCTGCTGATTAATGAGAGGTTCCCTCCACCTCTGCGAG 1223
QY 1081 GAGAGTGAGAGAAA 1094
DB 1224 GAGAGTGAGAGAAA 1237

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RESULT 5

ABX72029 standard; DNA; 5540 BP.

ABX72029;

12-MAR-2003 (first entry)

DNA encoding human tumour endothelial marker TEM 19.

Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;

Tumour endothelial marker; normal endothelial marker; PEM;

pan-endothelial marker; polycystic kidney disease; psoriasis;

diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;

neovascularization; immune response; cytoskeletal; antidiabetic; gene;

ophthalmological; antirheumatic; antirheumatic; antipsoriatic; ds.

Homo sapiens.

MO200283874-A2.

24-OCT-2002.

10-Apr-2002; 2002MO-US008253.

11-APR-2001; 2001US-0282850P.

06-FEB-2002; 2002US-0354262P.

(UJJO) UNIV JOHNS HOPKINS.

Carson-Walter E, St Croix B, Kinzler KM, Vogelstein B;

WPI; 2003-093016/08.

P-PSDB; ABUS4457.

New purified human transmembrane protein, designated as tumor endothelial

marker (TEM) 3, useful for detecting, diagnosing or treating tumors,

polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or

psoriasis.

Disclosure; Page 223-225; 374pp; English.

The present invention relates to a novel method for the isolation of

endothelial cells (ECs), and the identification of genes expressed in

normal and tumour ECs. Tumour endothelial marker (TEM), normal

endothelial marker (NEM), and pan-endothelial marker (PEM) genes are

identified in human ECs. The human EC marker proteins and the

polynucleotide sequences encoding them are useful for detecting,

diagnosing or treating tumours as well as polycystic kidney disease,

diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

useful for inhibiting neovascularization or tumour angiogenesis, for

identifying an immune response to tumour endothelial cells in a patient, or

for identifying candidate drugs for treating tumours. The present

sequence represents a human TEM or NEM gene of the invention

Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

Query Match 98.8%; Score 1090.8; DB 10; Length 5540;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ATGGCCACGGCGAGGAGAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 144 ATGGCCACGGCGAGGAGAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACT 203
QY 61 CTGGTCTCATCTGCGCCCGGGCAAGGGGGAACGAGAGAGAGTGGGGTCCAGCTGTAC 120
DB 204 CTGGTCTCATCTGCGCCCGGGCAAGGGGGAACGAGAGAGAGTGGGGTCCAGCTGTAC 263
QY 121 GGGGATTGACCTGACTTCAATTTGGACAAATCAAGAAAGTGTGTGACCACTGGAAT 180
DB 264 GGGGATTGACCTGACTTCAATTTGGACAAATCAAGAAAGTGTGTGACCACTGGAAT 323
QY 181 GAAATCTAATTAATTTGGAACAGTTGGCTCAAAAATTCATCAGCCCAAGTTGAGAAATG 240
DB 324 GAAATCTAATTAATTTGGAACAGTTGGCTCAAAAATTCATCAGCCCAAGTTGAGAAATG 383
QY 241 TCTTTATTTGTTTCTTCACCCGAGAAACAATTAATGAAGAACTGACAGAGACAGAA 300
DB 384 TCTTTATTTGTTTCTTCACCCGAGAAACAATTAATGAAGAACTGACAGAGACAGAA 443
QY 301 CAAATCGCTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGAGGAGAGCACTTACATG 360
DB 444 CAAATCGCTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGAGGAGAGCACTTACATG 503
QY 361 CATGAAGATTGGAAGGCGCAGTGAGCAGATTTATTAAGAAAACAGACAGGGTACAG 420
DB 504 CATGAAGATTGGAAGGCGCAGTGAGCAGATTTATTAAGAAAACAGACAGGGTACAG 563
QY 421 ACAGCCAGGCTCATCTTTGTTGACTGATGAGAACTCATGAAAGTCTCTTTTCTAT 480
DB 564 ACAGCCAGGCTCATCTTTGTTGACTGATGAGAACTCATGAAAGTCTCTTTTCTAT 623
QY 481 TCAGAGGGGAGGCTAATAGTCTCGAGATCTTGAGCAATGTTACTGTGTGTGAG 540
DB 624 TCAGAGGGGAGGCTAATAGTCTCGAGATCTTGAGCAATGTTACTGTGTGTGAG 683
QY 541 AAAGATTTCAATGAGACACAGCTGCGCCCGGATTCGAGACAGTAAGATCATGTGTTCC 600
DB 684 AAAGATTTCAATGAGACACAGCTGCGCCCGGATTCGAGACAGTAAGATCATGTGTTCC 743
QY 601 GTGAATGAGCGGCTTTCAGGCTGTGCAAGGATCATCACTCAATTTGAAAGAGTCTG 660
DB 744 GTGAATGAGCGGCTTTCAGGCTGTGCAAGGATCATCACTCAATTTGAAAGAGTCTG 803
QY 661 ATGGAATTTCTAGCAGTGAAACATGCAATATGTGAGAGAGTCAATTTCAAGTTGTC 720
DB 804 ATGGAATTTCTAGCAGTGAAACATGCAATATGTGAGAGAGTCAATTTCAAGTTGTC 863
QY 721 GTGAGAGAAACGGCTTCCGACATGCGCCGCAACGTGAGACAGGCTCTGTGACGCTTCA 780
DB 864 GTGAGAGAAACGGCTTCCGACATGCGCCGCAACGTGAGACAGGCTCTGTGACGCTTCA 923
QY 781 ATCAATGATCGGCTCACACTCAATGAGAAAGCCCTTTTCTGTGAAAGCACTTATTTACTG 840
DB 924 ATCAATGATCGGCTCACACTCAATGAGAAAGCCCTTTTCTGTGAAAGCACTTATTTACTG 983
QY 841 TGTCCAGCGCTTCTTAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCACATGAAC 900
DB 984 TGTCCAGCGCTTCTTAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCACATGAAC 1043
QY 901 GATGAGCTCTCTTTTATCTCAAGTTCTGATCATCAACACACAGACTGTTTGAAGCT 960
DB 1044 GATGAGCTCTCTTTTATCTCAAGTTCTGATCATCAACACACAGACTGTTTGAAGCT 1103
QY 961 TCCATCTTGCCATTCGCGCTGTGATCTGTCTGTCTGTCTGTAGCCCTGCTCTCTG 1020
DB 1104 TCCATCTTGCCATTCGCGCTGTGATCTGTCTGTCTGTCTGTAGCCCTGCTCTCTG 1163
QY 1021 TGGTCTGAGCGCTCTGCTGACATGATATCAAGAGAGTCCCTCAACCCCTGCGAG 1080
DB 1164 TGGTCTGAGCGCTCTGCTGACATGATATCAAGAGAGTCCCTCAACCCCTGCGAG 1223
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```
QY 1081 GAGAGTGAGAAAA 1094
DB 1224 GAGAGTGAGAGAGA 1237

RESULT 6
ABX72003
ID ABX72003 standard; DNA; 5540 BP.
XX
XX ABX72003;
AC
XX
XX 12-MAR-2003 (first entry)
DT
XX
DE DNA encoding human tumour endothelial marker TEM 8.
XX
XX
XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
XX Tumour endothelial marker; normal endothelial marker; PEM;
XX pan-endothelial marker; polycystic kidney disease; psoriasis;
XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
XX neovascularization; immune response; cytosolic; antidiabetic; gene;
XX ophthalmological; antineoplastic; antirheumatic; antidiabetic; da.
XX
XX Homo sapiens.
OS
XX
XX WO200283874-A2.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 10-APR-2002; 2002WO-US008253.
PF
XX
XX 11-APR-2001; 2001US-0282850P.
PR
XX
XX 06-FEB-2002; 2002US-0354262P.
PA
XX
XX (UYPD ) UNIV JOHNS HOPKINS.
PI
XX
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2003-093016/08.
DR
XX
XX P-PSDB; ABUS4430.
PT
XX
XX New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX
XX
XX Disclosure; Page 117-120; 374pp; English.
XX
XX
XX The present invention relates to a novel method for the isolation of
XX endothelial cells (ECs), and the identification of genes expressed in
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
XX identified in human ECs. The human EC marker proteins and the
XX polynucleotide sequences encoding them are useful for detecting,
XX diagnosing or treating tumours as well as polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
XX useful for inhibiting neovascularization or tumour angiogenesis, for
XX inducing an immune response to tumour endothelial cells in a patient, or
XX for identifying candidate drugs for treating tumours. The present
XX sequence represents a human TEM or NEM gene of the invention
XX
XX
XX Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
SQ

Query Match 98.8%; Score 1090.8; DB 10; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGGCGAGGAGAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 144 ATGGCCACGGCGAGGAGAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACT 203
QY 61 CTGGTCTCATCTGCGCCCGGGCAAGGGGGAACGAGAGAGAGTGGGGTCCAGCTGTAC 120
DB 204 CTGGTCTCATCTGCGCCCGGGCAAGGGGGAACGAGAGAGAGTGGGGTCCAGCTGTAC 263
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QY 121 GGGGATTTGACCTGTAATTTGACAAATCAGAAAGTGTGACCACTGGAAAT 180
DB 264 GGGGATTTGACCTGTAATTTGACAAATCAGAAAGTGTGACCACTGGAAAT 323
QY 181 GAAATCTAATCTTTGTGAAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAAATG 240
DB 324 GAAATCTAATCTTTGTGAAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAAATG 383
QY 241 TCTTTATTTGTTTTTCTCCACCGAGAAACAACCTTAATGAATCTGACAGAAACAGAGAA 300
DB 384 TCTTTATTTGTTTTTCTCCACCGAGAAACAACCTTAATGAATCTGACAGAAACAGAGAA 443
QY 301 CAAATCCGTCAGAGCCCTGAGAAAGAACTCCAGAAAGTTCTGCGACAGAGAGACCTTACATG 360
DB 444 CAAATCCGTCAGAGCCCTGAGAAAGAACTCCAGAAAGTTCTGCGACAGAGAGACCTTACATG 503
QY 361 CATGAAGATTTGAAAGGGCCAGTGAAGACATTTATATGAAGACAGAAAGGTAACAGG 420
DB 504 CATGAAGATTTGAAAGGGCCAGTGAAGACATTTATATGAAGACAGAAAGGTAACAGG 563
QY 421 ACAGCCAGCGTCATCATTTGCTTGAATGAGAACTCCATGAAGATCTTTTCTAT 480
DB 564 ACAGCCAGCGTCATCATTTGCTTGAATGAGAACTCCATGAAGATCTTTTCTAT 623
QY 481 TCAAGAGAGGAGCTAATAGTCTCCAGATCTTGTGTGCAATTTGTAATCTGTGTGATG 540
DB 624 TCAAGAGGAGGAGCTAATAGTCTCCAGATCTTGTGTGCAATTTGTAATCTGTGTGATG 683
QY 541 AAAGATTTCAATGAGACAGAGCTGGCCCGGATTTGGGAGAGTATCATGTGTTTCCC 600
DB 684 AAAGATTTCAATGAGACAGAGCTGGCCCGGATTTGGGAGAGTATCATGTGTTTCCC 743
QY 601 GTGATGACCGCTTTTCAGGCTCTGCAAGGCAATCATCTCAATTTTGAAGAACTCTGC 660
DB 744 GTGATGACCGCTTTTCAGGCTCTGCAAGGCAATCATCTCAATTTTGAAGAACTCTGC 803
QY 661 ATGGAATTTAGACAGCTGAACCATCCATATGTGACAGAGAGTATTTCAAGTTGTC 720
DB 804 ATGGAATTTAGACAGCTGAACCATCCATATGTGACAGAGAGTATTTCAAGTTGTC 863
QY 721 GTGAGAGGAAAGCGCTTCGACATGCGCGCAAGTGAGAGGGCTCTGACAGTTCAAG 780
DB 864 GTGAGAGGAAAGCGCTTCGACATGCGCGCAAGTGAGAGGGCTCTGACAGTTCAAG 923
QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACACTTAATTA 840
DB 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACACTTAATTA 983
QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAGCTGATCCAGGTCCAGATGAAC 900
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAGCTGATCCAGGTCCAGATGAAC 1043
QY 901 GATGGCGCTCTTTTATCTCCAGTCTGTATCATCAACCAACACACTGTTCTGACGGT 960
DB 1044 GATGGCGCTCTTTTATCTCCAGTCTGTATCATCAACCAACACACTGTTCTGACGGT 1103
QY 961 TCCATCTGCGCATCGGCTGCTGATCTGTTCTGCTCTGAGCCCTGCTCTCTCTG 1020
DB 1104 TCCATCTGCGCATCGGCTGCTGATCTGTTCTGCTCTGAGCCCTGCTCTCTCTG 1163
QY 1021 TGTGTTCTGGCCCTCTGCTGATCTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1080
DB 1164 TGTGTTCTGGCCCTCTGCTGATCTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1223
QY 1081 GAGAGTGAGGAAAA 1094
DB 1224 GAGAGTGAGGAAAA 1237
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RESULT 7
ADR48215
ID ADR48215 standard; cDNA; 5540 BP.

```
XX AC ADR48215;
XX XX 18-NOV-2004 (first entry)
XX DT
XX DE Human tumour endothelial marker 8 precursor encoding cDNA SEQ.3.
XX XX pancreatic cancer-associated transcript; pancreatic cancer; human;
XX KW cytostatic; gene therapy; protein therapy;
XX KW tumour endothelial marker 8 precursor; TM8; gene; ss.
XX OS Homo sapiens.
XX XX
XX FT Key Location/Qualifiers
XX FT CDS 144..1038
XX FT /tag a
XX FT /product= "tumour endothelial marker 8 precursor (TM8)"
XX PD MO2004074510-AI.
XX XX
XX PF 02-SEP-2004.
XX XX
XX PF 18-FEB-2004; 2004MO-AU000194.
XX XX
XX PR 18-FEB-2003; 2003AU-00900747.
XX XX
XX PA (GARY-) GARYAN INST MEDICAL RES.
XX PI Biankin A, Segara D, Henshall S, Sutherland R,
XX DR WPI; 2004-635591/61.
XX DR P-PADB; ADR48216.
XX XX
XX PT Detecting pancreatic cancer-associated transcript in a biological sample,
XX PT useful for diagnosing or treating the disease, comprises contacting the
XX PT sample with a polynucleotide that selectively hybridizes to a specific
XX PT sequence.
XX XX
XX PS Claim 70; SEQ ID NO 3; 263bp; English.
XX XX
XX CC The present invention describes a method for detecting a pancreatic
XX CC cancer-associated transcript in a biological sample. The method comprises
XX CC contacting the biological sample with a polynucleotide that selectively
XX CC hybridizes to a sequence at least 80% identical to a sequence as shown in
XX CC any one of Tables 3 to 25 in the specification or having the Genbank
XX CC Accession Number AF279145. Also described: (1) diagnosing pancreatic
XX CC cancer in a human or animal subject being tested; determining the
XX CC likelihood that a subject having a pancreatic cancer will survive, or
XX CC determining the suitability of a subject having a pancreatic cancer for
XX CC surgical resection therapy; (2) detecting a pancreatic cancer-associated
XX CC polypeptide in a biological sample; (3) determining the likelihood that a
XX CC subject having a pancreatic cancer will survive; and (4) monitoring the
XX CC efficacy of a therapeutic treatment of pancreatic cancer. A pancreatic
XX CC cancer-associated transcript has cytostatic activity, and can be used in
XX CC gene and protein therapy. A pancreatic cancer-associated transcript
XX CC polynucleotide, a vector comprising the polynucleotide, an isolated
XX CC polypeptide or an antibody that binds to the isolated polypeptide can be
XX CC used for diagnosing or prognosing pancreatic cancer or for preparing a
XX CC medicament for the treatment of pancreatic cancer. The prognostic or
XX CC diagnostic methods are useful for the early detection of pancreatic
XX CC cancer or its metastases, and for monitoring the progress of disease such
XX CC as during remission or following surgery or chemotherapy. The present
XX CC sequence encodes human tumour endothelial marker 8 precursor (TM8),
XX CC which is used in the exemplification of the present invention.
XX XX
XX SO Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
```

Query Match 98.8%; Score 1090.8; DB 13; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGCCACGCGGAGGAGAGCCCTGCGATCGGCTTCCAGTGGCTCTTTGGCACT 60
|||||

Db 144 ATGGCCACGGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 203
Qy 61 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGACGAGGAGATGGGGGTCCAGCCTGCTAC 120
Db 204 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGACGAGGAGATGGGGGTCCAGCCTGCTAC 263
Qy 121 GGGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 180
Db 264 GGGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 323
Qy 181 GAAATCTATTAATCTTTGGAACAGTTGGTCAACAAATTCATGACCCCAAGTTGAAATG 240
Db 324 GAAATCTATTAATCTTTGGAACAGTTGGTCAACAAATTCATGACCCCAAGTTGAAATG 383
Qy 241 TCCCTATTTGTTTCTCCACCCGAGAACACCTTAATGAAAATGACAGAAACAGAGAA 300
Db 384 TCCCTATTTGTTTCTCCACCCGAGAACACCTTAATGAAAATGACAGAAACAGAGAA 443
Qy 301 CAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAGTTCTGCGCAGAGAGAGACCTTACATG 360
Db 444 CAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAGTTCTGCGCAGAGAGAGACCTTACATG 503
Qy 361 CATGAGATTTGAAAGGGCCAGTGAAGCATTTATTAAGAAAACGACAAAGGTCAAG 420
Db 504 CATGAGATTTGAAAGGGCCAGTGAAGCATTTATTAAGAAAACGACAAAGGTCAAG 563
Qy 421 ACAGCAGGCTCATCTGCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTAT 480
Db 564 ACAGCAGGCTCATCTGCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTAT 623
Qy 481 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGTGCAATGTTTACTGTGTGTGTG 540
Db 624 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGTGCAATGTTTACTGTGTGTGTG 683
Qy 541 AAAAGATTTCAATGAGACAGCTGGCCCGGATGGCGACAGTGAAGATCATGTGTTCCC 600
Db 684 AAAAGATTTCAATGAGACAGCTGGCCCGGATGGCGACAGTGAAGATCATGTGTTCCC 743
Qy 601 GTGAATGACGGCTTTAGAGGCTTGCAAGGATCATCTCAATTTTGAAGAAAGTCTGCG 660
Db 744 GTGAATGACGGCTTTAGAGGCTTGCAAGGATCATCTCAATTTTGAAGAAAGTCTGCG 803
Qy 661 ATCGAAATTTCTAGCAGCTGAAACCATTCACCAATGTGCAAGAGAGTCAATTTCAAGTTGTC 720
Db 804 ATCGAAATTTCTAGCAGCTGAAACCATTCACCAATGTGCAAGAGAGTCAATTTCAAGTTGTC 863
Qy 721 GTGAGAGGAAACGGCTTCCGACATGCCCCGCAAGCTGGAAGAGGTCTCTGCAAGCTTCAAG 780
Db 864 GTGAGAGGAAACGGCTTCCGACATGCCCCGCAAGCTGGAAGAGGTCTCTGCAAGCTTCAAG 923
Qy 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACCTTATTACTG 840
Db 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACCTTATTACTG 983
Qy 841 TGTCCAGCGCTAATCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAC 900
Db 984 TGTCCAGCGCTAATCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAC 1043
Qy 901 GATGGGCTCTCTTTATCTTCAATTTCTGTATCATATCAACCAACCAACATGTTTGACGCT 960
Db 1044 GATGGGCTCTCTTTATCTTCAATTTCTGTATCATATCAACCAACCAACATGTTTGACGCT 1103
Qy 961 TCCATCTGGCCATCGCCCTGATCTGATCTGTCCTGCTTACGCTTGGCTCTCTCTG 1020
Db 1104 TCCATCTGGCCATCGCCCTGATCTGATCTGTCCTGCTTACGCTTGGCTCTCTCTG 1163
Qy 1021 TGGTCTGCGCCCTCTGCTGCACTGTGATTAATCAGAGAGTCCCTCAACCCCTGCGAG 1080
Db 1164 TGGTCTGCGCCCTCTGCTGCACTGTGATTAATCAGAGAGTCCCTCAACCCCTGCGAG 1223
Qy 1081 GAGAGTGAGGAAAA 1094
Db 1224 GAGAGTGAGGAAAA 1237

RESULT 8
AD270742
ID AD270742 standard; cDNA; 5540 BP.
XX
AC AD270742;
XX
DT 14-JUL-2005 (first entry)
XX
DE Tumor endothelial marker 8 precursor (Tem8) cDNA.
XX
KW osteopathic; antiarthritic; gene expression; differentiation;
KW transcription; bone disease; osteoarthritis; antiarthritic; osteopathic;
KW musculoskeletal disease; tumor endothelial marker 8 precursor; Tem8; gene;
KW 8.
XX
OS Homo sapiens.
XX
PN WO2005038022-A1.
PN
PD 28-APR-2005.
XX
PF 20-OCT-2004; 2004WO-JP015879.
XX
PR 20-OCT-2003; 2003JP-00359172.
XX
PA (TEIJ-) TEIJIN PHARMA LTD.
PA (KOMORI) KOMORI T.
XX
PI Komori T, Kanatani N, Yoshida CA, Zama A, Kobayashi S, Yamana K;
DR WPI; 2005-322866/33.
XX
DR P-PSDB; AD270743.
XX
PT Acquiring chondrogenic differentiation control related gene Runx2/Cbfa1,
PT by forcibly expressing transcriptional factor related to pathological
PT condition in cell strain lacking transcriptional factor and screening for
PT gene.
XX
PS Claim 15; SEQ ID NO 27; 357bp; Japanese.
XX
CC The invention describes acquiring (M1) a pathological condition related
CC gene, preferably chondrogenic differentiation control related gene
CC Runx2/Cbfa1, comprising forcibly expressing a transcriptional factor
CC related to pathological condition, preferably Runx2/Cbfa1 in a cell
CC strain or a primary culture cell lacking the transcriptional factor, and
CC screening for the gene whose expression is induced or suppressed. (M1) is
CC useful for acquiring a pathological condition related gene, preferably
CC chondrogenic differentiation control related gene Runx2/Cbfa1.
CC Polynucleotides detailed in the invention are useful for screening a
CC preventive and/or therapeutic agent of bone and/or articular disease such
CC as osteoarthritis. This sequence encodes tumor endothelial marker 8
CC precursor (Tem8) associated with isolation of a pathological condition
CC related gene.
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
XX
Query Match 98.8%; Score 1090.8; DB 14; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCCACGGGAGGAGAGCCCTCGGCATCGGCTTCAAGTGGCTCTCTTTGGCCACT 60
Db 144 ATGGCCACGGGAGGAGAGCCCTCGGCATCGGCTTCAAGTGGCTCTCTTTGGCCACT 203
Qy 61 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGACGAGGAGATGGGGGTCCAGCCTGCTAC 120
Db 204 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGACGAGGAGATGGGGGTCCAGCCTGCTAC 263
Qy 121 GGGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 180
Db 264 GGGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 323

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QY 181 GAAATCTATTACTTTGGTGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 240
XX |||||
DB 324 GAAATCTATTACTTTGGTGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 383
QY 241 TCCCTTATTGTTTTTCTCCACCCGAGAACAACTTAAATGAAATGACAGAAAGACAGAA 300
XX |||||
DB 384 TCCCTTATTGTTTTTCTCCACCCGAGAACAACTTAAATGAAATGACAGAAAGACAGAA 443
QY 301 CAAATCCGTCAAGGCTTGAAGAACTTCAGAAAGTTCTGCAGAGAGACACTTACATG 360
XX |||||
DB 444 CAAATCCGTCAAGGCTTGAAGAACTTCAGAAAGTTCTGCAGAGAGACACTTACATG 503
QY 361 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTTATATGAAACAGCAAGGGTACAG 420
XX |||||
DB 504 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTTATATGAAACAGCAAGGGTACAG 563
QY 421 ACAGCCAGCTCATCATTTGCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTAT 480
XX |||||
DB 564 ACAGCCAGCTCATCATTTGCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGGTGTG 540
XX |||||
DB 624 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGGTGTG 683
QY 541 AAAGATTTCAATAGACACAGCTGGCCCGGATTTGCCGACAGTAAGATCAATGTTTCCC 600
XX |||||
DB 684 AAAGATTTCAATAGACACAGCTGGCCCGGATTTGCCGACAGTAAGATCAATGTTTCCC 743
QY 601 GTGAATGACGGCTTTCAGGCTCTGCAGAGCATCATCAATTTTGAAGAGTCCG 660
XX |||||
DB 744 GTGAATGACGGCTTTCAGGCTCTGCAGAGCATCATCAATTTTGAAGAGTCCG 803
QY 661 ATCGAAATTTGACAGCTGAACCATCCATATGTGTCAGAGAGATCATTTCAAGTTGTC 720
XX |||||
DB 804 ATCGAAATTTGACAGCTGAACCATCCATATGTGTCAGAGAGATCATTTCAAGTTGTC 863
QY 721 GTGAGAGGAAACGGCTTCCGACATGCCCCGACAGTGAACAGGGTCTCTGCAGCTTCAAG 780
XX |||||
DB 864 GTGAGAGGAAACGGCTTCCGACATGCCCCGACAGTGAACAGGGTCTCTGCAGCTTCAAG 923
QY 781 ATCAATGACTCGGTCACTCAATGAGAACCCCTTTCTGTGGAAGACACTTATTTACTG 840
XX |||||
DB 924 ATCAATGACTCGGTCACTCAATGAGAACCCCTTTCTGTGGAAGATCTTATTTTACTG 983
QY 841 TGTCCAGCGGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCAGGTCAGCATGAAC 900
XX |||||
DB 984 TGTCCAGCGGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCAGGTCAGCATGAAC 1043
QY 901 GATGGGCTCTCTTTTATCTCGAGTCTGTCACTATCAACACACACACTGTGTGAGCGT 960
XX |||||
DB 1044 GATGGGCTCTCTTTTATCTCGAGTCTGTCACTATCAACACACACACTGTGTGAGCGT 1103
QY 961 TCCATCTCTGGAGCATCGGCTGTGATCTGTCTCTGCTGAGCCCTGGCTCTCTCTG 1020
XX |||||
DB 1104 TCCATCTCTGGAGCATCGGCTGTGATCTGTCTCTGCTGAGCCCTGGCTCTCTCTG 1163
QY 1021 TGGTTCTGGCCCTCTCTGCTGACATGTGATTAATCAAGAGAGTCCCTCCACCCCTGCCGAG 1080
XX |||||
DB 1164 TGGTTCTGGCCCTCTCTGCTGACATGTGATTAATCAAGAGAGTCCCTCCACCCCTGCCGAG 1223
QY 1081 GAGAGTGAAGAAA 1094
XX |||||
DB 1224 GAGAGTGAAGAAA 1237
XX |||||

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RESULT 9
AEA29804
ID AEA29804 standard; DNA; 5540 BP.
XX
AC AEA29804;
XX
DT 11-AUG-2005 (first entry)

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XX XX
DE DNA encoding a human tumor endothelial marker 8 protein.
XX XX
KW synergistic induction; tumor-associated antigen; vaccine;
XX tumor endothelial marker 8; immune stimulation; cytostatic; gene; da.
XX XX
OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT CDS 144..1838
FT /tag=a
FT /product= "Human tumor endothelial marker 8 protein"
XX XX
PN MO2005048943-A2.
XX XX
PD 02-JUN-2005.
XX XX
PF 15-NOV-2004; 2004WO-US038022.
XX XX
PR 13-NOV-2003; 2003US-0519498P.
XX XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX XX
PI Gregor P. Houghton A, Concetti A, Venanzi FM;
XX XX
DR WPI: 2005-395941/40.
DR P-PSDB; AEA29805.
XX XX
PT New composition useful as a vaccine for inducing anti-tumor immune
PT response and having a vector with a nucleic acid sequence encoding a
PT tumor-associated antigen and/or encoding a tumor endothelial marker 8.
XX XX
PS Claim 6; SEQ ID NO 4; 54bp; English.
XX XX
CC The invention relates to novel compositions and methods for the
CC synergistic induction of antitumor immunity. The invention discloses a
CC synergistic effect between vaccines encoding a tumor-associated antigen
CC and vaccines encoding a tumor endothelial marker 8 (TEM8). The invention
CC further includes a method of inducing anti-tumor immune responses in an
CC individual, comprising administering to the individual a composition
CC cited above or dendritic cells comprising a nucleic acid or protein
CC selected from the composition cited above and proteins encoded by the
CC vectors of the composition. The methods and compositions of the present
CC invention are useful in the field of anti-tumor immunity, in particular
CC for inducing an anti-tumor immune response by targeting both tumor-
CC associated antigens and tumor endothelia, hence have cytostatic activity.
CC This polynucleotide sequence represents the DNA encoding a human tumor
CC endothelial marker 8 protein of the invention.
XX XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

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Query Match 98.8%; Score 1090.8; DB 14; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGGCCACGGCGGAGGAGAGCCCTCGGATGAGGCTTCAGAGGCTCTCTTGGGCACT 60
DB 144 ATGGCCACGGCGGAGGAGAGCCCTCGGATGAGGCTTCAGAGGCTCTCTTGGGCACT 203
QY 61 CTGGTCTCATCTGCGCCCGGCAAGGGGACGCGAGGAGATGGGGTCCAGCTTCTAC 120
DB 204 CTGGTCTCATCTGCGCCCGGCAAGGGGACGCGAGGAGATGGGGTCCAGCTTCTAC 263
QY 121 GCGGATTTGACCTGTACTTCAATTTTGGACAAATTCAGAAAGTGTCTGCACCACTGGAAT 180
DB 264 GCGGATTTGACCTGTACTTCAATTTTGGACAAATTCAGAAAGTGTCTGCACCACTGGAAT 323
QY 181 GAAATCTATTACTTTGGTGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 240
DB 324 GAAATCTATTACTTTGGTGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 383
QY 241 TCCCTTATTGTTTTTCTCCACCCGAGAACAACTTAAATGAAATGACAGAAAGACAGAA 300
DB 384 TCCCTTATTGTTTTTCTCCACCCGAGAACAACTTAAATGAAATGACAGAAAGACAGAA 443

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Db 384 TCCTTATTGTTTTCACCCGAGAACACCTTAATGAACTGACAGAGACAGAGAA 443
Qy 301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
Db 444 CAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
Qy 361 CATGAAGATTGAAAGGGCCAGTAGAGCAGATTATTAATGAAACAGACAGAGGTACAG 420
Db 504 CATGAAGATTGAAAGGGCCAGTAGAGCAGATTATTAATGAAACAGACAGAGGTACAG 563
Qy 421 ACAGCCAGGCTCATCTGTTGATGATGAGAACTCCATGAAATCTCTTTTCTAT 480
Db 564 ACAGCCAGGCTCATCTGTTGATGATGAGAACTCCATGAAATCTCTTTTCTAT 623
Qy 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGAGCAATTGTTACTGTGTGTG 540
Db 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGAGCAATTGTTACTGTGTGTG 683
Qy 541 AAAGATTTCATAGACACAGCTGGCCCGAATTGCCGACAGTAAGATCATGTGTTCC 600
Db 684 AAAGATTTCATAGACACAGCTGGCCCGAATTGCCGACAGTAAGATCATGTGTTCC 743
Qy 601 GTGAATGAGCGGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAAGTCTGC 660
Db 744 GTGAATGAGCGGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAAGTCTGC 803
Qy 661 ATCGAATTTCTAGCAGCTGAAACCATCACTATGTGCAAGAGTCAATTTCAAGTTGTC 720
Db 804 ATCGAATTTCTAGCAGCTGAAACCATCACTATGTGCAAGAGTCAATTTCAAGTTGTC 863
Qy 721 GTGAGAGAAACGGCTTCCGACATGCCCCGACAGTGAACAGGCTCTGACAGTTCAAG 780
Db 864 GTGAGAGAAACGGCTTCCGACATGCCCCGACAGTGAACAGGCTCTGACAGTTCAAG 923
Qy 781 ATCAATGATCTCGGTCACTCACTGAAAGCCCTTTCTGTGAAGACCTTATTACATG 840
Db 924 ATCAATGATCTCGGTCACTCACTGAAAGCCCTTTCTGTGAAGACCTTATTACATG 983
Qy 841 TGTCACAGCGCTTCTTAAAGAGTTGGCATGAAAGTGCATCTCAGGTACAGCATGAAC 900
Db 984 TGTCACAGCGCTTCTTAAAGAGTTGGCATGAAAGTGCATCTCAGGTACAGCATGAAC 1043
Qy 901 GATGCGCTCTCTTTTATCTTCAGTTCTGTCAATGACACACACACTGTTTGAAGGT 960
Db 1044 GATGCGCTCTCTTTTATCTTCAGTTCTGTCAATGACACACACACTGTTTGAAGGT 1103
Qy 961 TCATCTCTGCGCATGCGCCCTGCTGATCTCTGCTCTGCTGCTCTCTCTCTG 1020
Db 1104 TCATCTCTGCGCATGCGCCCTGCTGATCTCTGCTCTGCTCTCTCTCTCTCTG 1163
Qy 1021 TGGTTCGCGCCCTCTGCTGCACTGTGATTAATGAGAGGTCCCTCCACCCCTGCGAG 1080
Db 1164 TGGTTCGCGCCCTCTGCTGCACTGTGATTAATGAGAGGTCCCTCCACCCCTGCGAG 1223
Qy 1081 GAGAGTGAGGAAAA 1094
Db 1224 GAGAGTGAGGAAAA 1237

RESULT 10
AAD05303
ID AAD05303 standard; cDNA; 2447 BP.
XX
AC AAD05303;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human secreted protein-encoding gene 4 cDNA clone HMLFR02, SEQ ID NO:14.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
foetal abnormality; developmental abnormality; haematopoietic disorder;
immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
inflammation; allergy; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiodysplasia; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery; cell culture;
KW chemotaxis; food additive; gene therapy; binding partner identification;
KW chromosome 19; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 140..1351
FT /tag= a
FT /product= "Human secreted protein"
FT sig_peptide 140..220
FT /tag= b
FT mat_peptide 221..1348
FT /tag= c
FT /product= "Mature human secreted protein"
XX
PN MO200134626-A1.
XX
PD 17-MAY-2001.
XX
PF 01-NOV-2000; 2000MO-US030045.
XX
PR 05-NOV-1999; 99US-0163581P.
XX 30-JUN-2000; 2000US-0215133P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Moore PA, Birse CE, Ni J,
PI MPI: 2001-308778/32.
XX P-PSDB; AAE01439.
DR
DR New nucleic acid molecules encoding 28 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX Claim 1; Page 425-426; 562pp; English.
XX
XX AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE01436-AAE01513 represent the proteins they encode.
CC AAB01514-AAE01544 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 28 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or a
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein-encoding cDNA of the
CC invention
XX
SQ Sequence 2447 BP; 673 A; 562 C; 587 G; 625 T; 0 U; 0 Other;

AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. CC Pathological conditions can be diagnosed by determining the amount of the CC new protein in a sample or by determining the presence of mutations in CC the new genes. Specific uses are described for each of the 28 genes, CC based on the tissues in which they are most highly expressed, and include CC developing products for the diagnosis or treatment of proliferative CC disorders, cancer, tumours, foetal and developmental abnormalities, CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, CC angiogenic disorders, kidney disorders, gastrointestinal disorders, CC pregnancy-related disorders, endocrine disorders, and infections. The CC proteins can also be used to aid wound healing and epithelial cell CC proliferation, to prevent skin aging due to sunburn, to maintain organs CC before transplantation, for supporting cell culture of primary tissues, CC to regenerate tissues, to identify their cognate ligands or binding CC partners, and in chemotaxis, and can be used as a food additive or CC preservative to modify storage properties. Antibodies specific for a CC protein of the invention can be used in alleviating symptoms associated CC with the disorders mentioned above, and in diagnostic immunoassays e.g., CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The CC present sequence represents a human secreted protein-encoding cDNA of the CC invention

XX Sequence 2086 BP; 544 A; 491 C; 538 G; 501 T; 0 U; 12 Other;

Query Match 98.7%; Score 1089.4; DB 4; Length 2086;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1090; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGSCCAACGGCGGAGGAGAGCCCTCGGATCGCTTCCAGTGGCTCTTTGGCACT 60
DB 166 ATGGCCACGCGCGGAGGAGAGCCCTCGGATCGCTTCCAGTGGCTCTTTGGCACT 225
QY 61 CTGGTCTCATCTGCGCGCGGAGGAGGAGGAGGATGGGGGTCAGGCTGCTAC 120
DB 226 CTGGTCTCATCTGCGCGCGGAGGAGGAGGAGGATGGGGGTCAGGCTGCTAC 285
QY 121 GGGGGAATTTGACCTGTATCTTCAATTTTGGACAAATTCAGAAATGTGTGACCACTGGAAT 180
DB 286 GGGGGAATTTGACCTGTATCTTCAATTTTGGACAAATTCAGAAATGTGTGACCACTGGAAT 345
QY 181 GAAATCTATTAATCTTTGTGGAAACAGTTGGCTCACAATTCACGCCCAAGTTGAGAAAG 240
DB 346 GAAATCTATTAATCTTTGTGGAAACAGTTGGCTCACAATTCACGCCCAAGTTGAGAAAG 405
QY 241 TCCTTATTTGTTTTCACCCGAGGAAACAACCTTATGAAATCTGACAGAAAGACAGAA 300
DB 406 TCCTTATTTGTTTTCACCCGAGGAAACAACCTTATGAAATCTGACAGAAAGACAGAA 465
QY 301 CAAATCGTCAAGGCTAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
DB 466 CAAATCGTCAAGGCTAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 525
QY 361 CATGAAGATTTGAAAGGGGCAAGTGAAGCAATTTATTAAGAAACAGCAAGGTTACAG 420
DB 526 CATGAAGATTTGAAAGGGGCAAGTGAAGCAATTTATTAAGAAACAGCAAGGTTACAG 585
QY 421 ACAGCAGAGGTCATCTGCTTGAAGTGAAGAACTCATGAAGATCTTTTCTAT 480
DB 586 ACAGCAGAGGTCATCTGCTTGAAGTGAAGAACTCATGAAGATCTTTTCTAT 645
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGCAATCTGTGTTGTTGTTG 540
DB 646 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGCAATCTGTGTTGTTGTTGTTG 705
QY 541 AAAGATTTCAATAGACACAGCTGGCCGGATGGCGACATGAAGATCATGTGTTCCC 600
DB 706 AAAGATTTCAATAGACACAGCTGGCCGGATGGCGACATGAAGATCATGTGTTCCC 765

QY 601 GTGAATGACGCGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAATCTTGC 660
DB 766 GTGAATGACGCGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAATCTTGC 825
QY 661 ATCGAAATTTTACGACGTGGAACCATCCATCATATGTGACAGAGATCATTTCAAGTTGTC 720
DB 826 ATCGAAATTTTACGACGTGGAACCATCCATCATATGTGACAGAGATCATTTCAAGTTGTC 885
QY 721 GTGAGAGGAAACGGCTTCGACATGCGCGCAACGTGACAGGGTCTCTGACGTTCAAG 780
DB 886 GTGAGAGGAAACGGCTTCGACATGCGCGCAACGTGACAGGGTCTCTGACGTTCAAG 945
QY 781 ATCAATGACTCGGTCACTCAATGAGAGCCCTTTCTGTGGAAGACATTAATTAATCTG 840
DB 946 ATCAATGACTCGGTCACTCAATGAGAGCCCTTTCTGTGGAAGATTAATTAATCTG 1005
QY 841 TGTCCAGGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCATCGAGTCAAGTGAAC 900
DB 1006 TGTCCAGGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCATCGAGTCAAGTGAAC 1065
QY 901 GATGCGCTCTCTTTATCTCCAGTCTGTATCATCATCACACACACACTGTTCTGACGCT 960
DB 1066 GATGCGCTCTCTTTATCTCCAGTCTGTATCATCATCACACACACTGTTCTGACGCT 1125
QY 961 TCCATCTGCGCCATGCGCCCTGCTGATCTGTTCTGCTCTTACGCCCTGCTCTCTG 1020
DB 1126 TCCATCTGCGCCATGCGCCCTGCTGATCTGTTCTGCTCTTACGCCCTGCTCTCTG 1185
QY 1021 TGTGTTGCGCCCTCTGCTGCACTGTGATTAACAAGAGTCCCTCCACCCCTGCGAG 1080
DB 1186 TGTGTTGCGCCCTCTGCTGCACTGTGATTAACAAGAGTCCCTCCACCCCTGCGAG 1245
QY 1081 GAGAGTGAAGAAATTA 1097
DB 1246 GAGAGTGAAGTAACTGA 1262

RESULT 12

AD100549
ID AD100549 standard; DNA; 1674 BP.

AC AD100549;

DT 22-APR-2004 (first entry)

XX Human TANGO 197 Ig fusion mutated DNA - plasmid p0610.

KW fusion; von Willlebrand factor A-like domain; vWF; antibacterial;
KW cutaneous; inhalation anthrax; human; TANGO 197 Ig fusion; mutant;
KW plasmid p0610; ds; gene.

XX Homo sapiens.

OS Synthetic.

PN US2003144193-A1.

PD 31-JUL-2003.

PF 24-JUL-2002; 2002US-00201292.

PR 20-DEC-2001; 2001US-00038307.

PA (ROTT/) ROTTMAN J B.

PA (OKER/) O'KEEFE T L.

PA (OZKA/) OZKAYNAK E.

PA (HEAL/) HEALEY J J.

PI Rotman JB, O'keefe TL, Ozkaynak E, Healey JJ;

DR WPI; 2003-720708/68.

DR P-PSDB; AD100550.

XX

PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
PT to the vWF.

XX Example; SEQ ID NO 17; 86bp; English.

XX The invention relates to a novel fusion polypeptide comprising a von
CC Willebrand factor A-like domain (vWF) amino acid sequence and an amino
CC acid sequence heterologous to the vWF. The polypeptide of the invention
CC demonstrates antibacterial activities whilst the composition and method
CC may be useful in preventing or ameliorating the symptoms of cutaneous
CC and/or inhalation anthrax. The current sequence is that of the human
CC TANGO 197 Ig mutated fusion DNA of the invention.

XX Sequence 1674 BP; 433 A; 461 C; 424 G; 356 T; 0 U; 0 Other;

XX Query Match 87.0%; Score 960.8; DB 10; Length 1674;

XX Best Local Similarity 99.8%; Pred. No. 4,4e-284;
Matches 962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGGCGGAGCGGAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTGGCCACT 60

DB 13 ATGGCCACGGCGGAGCGGAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTGGCCACT 72

QY 61 CTGCTGCTCATCTGCGCGCGGCAAGGGGAGACGACGAGAGATGGGGGTCCAGCTGTCTAC 120

DB 73 CTGCTGCTCATCTGCGCGCGGCAAGGGGAGACGACGAGAGATGGGGGTCCAGCTGTCTAC 132

QY 121 GGGGGAATTTGACCTGTAATTTTGGACAAATCAGGAAGTGTGTCACCACTGGAT 180

DB 133 GGGGGAATTTGACCTGTAATTTTGGACAAATCAGGAAGTGTGTCACCACTGGAT 192

QY 181 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 240

DB 193 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 252

QY 241 TCCCTTATTTGTTTCTCCACCCGAGAAACAACTTATATGAAATCAGACAAAGACAGAA 300

DB 253 TCCCTTATTTGTTTCTCCACCCGAGAAACAACTTATATGAAATCAGACAAAGACAGAA 312

QY 301 CAATCCGTCAGGCGCTAGAAAGAACTCAGAAAGTTCTGCGAGGAGAGACCTTACATG 360

DB 313 CAATCCGTCAGGCGCTAGAAAGAACTCAGAAAGTTCTGCGAGGAGAGACCTTACATG 372

QY 361 CATGAAGATTTGAAAGGCGCAGTGAAGCAGATTATTATGAAACAGACAAAGGTACAGG 420

DB 373 CATGAAGATTTGAAAGGCGCAGTGAAGCAGATTATTATGAAACAGACAAAGGTACAGG 432

QY 421 ACAGCCAGGCTCATCTGTTGATGATGAGAACTCCATGAAGTCTTTTCTTAT 480

DB 433 ACAGCCAGGCTCATCTGTTGATGATGAGAACTCCATGAAGTCTTTTCTTAT 492

QY 481 TCAGAGGAGGAGGTATAGGTCGAGATCTTGATGATGATGATGATGATGATGATGATG 540

DB 493 TCAGAGGAGGAGGTATAGGTCGAGATCTTGATGATGATGATGATGATGATGATGATG 552

QY 541 AAGATTTCAATGAGACACAGCTGGCCCGATGCGGACAGTAAGATCATGTGTTTCCC 600

DB 553 AAGATTTCAATGAGACACAGCTGGCCCGATGCGGACAGTAAGATCATGTGTTTCCC 612

QY 601 GTGAATACGGGCTTTCAGGCTTCCAGAGGATCATCTCAATTTGAAAGAGTCTTGC 660

DB 613 GTGAATACGGGCTTTCAGGCTTCCAGAGGATCATCTCAATTTGAAAGAGTCTTGC 672

QY 661 ATGAAATTTCTAGACGCTGAACCATCCACCTATAGTGAAGAGATGATTTCAAGTTGTC 720

DB 673 ATGAAATTTCTAGACGCTGAACCATCCACCTATAGTGAAGAGATGATTTCAAGTTGTC 732

QY 721 GTGAGAGAAACGGCTTCCGACATGCCGCAACGTGACAGAGGCTCTGACGCTTCAAG 780

DB 733 GTGAGAGAAACGGCTTCCGACATGCCGCAACGTGACAGAGGCTCTGACGCTTCAAG 792

QY 781 ATCAATAGCTCGGTGCACACTCATATGAGAAAGCCCTTCTGTGGAGACATTAATTACTG 840

DB 793 ATCAATAGCTCGGTGCACACTCATATGAGAAAGCCCTTCTGTGGAGACATTAATTACTG 852

QY 841 TGTCCAGCGGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAC 900

DB 853 TGTCCAGCGGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAC 912

QY 901 GATGCGCTCTCTTTTATCTTCAGATTCTGTCAATCATACACACACACACTGTTGACGGT 960

DB 913 GATGCGCTCTCTTTTATCTTCAGATTCTGTCAATCATACACACACACACTGTTGACGGT 972

QY 961 TCCA 964

DB 973 CCGA 976

RESULT 13

ADM64575
ID ADM64575 standard; DNA; 1674 BP.

XX ADM64575;

XX 03-JUN-2004 (first entry)

XX Mouse TANGO197-immunoglobulin (Ig) fusion protein DNA.

XX antibacterial; gene therapy;

XX von Willebrand factor A-like domain amino acid sequence;

XX vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;

XX inhalation anthrax; mouse; TANGO197; immunoglobulin; Ig; fusion protein;

XX gene; ds.

XX Mus sp.

XX Synthetic.

XX US2003134786-A1.

XX 17-JUL-2003.

XX 20-DEC-2001; 2001US-00038307.

XX 20-DEC-2001; 2001US-00038307.

XX (ROTT/) ROTTMAN J B.

XX (OKEE/) O'KEEFE T L.

XX (OZKA/) OZKAYNAK E.

XX (HEAL/) HEALEY J J.

XX Rottman JB, O'Keefe TL, Ozkaynak E, Healey JJ;

XX WPI; 2003-829643/77.

XX P-PSDB; ADM64576.

XX New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or

XX ameliorating symptoms of anthrax comprises a von Willebrand factor A-like

XX domain (vWF) amino acid sequence and an amino acid sequence heterologous

XX to the vWF.

XX Example; SEQ ID NO 17; 64bp; English.

XX The invention describes a fusion polypeptide comprising a von Willebrand

XX factor A-like domain (vWF) amino acid sequence and an amino acid sequence

XX heterologous to the vWF. Also described are: a method of preventing or

XX ameliorating a symptom of anthrax in a subject thought to be at risk for

XX exposure to or suspected of having been exposed to Bacillus anthracis;

XX and a pharmaceutical composition comprising the novel fusion polypeptide.

XX The composition and method are useful in preventing or ameliorating

XX symptoms of cutaneous and/or inhalation anthrax. This sequence encodes a

XX fusion protein comprising mouse TANGO197 and immunoglobulin (Ig) that can

XX be used to treat exposure to or prevent a symptom of anthrax.

XX Sequence 1674 BP; 433 A; 461 C; 424 G; 356 T; 0 U; 0 Other;

Query Match 87.0%; Score 960.8; DB 11; Length 1674;
 Best Local Similarity 99.8%; Pred. No. 4.4e-284;
 Matches 962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 ATGGCCAGCGCGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 13 ATGGCCAGCGCGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 72
QY 61 CTGGGTCTATCTGCGCCCGGCGAAGGGGAGCCGAGGAGAGATGGGGGTCCACCTGCTAC 120
DB 73 CTGGGTCTATCTGCGCCCGGCGAAGGGGAGCCGAGGAGAGATGGGGGTCCACCTGCTAC 132
QY 121 GCGGATTTGACCTGACTTCAATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAAAT 180
DB 133 GCGGATTTGACCTGACTTCAATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAAAT 192
QY 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGATG 240
DB 193 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 252
QY 241 TCCCTTATTGTTTTTCTCCACCCGAGAGAACACCTTAATGAAACTGACAGAAACAGAGA 300
DB 253 TCCCTTATTGTTTTTCTCCACCCGAGAGAACACCTTAATGAAACTGACAGAAACAGAGA 312
QY 301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
DB 313 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 372
QY 361 CATGAAGATTGAAAAGGCGCAGTAGACAGATTTATTATGAAAACAGACAGAGGTACAG 420
DB 373 CATGAAGATTGAAAAGGCGCAGTAGACAGATTTATTATGAAAACAGACAGAGGTACAG 432
QY 421 ACAGCCAGGCTATCATTTGCTTGTGATGATGAGAACTCCAGAGAAATCTCTTTTCTAT 480
DB 433 ACAGCCAGGCTATCATTTGCTTGTGATGAGAACTCCAGAGAAATCTCTTTTCTAT 492
QY 481 TCAGAGAGGAGGCTATAGAGTCTCGAGATCTTGGTGCAATTTGTTACTGTGTGGTGTG 540
DB 493 TCAGAGAGGAGGCTATAGAGTCTCGAGATCTTGGTGCAATTTGTTACTGTGTGGTGTG 552
QY 541 AAGATTTCAATGAGACACAGCTGCGCCGAGATTGCGAGACAGTAAAGATCATGTGTTCCC 600
DB 553 AAGATTTCAATGAGACACAGCTGCGCCGAGATTGCGAGACAGTAAAGATCATGTGTTCCC 612
QY 601 GTGAATGAGAGGCTTTTNAAGGCTCTGCAAGGATCATCACTCAATTTTGAAGAAGTCTGC 660
DB 613 GTGAATGAGAGGCTTTTNAAGGCTCTGCAAGGATCATCACTCAATTTTGAAGAAGTCTGC 672
QY 661 ATCGAATTTCTAGCAGCTGACCATCCACATATATGTCAGAGAGATCATTTTCAAGTTGTC 720
DB 673 ATCGAATTTCTAGCAGCTGACCATCCACATATATGTCAGAGAGATCATTTTCAAGTTGTC 732
QY 721 GTGAGAGGAAAAGCGCTTCCGACATGCGCCGACAGTGAACAGGCTCTTGCAGCTTCAAG 780
DB 733 GTGAGAGGAAAAGCGCTTCCGACATGCGCCGACAGTGAACAGGCTCTTGCAGCTTCAAG 792
QY 781 ATCAATGACTCGGTTCACCTCACTCAATGAGAGCCCTTTTCTGTGAAATACCTTATTACG 840
DB 793 ATCAATGACTCGGTTCACCTCACTCAATGAGAGCCCTTTTCTGTGAAATACCTTATTACG 852
QY 841 TGTCCAGCGCCTATCTTTAAAGAGTGGCATGAAAGCTGCACTCAGAGTCAAGCATGAAC 900
DB 853 TGTCCAGCGCCTATCTTTAAAGAGTGGCATGAAAGCTGCACTCAGAGTCAAGCATGAAC 912
QY 901 GATGCGCTCTCTTTTATCTTCAGATTGTGCATCATCAACACACAGCTGTTTGAAGGT 960
DB 913 GATGCGCTCTCTTTTATCTTCAGATTGTGCATCATCAACACACAGCTGTTTGAAGGT 972
QY 961 TCCA 964
DB 973 CCGA 976

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RESULT 14
 AD100545
 ID AD100545 standard; DNA; 1650 BP.

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XX AC AD100545;
XX DT 22-APR-2004 (first entry)
XX DE Human TANGO 197 Ig FcR mutated fusion DNA - plasmid pUKTOK127.
XX XX fusion; von Willebrand factor A-like domain; vWF; antibacterial;
XX KW cutaneous; inhalation anthrax; human; TANGO 197 Ig FcR fusion; mutant;
XX KW plasmid pUKTOK127; de; gene.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2003144193-A1.
XX PD 31-JUL-2003.
XX XX 24-JUL-2002; 2002US-00201292.
XX PR 20-DEC-2001; 2001US-00038307.
XX PA (ROTT/) ROTTMAN J B.
XX PA (OKEB/) O'KEEFE T L.
XX PA (OZKA/) OZKAYNAK E.
XX PA (HEAL/) HEALEY J J.
XX PI Rotman JB, O'keefe TL, Ozkaynak E, Healey JJ;
XX DR MPI: 2003-720708/68.
XX DR P-PsDB: AD100546.
XX PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
XX PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
XX PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
XX PT to the vWF.
XX PS Example; SEQ ID NO 13; 86pp; English.
XX CC The invention relates to a novel fusion polypeptide comprising a von
XX CC Willebrand factor A-like domain (vWF) amino acid sequence and an amino
XX CC acid sequence heterologous to the vWF. The polypeptide of the invention
XX CC demonstrates antibacterial activities whilst the composition and method
XX CC may be useful in preventing or ameliorating the symptoms of cutaneous
XX CC and/or inhalation anthrax. The current sequence is that of the human
XX CC TANGO 197 Ig FcR mutated fusion DNA of the invention.
XX SO Sequence 1650 BP; 427 A; 454 C; 419 G; 350 T; 0 U; 0 Other;

Query Match 86.3%; Score 952.4; DB 10; Length 1650;
Best Local Similarity 99.4%; Pred. No. 1.7e-281;
Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGCCAGCGCGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 1 ATGGCCAGCGCGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
QY 61 CTGGGTCTATCTGCGCCCGGCGAAGGGGAGCCGAGGAGAGATGGGGGTCCACCTGCTAC 120
DB 61 CTGGGTCTATCTGCGCCCGGCGAAGGGGAGCCGAGGAGAGATGGGGGTCCACCTGCTAC 120
QY 121 GCGGATTTGACCTGACTTCAATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAAAT 180
DB 121 GCGGATTTGACCTGACTTCAATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAAAT 180
QY 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 240
DB 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 240

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QY 241 TCCTTATTGTTTCTCCACCCGAGNACCACTTAATGAACTGACAGAGAGAA 300
 XX |||||
 DB 241 TCCTTATTGTTTCTCCACCCGAGAGAACCTTAATGAACTGACAGAGAGAA 300
 QY 301 CAAATCCGTCAGGCTTGAAGAACTTCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
 DB 301 CAAATCCGTCAGGCTTGAAGAACTTCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
 QY 361 CATGAAGAGATTGAAAGGGCCAGTGAAGCAATTTATTAATAAAGCAAGAGGTACAG 420
 DB 361 CATGAAGAGATTGAAAGGGCCAGTGAAGCAATTTATTAATAAAGCAAGAGGTACAG 420
 QY 421 ACAGCAGAGCTCATCATTTGCTTGAATGAGAACTCCATGAAGATCTCTTTTCTAT 480
 DB 421 ACAGCAGAGCTCATCATTTGCTTGAATGAGAACTCCATGAAGATCTCTTTTCTAT 480
 QY 481 TCAGAGAGGAGGCTAATAGGTTCTCGAGATCTTGTCGAATTTGTTTACTGTGGTG 540
 DB 481 TCAGAGAGGAGGCTAATAGGTTCTCGAGATCTTGTCGAATTTGTTTACTGTGGTG 540
 QY 541 AAAGATTTCAATGACACAGCTGGCCCGGATGGCGAGAGTAAGATCATGTTTCCC 600
 DB 541 AAAGATTTCAATGACACAGCTGGCCCGGATGGCGAGAGTAAGATCATGTTTCCC 600
 QY 601 GTGAATGACGCTTTCAGGCTTTCAGAGGATCATCATCAATTTTGAAGAAGTCTG 660
 DB 601 GTGAATGACGCTTTCAGGCTTTCAGAGGATCATCATCAATTTTGAAGAAGTCTG 660
 QY 661 ATCGAAATTTCTAGCAGCTGAACCATCCCATATGTGCAAGAGAGTCAATTTCAAGTTGTC 720
 DB 661 ATCGAAATTTCTAGCAGCTGAACCATCCCATATGTGCAAGAGAGTCAATTTCAAGTTGTC 720
 QY 721 GTGAGAGGAAAGCGCTTCCGACATGCCCCGACAGTGAACAGGCTCTGCACTTCAAG 780
 DB 721 GTGAGAGGAAAGCGCTTCCGACATGCCCCGACAGTGAACAGGCTCTGCACTTCAAG 780
 QY 781 ATCAATGACTCGGTCACACTCAATGAGAGACCTTTTCTGTGGAAGACCTTATTTACTG 840
 DB 781 ATCAATGACTCGGTCACACTCAATGAGAGACCTTTTCTGTGGAAGACCTTATTTACTG 840
 QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAC 900
 DB 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAC 900
 QY 901 GATGGCTCTCTTTTATCTCCAGGTTCTGTATCATCAACCAACACACTGTTCTGAGG 960
 DB 901 GATGGCTCTCTTTTATCTCCAGGTTCTGTATCATCAACCAACACTGTTCTGCCAAA 960
 QY 961 TC 962
 DB 961 TC 962
 RESULT 15
 ADI00547
 ID ADI00547 standard; DNA; 1650 BP.
 AC ADI00547;
 XX
 DT 22-APR-2004 (first entry)
 DE Human TANGO 197 Ig FCR WT fusion DNA - plasmid pLTKOK129.
 XX
 KW fusion; von Willebrand factor A-like domain; vWF; antibacterial;
 KM cutaneous; inhalation anthrax; human; TANGO 197 Ig FCR fusion; wild-type;
 XX plasmid pLTKOK129; ds; gene.
 OS Homo sapiens.
 XX
 PN US2003144193-A1.
 XX
 PD 31-JUL-2003.
 XX

PF 24-JUL-2002; 2002US-00201292.
 XX
 PR 20-DEC-2001; 2001US-00038307.
 XX
 PA (ROTT/) ROTTMAN J B.
 PA (OKEE/) O'KEEFE T L.
 PA (OZKA/) OZKAYNAK E.
 PA (HEAL/) HEALEY J J.
 XX
 PI Rottman JB, O'keefe TL, Ozkaynak E, Healey JJ,
 XX
 DR WPI; 2003-720708/68.
 DR P-PSDB; ADI00548.
 XX
 PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
 PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
 PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
 PT to the vWF.
 XX
 PS Example; SEQ ID NO 15; 86pp; English.
 CC The invention relates to a novel fusion polypeptide comprising a von
 CC Willebrand factor A-like domain (vWF) amino acid sequence and an amino
 CC acid sequence heterologous to the vWF. The polypeptide of the invention
 CC demonstrates antibacterial activities whilst the composition and method
 CC may be useful in preventing or ameliorating the symptoms of cutaneous
 CC and/or inhalation anthrax. The current sequence is that of the human
 CC TANGO 197 Ig FCR wild-type fusion DNA of the invention.
 XX
 SQ Sequence 1650 BP; 427 A; 453 C; 419 G; 351 T; 0 U; 0 Other;
 XX
 Query Match 86.3%; Score 952.4; DB 10; Length 1650;
 Best Local Similarity 99.4%; Pred. No. 1.7e-281;
 Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ATGGCCACGCGCGAGGAGAGAGCCCTCGGATGAGGCTTCAGTGGCTCTTTGGCACT 60
 DB 1 ATGGCCACGCGCGAGGAGAGAGCCCTCGGATGAGGCTTCAGTGGCTCTTTGGCACT 60
 QY 61 CTGGTGTCTATCTGCGCCCGGCAAGGGGAGCGAGAGAGATGGGGGTCCAGCTGTAC 120
 DB 61 CTGGTGTCTATCTGCGCCCGGCAAGGGGAGCGAGAGAGATGGGGGTCCAGCTGTAC 120
 QY 121 GCGGATTTGACCTGTACTTCAATTTGGAACAATGAGAAAGTGTGTCACCACTGGAAT 180
 DB 121 GCGGATTTGACCTGTACTTCAATTTGGAACAATGAGAAAGTGTGTCACCACTGGAAT 180
 QY 181 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCACGCCACAGTTGAGAAATG 240
 DB 181 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCACGCCACAGTTGAGAAATG 240
 QY 241 TCCTTATTGTTTCTCCACCCGAGAGAACCTTAAATGAACTGACAGAGAGAGAA 300
 DB 241 TCCTTATTGTTTCTCCACCCGAGAGAACCTTAAATGAACTGACAGAGAGAGAA 300
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 QY 421 ACAGCAGAGCTCATCATTTGCTTGAATGAGAACTCCATGAAGATCTCTTTTCTAT 480
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 DB 541 AAAGATTTCAATGACACAGCTGGCCCGGATGGCGAGAGTAAGATCATGTTTCCC 600

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Db      541 AAAGATTTCAATGAGACACAGCTGGCCCGAATTGCGGACGTAAGANTCATGTGTTCCC 600
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QY      961 TC 962
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Search completed: December 17, 2005, 19:23:03
Job time : 739.269 secs

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| Query Match | 86.0% | Score 949.4; | DB 4; | Length 1957; |
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| | | | | Gaps 0 |

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QY 421 ACAGCCAGGCTCATCTGCTTTGACTGATGGAACCTCCATGAAAGATCTCTTTTCTAT 480
DB 615 ACAGCCAGGCTCATCTGCTTTGACTGATGGAACCTCCATGAAAGATCTCTTTTCTAT 674
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGAGCAATGTTTACTGTGTTGATG 540
DB 675 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGAGCAATGTTTACTGTGTTGATG 734
QY 541 AAAGATTTCAATGAGACACAGCTGCGCCGGATTGCGAGACATGATCATGTGTTCC 600
DB 735 AAAGATTTCAATGAGACACAGCTGCGCCGGATTGCGAGACATGATCATGTGTTCC 794
QY 601 GTGAATGAGCGGCTTTCAAGGCTTCGCAAGGATCATCTCAATTTTGAAGAAGTCTG 660
DB 795 GTGAATGAGCGGCTTTCAAGGCTTCGCAAGGATCATCTCAATTTTGAAGAAGTCTG 854
QY 661 ATGGAATTTAGACAGTGAACCATCAATATGTCAGAGAGAGTCAATTTCAAGTTGTC 720
DB 855 ATGGAATTTAGACAGTGAACCATCAATATGTCAGAGAGAGTCAATTTCAAGTTGTC 914
QY 721 GTGAGAGAAACGGCTTCCGACATGCGCCGACATGCGAGAGGCTCTGACAGTTCAAG 780
DB 915 GTGAGAGAAACGGCTTCCGACATGCGCCGACATGCGAGAGGCTCTGACAGTTCAAG 974
QY 781 ATCAATGACTCGGTTCACACTCAATGAGAGCCCTTTTCTGTGGAAGACACTTATTTAC 840
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RESULT 2
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LOCUS AK031465
DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030436p19 product:ANTHRAX TOXIN RECEPTOR
PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], full
insert sequence.
ACCESSION AK031465

VERSION AK031465.1 GI:26082340
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Carninci, P., and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, Y.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
JOURNAL sequencing pipeline with 384 multicapillary sequencer
PUBMED Genome Res. 10 (11), 1757-1771 (2000)
11076861
REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
5
TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
JOURNAL Group Phase I & II Team.
REFERENCE Analysis of the mouse transcriptome based on functional annotation
AUTHORS of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
6 (bases 1 to 3161)
ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P.,
FUKUDA, S., FURUKO, M., HANAGAKI, T., HARA, A., HASHIZUME, M.,
HAYASHIDA, K., HAYASE, N., HIRAMOTO, K., HIROCKA, T., HIROZANE, T.,
HOIT, P., IMOTANI, K., ISHII, Y., ITOH, M., KAGAWA, I., KANUKAWA, T.,
KATO, H., KAWAI, D., KOJIMA, Y., KONDO, S., KONO, H., KOUNDA, M.,
KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., MURATA, M.,
NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSAKI, N.,
OKAZAKI, Y., SAITO, R., SAITOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N.,
SANO, H., SASAKI, D., SHIBATA, K., SHINGAWA, A., SHIRAKI, T.,
SOGABE, Y., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKEKI, A.,
TAKEDA, Y., TANAKA, T., TOMARU, A., TOYA, T., YASUNISHI, A.,
MURAMATSU, M., and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suenitcho, Tsukuba, Ibaraki, Japan,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
URL: http://fantom.qualifere
FEATURES
source location/Qualifere
1. 3161

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RESULT 4
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LOCUS 603039031F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:517974 5',
DEFINITION mRNA sequence.
ACCESSION B1823853
VERSION B1823853.1 GI:15935416
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 878)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph. D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M11448 row: n column: 07
High quality sequence stop: 804.

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:517974"
/lab_host="DH10B"
/clone_11b="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."
ORIGIN
Query Match 62.0%; Score 684.6; DB 3; Length 878;
Best Local Similarity 95.1%; Pred. No. 1.2e-191;
Matches 783; Conservative 0; Mismatches 29; Indels 11; Gaps 7;
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| DEFINITION | AK013005 | 1614 bp | mRNA |
| | | | linear |
| | | | HTC 03-APR-2004 |
| | | | Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length |
| | | | enriched library, clone:281045N18 product:ANTPAX TOXIN RECEPTOR |
| | | | PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], fulll |
| | | | insert sequence. |
| ACCESSION | AK013005 | | |
| VERSION | AK013005.1 | GI:12850099 | |
| KEYWORDS | HTC, CAP trapper. | | |
| SOURCE | Mus musculus (house mouse) | | |
| ORGANISM | Mus musculus | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; | | |
| | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; | | |
| | Sciurognathi; Muridae; Murinae; Mus. | | |
| REFERENCE | | | |
| AUTHORS | Carninci, P. and Hayashizaki, Y. | | |
| TITLE | High-efficiency full-length cDNA cloning | | |
| JOURNAL | Meth. Enzymol. 303, 19-44 (1999) | | |
| PUBMED | 10349636 | | |
| REFERENCE | | | |
| AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., | | |
| TITLE | 1 | | |
| | Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | | |
| | Normalization and substructure of cap-trapper-selected cDNAs to | | |
| | prepare full-length cDNA libraries for rapid discovery of new genes | | |
| | Genome Res. 10 (10), 1617-1630 (2000) | | |
| JOURNAL | 11042159 | | |
| PUBMED | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | 3 | | |
| | Shibata, K., Itch, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P., | | |
| | Kono, H., Akiyama, J., Nishi, K., Kitsuami, T., Teshiro, H., Itch, M., | | |
| | Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., | | |
| | Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., | | |
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| | Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | | |
| | RIKEN integrated sequence analysis (RISA) system-384-format | | |
| | sequencing pipeline with 384 multichannel sequencer | | |
| | Genome Res. 10 (11), 1757-1771 (2000) | | |
| JOURNAL | 11076861 | | |
| PUBMED | | | |
| REFERENCE | | | |
| AUTHORS | 4 | | |
| | The RIKEN Genome Exploration Research Group Phase II Team and the | | |
| | FANTOM Consortium. | | |
| TITLE | Functional annotation of a full-length mouse cDNA collection | | |
| JOURNAL | Nature 409, 685-690 (2001) | | |
| REFERENCE | | | |
| AUTHORS | 5 | | |
| | The FANTOM Consortium and the RIKEN Genome Exploration Research | | |
| | Group Phase I & II team. | | |
| | Analysis of the mouse transcriptome based on functional annotation | | |
| | of 60,770 full-length cDNAs | | |
| | Nature 420, 563-573 (2002) | | |
| JOURNAL | 6 (bases 1 to 1614) | | |
| REFERENCE | | | |
| AUTHORS | Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., | | |
| | Araiawa, T., Bono, H., Carninci, P., Fukuda, S., Furumishi, Y., | | |
| | Furuno, M., Hanagaki, T., Harada, A., Hayatsu, N., Hiramoto, K., | | |
| | Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itch, M., Izawa, M., | | |
| | Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., | | |
| | Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., | | |
| | Nomura, K., Nunazaki, R., Ohno, M., Okazaki, Y., Okido, T., Osa, C., | | |
| | Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., | | |
| | Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., | | |
| | Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., | | |
| | Tejima, Y., Toyu, T., Yamamura, T., Yasunishi, A., Yoshida, K., | | |
| | Yoshino, M., Muramatsu, M. and Hayashizaki, Y. | | |
| TITLE | Direct Subtraction | | |
| JOURNAL | Submitted (10-JUL-2000) | | |

| | | COMMENT |
|--------------|--|---|
| | | cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGGAAGATCCCAAGACCTCTTTTCTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCCTGAGTTAATTAAATATGCCCCCCCCC 3']. cDNA was cleaved with XhoI and SctI. Cloning sites, 5' end: XhoI, 3' end: SctI. |
| | | Host: SOLR. |
| FEATURES | | |
| source | Location/Qualifiers | |
| | 1..1614 | |
| | /organism="Mus musculus" | |
| | /mol_type="mRNA" | |
| | /strain="C57BL/6J" | |
| | /db_xref="PANTOM_DB:2810405N18" | |
| | /db_xref="taxon:10090" | |
| | /clone="2810405N18" | |
| | /cissue_type="whole body" | |
| | /clone_lib="RIKEN full-length enriched mouse cDNA library" | |
| | /dev_stage="10, 11 days embryo" | |
| | 11..1306 | |
| CDS | /note="unnamed protein product; ANTRAX TOXIN RECEPTOR PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [mus musculus] (SWISSPROT O9CZ52, evidence: FASTV, 100%ID, 84.6%length, match=1428) | |
| | putative | |
| | /codon_start=1 | |
| | /protein_id="BAB28591.1" | |
| | /db_xref="GI:12850100" | |
| | /translation="MKLTEDREQIRQGLEELKQVLPGADTYMHEGPASBOIYENS QGYRTAVDIIADTGELHDLPTFSSEARNSRLGAIIVCVKGDNEQNLARIADS KDHFPPNDSPFOALOGITIHSLFKSCIEILAEBSSTICAKESPOVVNRNFRRANVR DRLVCFPRINDSVTLNKEPRAVEDTVYLCPAPLILKEBGMALDVSNKDGLSFSSSY IITTHCSDDSIILAILLVFLMLALWMPWLCTVTIIXEVPVPEESDEDDIGLPKKMPTVDASYGGRGVGGI KRMLEVRNGESTEGALKAEKANRVVMSPOBYEH FPERRNINNMNRBRPSRKMYSPIKGIDLMTVLRLRGYDRVSVMR PQGPDTRFRGNMR LTIETLSKNYHRHGHDKGRPTPLLKQAMFSSFLERAFO" | |
| | 1592..1597 | |
| polya_signal | /note="putative" | |
| | 1614 | |
| polya_site | /note="putative" | |
| ORIGIN | | |
| | Query Match 61.7%; Score 681.4; DB 4; Length 1614; | |
| | Best Local Similarity 89.0%; Pred. No. 1.3e-190; | |
| | Matches 736; Conservative 0; Mismatches 91; Indels 0; Gaps 0; | |
| Gy | 268 ACAACCTTAATGAACAATGCACGAAGACAGACAGAACAAATCCGTCAAGCGCTGAGGAATC 327 | |
| Dd | 2 ACAACTTAAAGAACTACTACGAGACAGGGGAAACAGATCCACAAAGGCTTAGAAGAGCTC 61 | |
| Gy | 328 CAGAAAGTTCTGCACGAGAGAGACACTTACATGCATGACGAAAGATTGAAAGGCCACGTGAG 387 | |
| Dd | 62 CAGAAAGTTCTGCACGAGAGAGACACTTACATGCACGAAAGATTGAAAGGCCACGTGAG 121 | |
| Gy | 388 CAGATTATTTATGAAAAAGACAGCAAGGGTACAGACAGCCAGCGTCATCATTTGCTTGACT 447 | |
| Dd | 122 CAGATTATTTATGAAAGACAGTCAAGGATACAGACAGCGGAGCGTCATCATCGCGTTGCG 181 | |
| Gy | 448 GATGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGAGAGGAGGCTTAATAGTCTCGA 507 | |

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|||||
Db      182 GATGGGAGACTGACACAGGACCTCTTCTACTCAGAGAGGAGGCTAACGATCCCA 241
      508 GATCTTGGGCAATGTTTACTGTGTGGTGAAGATTTCAATGAGACAGCTGGCC 567
      242 GACCTTGGGCGATTTTACTGCGTTGGCGTGAAGATTTCAATGAATCTCAGTTGGCT 301
      568 CGGATTCGGGACAGTAAGATCATGTGTTCCTCGTGAATGACGGCTTTCAGGCTTCGAA 627
      302 CGGATTCGACAGATGAAGGACAGTGTTCCTGTAAGAGAGGCTTCAGGCTTCGAA 361
      628 GGCATATCACTCAATTTTGAAGAAGTCTGATGAATTTAGACAGTGAACATCC 687
      362 GGCATATCACTCAATTTTGAAGAAGTCTGATGAATTTAGACAGTGAACATCC 421
      688 ACCATATGTCAGGAGATCATTTCAAGTTGTGTGAGAGGAAAGGCTTCGACATGCC 747
      422 ACCATATGTCAGGAGAGTCTTTTCAAGTGTGTGAAGGAATGGCTTCGACATGCC 481
      748 CGCAACGTGACAGGCTCTCTGACAGCTTCAAGATCAATGACTCGGTCACTCATATGAG 807
      482 CGCAATGTGACAGGCTCTCTGACAGCTTCAAAATCAATGACTCAAGTCAAGCTCATATG 541
      808 AAGCCCTTTTCTGTGGAAGACACTTATTTACTGTGTCAAGCCCTTATCTTAAAGAAATT 867
      542 AAGCCCTTTTCTGTGGAAGACACTTATTTACTGTGTGTCCAGACCAATCTTGAAGAAATT 601
      868 GGCATGAAGCTGCACTCCAGGTGACAGATGAAGATGGGCTCTTTTATCTCAATGCT 927
      602 GGCATGAAGCTGCACTCCAGGTGACAGATGAAGATGGGCTCTTTTATCTCAATGCT 661
      928 GTTCATCATCACACACACACTGTTCGACGGTTCATCTGACATCGCCCTGTGATC 987
      662 GTTCATCATCACACACACACTGTTCGACGGTTCATCTGACATCGCCCTGTGATC 721
      988 CTGTTCTGCTCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
      722 CTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
      1048 ATTATCAAGAGAGTCCCTCCACCCCGGCGAGAGAGTGAAGAAA 1094
      782 ATCATCAAGAGAGTCCCTCCACCCCGTGTGAAGAGAGTGAAGAAA 828

RESULT 6
BM800898      1054 bp      mRNA      linear      EST 05-MAR-2002
LOCUS      AGENCOURT_6420797 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5541228
DEFINITION  5', mRNA sequence.
ACCESSION   BM800898
VERSION     BM800898.1 GI:19117721
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1054)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: ATCC/DCMP/DMP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LLAM12238 row: j column: 13
High quality sequence stop: 595.
Location/Qualifiers
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source      1..1054
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5541228"
            /tissue_type="melanotic melanoma"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: skin; Vector: pCMV-Sport6; Site: 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 2 kb. Library constructed by Life
            Technologies."

ORIGIN
Query Match      60.0%; Score 662; DB 3; Length 1054;
Best Local Similarity 97.5%; Pred. No. 6.6e-185;
Matches 704; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

      1 ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
      97 ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 156
      61 CTGGTGTCAATCTGGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
      157 CTGGTGTCAATCTGGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 216
      121 GCGGATTTGACCTGTACTTCAATTTTGGACAATCAGAAAGTGTGTCGACCACTGGAAT 180
      217 GCGGATTTGACCTGTACTTCAATTTTGGACAATCAGAAAGTGTGTCGACCACTGGAAT 276
      181 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 240
      277 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 336
      241 TCCCTTATTTGTTTCTCCACCGGAGGAACAACCTTAATGAATCTGACAGAGACAGAGA 300
      337 TCCCTTATTTGTTTCTCCACCGGAGGAACAACCTTAATGAATCTGACAGAGACAGAGA 396
      301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACATG 360
      397 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACATG 456
      361 CATGAAGATTGAAAAGGCGCAGTGAAGAGATTTATGAAAACAGCAAGGCTACAG 420
      457 CATGAAGATTGAAAAGGCGCAGTGAAGAGATTTATGAAAACAGCAAGGCTACAG 516
      421 AAGGCAAGGCTATCATTTGCTTGAATGAGAACTCCAGTAAGATCTCTTTCTAT 480
      517 AAGGCAAGGCTATCATTTGCTTGAATGAGAACTCCAGTAAGATCTCTTTCTAT 576
      481 TCAGAGAGGAGAGGCTAATAGTCTCGAGATCTTGTGCAATTTTACTGTGTGTGTG 540
      577 TCAGAGAGGAGAGGCTAATAGTCTCGAGATCTTGTGCAATTTTACTGTGTGTGTG 636
      541 AAGATTTCAATGAGACACAGCTGGCCGAGATTGCGGACAGTGAAGATCATGTGTTCCC 600
      637 AAGATTTCAATGAGACACAGCTGGCCGAGATTGCGGACAGTGAAGATCATGTGTTCCC 696
      601 GTGAATGAGAGGCTTTCAGGCTCTGCAAGGAGCATCATCAATTTTGAAGAAGTCTCG 660
      697 GTGAATGAGAGGCTTTCAGGCTCTGCG-AGGAGATCATCACTCCAGTTTGAAGAAGTCTCG 755
      661 ATGGAATTTCTAGACAGTGAACATCCACCAT-ATGTGCA-GGAGAGTCAATTTCAAGTTG 718
      756 ATGGAATTTCTAGACAGGTTGAACATCCCATGATGTGACAGGAGAGACATTTCCAGGTG 815
      719 TC 720
      816 TC 817

RESULT 7
CO245219
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LOCUS CO245219 833 bp mRNA linear EST 23-JUN-2004
DEFINITION AGENCOURT 26524177 NIH_MGC_212 Homo sapiens cDNA clone
IMAGE:30924322 5', mRNA sequence.
ACCESSION CO245219
VERSION CO245219.1 GI:49108057
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 833)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Mary Hendrix
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDAM1166 row: j column: 11
High quality sequence start: 6
High quality sequence stop: 688.
Location/Qualifiers
source 1..833
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30924322"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_1db="NIH_MGC_212"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATTAAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN
Query Match 59.7%; Score 658.8; DB 7; Length 833;
Best Local Similarity 97.9%; Pred. No. 5.4e-184;
Matches 689; Conservative 0; Mismatches 12; Indels 3; Gaps 2;
QY 1 ATGGCCACGGCGGAGGCGGAGAGCCCTTCGGCATCGGCTTCCTCTTTGGCACT 60
DB 100 ATGGCCACGGCGGAGGCGGAGAGCCCTTCGGCATCGGCTTCCTCTTTGGCACT 159
QY 61 CTGGTGTCAATCTGCGCGGCGGCGGAGGCGGAGGATGGGGGTCCAGCTGTAC 120
DB 160 CTGGTGTCAATCTGCGCGGCGGCGGAGGCGGAGGATGGGGGTCCAGCTGTAC 219
QY 121 GCGGATTTGACCTGTACTTCTTGGACAATCAGGAAGTGTCTGCACTGGAAAT 180
DB 220 GCGGATTTGACCTGTACTTCTTGGACAATCAGGAAGTGTCTGCACTGGAAAT 279
QY 181 GAAATCTATTACTTTTGGACAAGTGGCTCACAATTCATCAGCCCACTTGAAGATG 240
DB 280 GAAATCTATTACTTTTGGACAAGTGGCTCACAATTCATCAGCCCACTTGAAGATG 339
QY 241 TCCTTATTGTCTTCCACCGGAGGAACAACCTTAATGAACGACGAAGACAGAA 300

DB 340 TCCTTATTGTCTTCCACCGGAGGAACAACCTTAATGAACGACGAAGACAGAA 389
QY 301 CAAATCCGTCAAGCGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGCACTTACATG 360
DB 400 CAAATCCGTCAAGCGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGCACTTACATG 459
QY 361 CATGAAGAGTTTGAAGGGCGAGTGAAGAGATTATATGAAGAAACAGACAGGGTACAG 420
DB 460 CATGAAGAGTTTGAAGGGCGAGTGAAGAGATTATATGAAGAAACAGACAGGGTACAG 519
QY 421 ACAGCAGCGCTCATCTATGCTTTGAGTGAAGAGAACTCCATGAAGATCTTTTCTAT 480
DB 520 ACAGCAGCGCTCATCTATGCTTTGAGTGAAGAGAACTCCATGAAGATCTTTTCTAT 579
QY 481 TCAGAGAGGAGGCTTAATAGGCTCCAGATCTTGGTGAATTTGTTACTGTGTG 540
DB 580 TCAGAGAGGAGGCTTAATAGGCTCCAGATCTTGGTGAATTTGTTACTGTGTG 639
QY 541 AAGATTTCAATGAGACACAGCTGGCCCGGATTGGCGAGCATGATCATGTTTCCC 600
DB 640 AAGATTTCAATGAGACACAGCTGGCCCGGATTGGCGAGCATGATCATGTTTCCC 699
QY 601 GTGAATGACGCGCTTTCAGGCTCTGCAAGGCAATCATCAATTTGAAGAGTCTGC 660
DB 700 GTGAATGACGCGCTTTCAGGCTCTGCAAGGCAATCATCAATTTGAAGAGTCTGC 759
QY 661 ATGGAATTTAGACAGTGAACCATCCATATGTGCAGAGA 704
DB 760 ATGGAATTTAGACAGTGAAC--ATCCATATATGTGCAGAGA 800

RESULT 8
LOCUS BE741333 725 bp mRNA linear EST 15-SEP-2000
DEFINITION 601594179F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948114 5',
mRNA sequence.
ACCESSION BE741333
VERSION BE741333.1 GI:10155325
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LUCB810 row: n column: 19
High quality sequence stop: 711.
Location/Qualifiers
source 1..725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3948114"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1db="NIH_MGC_9"
/note="Organ: ovary; Vector: pOT87; Site 1: XhoI; Site 2:
EcorI; cDNA made by oligo-dT priming. Directionally
cloned into EcorI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

QY 361 CATGAAGATTGAAAAGGCGCAGTACAGATTTTATATGAAAACAGACAAAGGTACAGG 420
DB 491 CATGAAGATTGAAAAGGCGCAGTACAGATTTTATATGAAAACAGACAAAGGTACAGG 550
QY 421 ACAGCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 480
DB 551 ACAGCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 610
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTG 540
DB 611 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTG 670
QY 541 AAAGATTTCAATAGACACACGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTTCC 600
DB 671 AAAGATTTCAATAGACACACGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTTCC 720
QY 601 GTGAATGACGGCTT 614
DB 731 GTGAATGACGGCTT 744

RESULT 10
BG326444 963 bp mRNA linear EST 27-FEB-2001
LOCUS 602425082P1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4563020 5',
DEFINITION mRNA sequence.

ACCESSION BG326444
VERSION BG326444.1 GI:13132881
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straube, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LNCM276 row: c column: 21
High quality sequence stop: 718.
Location/Qualifiers

FEATURES
Source 1..963
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4563020"
/issue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_14"
/notes="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 53.0%; Score 585; DB 2; Length 963;
Best Local Similarity 96.3%; Pred. No. 5.2e-162;
Matches 621; Conservative 0; Mismatches 20; Indels 4; Gaps 2;

QY 1 ATGCCACGCGGAGGAGAGGCGCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 60
DB 114 ATGCCACGCGGAGGAGAGGCGCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 173
QY 61 CTGGTCTCATCTGCGCCGCGGCAAGGGAGCGAGGAGAGTGGGCTCCAGCTGTAC 120
DB 174 CTGGTCTCATCTGCGCCGCGGCAAGGGAGCGAGGAGAGTGGGCTCCAGCTGTAC 233
QY 121 GGGGATTGACCTGTACTTCAATTTTGGACAAATTCAGAAAGTGTCTGCACTGGAAT 180
DB 234 GGGGATTGACCTGTACTTCAATTTTGGACAAATTCAGAAAGTGTCTGCACTGGAAT 293
QY 181 GAAATCTATTCTTGGAAACAGTTGGCTCAAAATTCAGCCCAAGTGGAGATG 240
DB 294 GAAATCTATTCTTGGAAACAGTTGGCTCAAAATTCAGCCCAAGTGGAGATG 353
QY 241 TCCTTATGTTTCTCCACCCGAGAACCACTTAATGAACAGACAGAGAA 300
DB 354 TCCTTATGTTTCTCCACCCGAGAACCACTTAATGAACAGACAGAGAA 413
QY 301 CAAATCCGTACAGGCTTGAAGAACTCCAGAAAGTTCGACAGAGAGACATTACATG 360
DB 414 CAAATCCGTACAGGCTTGAAGAACTCCAGAAAGTTCGACAGAGAGACATTACATG 473
QY 361 CATGAAGATTGAAAAGGCGCAGTACAGATTTATATGAAAACAGACAAAGGTACAGG 420
DB 474 CATGAAGATTGAAAAGGCGCAGTACAGATTTATATGAAAACAGACAAAGGTACAGG 533
QY 421 ACAGCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 480
DB 534 ACAGCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 593
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTG 540
DB 594 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTG 653
QY 541 AAAGATTTCAATAGACACACGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTTCC 600
DB 654 AAAGATTTCAATAGACACACGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTTCC 711
QY 601 GTGAATGACGGCTTTCAGGCTTGCAGAGGATCATCATCAATT 645
DB 712 GTGAATGACGG--TTTAAGATCTGAAAGGATCATCATCAATT 754

RESULT 11
BG281561 820 bp mRNA linear EST 21-FEB-2001
LOCUS 602402412P1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544691 5',
DEFINITION mRNA sequence.
ACCESSION BG281561
VERSION BG281561.1 GI:13030486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 820)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straube, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
plate: LNCM228 row: h column: 04
High quality sequence stop: 815.
Location/Qualifiers

FEATURES

Query Match 53.0%; Score 585; DB 2; Length 963;
Best Local Similarity 96.3%; Pred. No. 5.2e-162;
Matches 621; Conservative 0; Mismatches 20; Indels 4; Gaps 2;

source

1. .820
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:454691"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 20"
/note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG (9). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 52.8%; Score 582.6; DB 2; Length 820;
Best Local Similarity 96.1%; Pred. No. 2,5e-161;
Matches 663; Conservative 0; Mismatches 19; Indels 9; Gaps 8;

QY 1 ATGGCCAGCGCGGAGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 112 ATGGCCAGCGCGGAGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 171
QY 61 CTGGTCTCATCTGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 172 CTGGTCTCATCTGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 231
QY 121 GCGGATTTGACCTGACTTCAATTTTGGACAAATTCAGAAAGTGTCTGACCACTGAAT 180
DB 232 GCGGATTTGACCTGACTTCAATTTTGGACAAATTCAGAAAGTGTCTGACCACTGAAT 291
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RESULT 12
CF132432

LOCUS CF132432 641 bp mRNA linear EST 05-AUG-2003
DEFINITION UI-HF-P00-awo-m-16-0-UI.r1 NIH MGC_215 Homo sapiens cDNA clone
IMAGE:30560079 5', mRNA sequence.
ACCESSION CF132432
VERSION CF132432.1 GI:33215693
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 641)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
COMMENT 8889548
CONTACT: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pyx-5.
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location/Qualifiers
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/note="Organ: Lung; Vector: pYX-AseI; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-AseI vector. The library tag
sequence located between the Not I site and the polyA tail
is GATTAAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN

Query Match 50.0%; Score 552; DB 6; Length 641;
Best Local Similarity 99.8%; Pred. No. 2,9e-152;
Matches 563; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 181 GAAATCTATTACTTTGTGAGACAGTTGGCTCAAAATTCATGACCCACAGTTGAGATG 240
DB 259 GAAATCTATTACTTTGTGAGACAGTTGGCTCAAAATTCATGACCCACAGTTGAGATG 318

University of Manchester Institute of Science and Technology
(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

source

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with the T-primed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Pu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
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containing BspI and BamHI sites
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Query Match 48.4%; Score 534; DB 5; Length 823;

Best Local Similarity 80.4%; Pred. No. 7.3e-147;

Matches 650; Conservative 0; Mismatches 155; Indels 3; Gaps 2;

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DB 63 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 122
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DB 243 GGAACAATTCATGATGATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302
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DB 303 CTTCAGAAAGTCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362
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ACCESSION CD664532
VERSION CD664532.1 GI:40546157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 564)
De Preter, K., Pattyn, F., Bex, G., Strueman, K., Mente, B., Van
Roy, F., De Paeye, A., Speleman, F., and Vandesompele, J.
Combined subtractive cDNA cloning and array CGH: an efficient
approach for identification of overexpressed genes in DNA amplicons
BMC Genomics 5 (1), 11 (2004)
15018647
Contact: Speleman, F.
Center for Medical Genetics
Ghent University Hospital
De Pintelaan 185, Medical Research Building, 2nd floor, 9000 Ghent,
Belgium
Tel: 3292406549
Fax: 3292404970
Email: franki.speleman@ugent.be.

FEATURES
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Location/Qualifiers

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/cell_type="Neuroblastoma"
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ORIGIN

Query Match 48.3%; Score 533.4; DB 6; Length 564;

Best Local Similarity 96.6%; Pred. No. 9.4e-147;

Matches 545; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

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GenCore version 5.1.6
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Scoring table: IDENTITY_NUC
Gapco 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Listing first 45 summaries

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SUMMARIES

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| 3 | 346.2 | 31.4 | 2234 | US-10-104-047-669 | Sequence 669, App |
| 4 | 307.4 | 27.8 | 1492 | US-09-774-528-297 | Sequence 297, App |
| 5 | 307.4 | 27.8 | 1492 | US-10-120-988-297 | Sequence 297, App |
| 6 | 79.4 | 7.2 | 450 | US-10-121-827-8330 | Sequence 8330, App |
| 7 | 47.4 | 4.3 | 7218 | US-08-232-463-14 | Sequence 14, Appl |
| 8 | 42.4 | 3.8 | 399 | US-09-621-976-8976 | Sequence 8976, App |
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| 12 | 37.6 | 3.4 | 1141 | US-09-806-7088-22 | Sequence 22, Appl |
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| 18 | 37.4 | 3.4 | 32207 | US-08-757-669A-20 | Sequence 20, Appl |
| 19 | 37.4 | 3.4 | 32207 | US-08-230-371A-20 | Sequence 20, Appl |
| 20 | 37.2 | 3.4 | 488 | US-09-385-982-368 | Sequence 368, App |
| 21 | 37 | 3.4 | 254366 | US-09-822-871-3 | Sequence 3, Appl1 |
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| 27 | 36.2 | 3.3 | 2198 | 3 | US-09-533-559-842 | Sequence 842, App |
| 28 | 36.2 | 3.3 | 5299 | 3 | US-09-902-540-645 | Sequence 645, App |
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| C 30 | 35.6 | 3.2 | 2278 | 3 | US-09-620-312D-1003 | Sequence 1003, App |
| C 31 | 35.6 | 3.2 | 2278 | 3 | US-09-148-545-78 | Sequence 78, Appl |
| C 32 | 35.6 | 3.2 | 2278 | 3 | US-09-148-545-131 | Sequence 131, App |
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| C 34 | 35.6 | 3.2 | 2278 | 3 | US-09-621-011-131 | Sequence 131, App |
| C 35 | 35.6 | 3.2 | 2368 | 3 | US-09-999-833A-471 | Sequence 471, App |
| C 36 | 35.6 | 3.2 | 2368 | 3 | US-10-020-445A-471 | Sequence 471, App |
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| C 41 | 35.2 | 3.2 | 1440 | 6 | US-09-009-656-13 | Sequence 13, Appl |
| C 42 | 35.2 | 3.2 | 1440 | 6 | PCT-US93-04493-3 | Sequence 3, Appl1 |
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| C 44 | 35.2 | 3.2 | 2409 | 3 | US-09-949-016-2968 | Sequence 2968, App |
| C 45 | 35.2 | 3.2 | 2422 | 2 | US-08-475-845-1 | Sequence 1, Appl1 |

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Lili, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aildong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_Fl_genes Version 1.0
SEQ ID NO 8
LENGTH: 1609
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (309) ..(1202)
US-09-620-312D-8
Query Match 72.8%; Score 803.8; DB 3; Length 1609;
Best Local Similarity 99.8%; Pred. No. 9e-250;
Matches 805; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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| : Patent No. 6919193 | | | |
| : GENERAL INFORMATION: | | | |
| : APPLICANT: Tang, Y. Tom | | | |
| : APPLICANT: Goodrich, Ryle | | | |
| : APPLICANT: Liu, Chenghua | | | |
| : APPLICANT: Ren, Felyan | | | |
| : APPLICANT: Wang, Dunrui | | | |
| : TITLE OF INVENTION: No. 6919193el Nucleic Acids and | | | |
| : FILE REFERENCE: 802CON | | | |
| : CURRENT APPLICATION NUMBER: US/10/120,988 | | | |
| : CURRENT FILING DATE: 2002-04-11 | | | |
| : PRIOR APPLICATION NUMBER: 09/774,528 | | | |
| : PRIOR FILING DATE: 2001-01-30 | | | |
| : NUMBER OF SEQ ID NOS: 441 | | | |
| : SOFTWARE: pc_FL_genes Version 2.0 | | | |
| : SEQ ID NO 297 | | | |
| : LENGTH: 1492 | | | |
| : TYPE: DNA | | | |
| : ORGANISM: Homo sapiens | | | |
| : FEATURE: | | | |
| : NAME/KEY: CDS | | | |
| : LOCATION: (79)..(1434) | | | |
| US-10-120-988-297 | | | |

| | | | | |
|-----------------------|-----------------|--------------------|-----------|--------------|
| Query Match | 27.8% | Score 307.4; | DB 3; | Length 1492; |
| Best Local Similarity | 59.2%; | Pred. No. 1.1e-88; | | |
| Matches 546; | Conservative 0; | Mismatches 371; | Indels 6; | Gaps 1. |

| | | | |
|----|------|--|------|
| OY | 155 | CAGGAAGTGTCTGCACACCTAGGATGAAATCTTATTACTTTGTGGAAACAGTGGCTGCACA | 214 |
| Db | 2 | CACGCCGCCGGCCGAAATACCTGGAATTTGAAATTTTATATTTTGGTACAGCAACTTGGGGAGA | 61 |
| OY | 215 | AATTCATCAGCCACAGTTGAGAAATGTCCTTATTTGTTTCTCCACCCGAGAACAACTT | 274 |
| Db | 62 | GATTTGTAGCCCTGAAATAGATTAATCTTTCATTTGTGTTTCTTCTCAAGCACTATTA | 121 |
| OY | 275 | TAAATGAATCTACAGAAACAGAGAACAAATCCCTCAGGCTTAAAGAACTCCAGAAAG | 334 |
| Db | 122 | TTTTGCCCTTAACTGGAGACAGAGCAAAATCAGTAAAGGCTTGGAGATTTAAACGTG | 181 |
| OY | 335 | TTCTGCCAGGAGAGACACTTACATGCAATGAAAGATTTGAAAGGGCCAGTGGAGATTT | 394 |
| Db | 182 | TTAGTCCAGTGTGGAGAGACATATATCTCATGAAAGCTAAAGCTACGAATGAACAAAT-- | 239 |
| OY | 395 | ATTATGAAACAGACAAAGGTACAGACAGCCAGGCTCATTTGCTTTGACTGATGAG | 454 |
| Db | 240 | ----TCAAGAAAGCAGAGGCTTGAAAACTCAGATCATTAATTTCTCTGACAGATGGCA | 295 |
| OY | 455 | AACTCATGAAGATCTCTTTTCTATTCTACAGAGGGAGGCTTAATAGTCTCGAATCTTG | 514 |
| Db | 296 | AGTTGAGACGCTGTGGTGCATCATATGACAGAGAAAGAGCAAAAGATATCCAGGTCACTTG | 355 |
| OY | 515 | GTGCAATTTGTTTACGTGTGTGTGTGGAAAGATTTCAATGAGACACAGCGGCCGGATTG | 574 |
| Db | 356 | GGGCTAGTGTATATGTGTGTGGGGCTCTTGATTTTGAACACAGCAAGCTTGAAAGATTTG | 415 |
| OY | 575 | CGGACAGTAAAGATCATGTGTTTCCCGTGAAATGACGCGCTTTCAGGCTCTGCAGGACATCA | 634 |
| Db | 416 | CTGATTTCAAGAGAGAAATTTTCCCTGTCAAAAGTGATTTTCAGGCTCTTAAAGAAATTA | 475 |
| OY | 635 | TCCACTCAATTTTGAAGAAGTCTGCAATGCAATTTCTAGAGCTAACCATCCACATAT | 694 |
| Db | 476 | TTAATTTCTATCTAGCTCAGTCACTGATCTGAATCTTAGAATTTGACGCCCTCMAAGTGTCT | 535 |
| OY | 695 | GTGACAGAGACATCAATTTCAAGTGTGCGTAGAGAGAAAGGCTTCCGACATGCCCGCAACG | 754 |
| Db | 536 | GTGTGGGGAGAAATTTAGATTTGTTCTTAAAGTGAAGAGATTTATGCTGGGCACTGCGA | 595 |
| OY | 755 | TGGAACAGGATCCTCTGCAGCTTCAAGATCAATGACTCGGTCACTCATATGAGAAAGCCT | 814 |
| Db | 596 | ATGGCAGTGTCTCTGCACCTTACCTGTAAATGAAACATATACACAGGTGTAAACAG | 655 |
| OY | 815 | TTTCTGTGAAGACATTAATTTACTGTGTCCAGCGCCTATCTTAAAGAAGATTTGGCATCA | 874 |
| Db | 656 | TAAAGTGTACACTTAATCTATGCTTGTCTGCGACCTATCTGAAATTAAGCTGGAGAA | 715 |
| OY | 875 | AAGCTGCACTCAGGTGACAGATGAACGATGGCTCTCTTTATATCCAGTTCTGTGCATCA | 934 |
| Db | 716 | CTTTGATGTTTCACTGAGCTTAAATGAGAGAAATCTGTCAATTTCCAGGATCATTTAATGG | 775 |
| OY | 935 | TCACCACCAACACTGTTCTGACGGTTCCATCTGGCCATCGCCCTGCTGATCTGTGCC | 994 |
| Db | 776 | TCACAGCCACAGAAATGTTCTTAACGGGATCGACGACATCATTTGTATTTTGGTGAATCTC | 835 |
| OY | 995 | TGCTCTTAGCCCTGGCTCTCTCTGTGTGTCTGGCCCTCTGCTGACCTGTGATTTATCA | 1055 |
| Db | 836 | TACTCTGGGATCGGTTGATGTGTGTGTGGCCCTTTGTGCTGCAAAAGTGTATTA | 895 |
| OY | 1055 | AGGAGGTCCCTCAACCCCTGCC | 1077 |
| Db | 896 | AGGATCTTCAACCAACCCCTCC | 918 |

RESULT 6
US-10-131-827-8330
; Sequence 8330, Application US/10131827


```

: Patent No. 6905827
: GENERAL INFORMATION:
: APPLICANT: Wohlgemuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Woodward, Robert
: APPLICANT: Ly, Ngoc
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
: TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
: FILE REFERENCE: 506612000120
: CURRENT APPLICATION NUMBER: US/10/131,827
: CURRENT FILING DATE: 2002-09-06
: PRIOR APPLICATION NUMBER: US 10/006,290
: PRIOR FILING DATE: 2001-10-22
: PRIOR APPLICATION NUMBER: US 60/296,764
: PRIOR FILING DATE: 2001-06-08
: NUMBER OF SEQ ID NOS: 9090
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 8330
: LENGTH: 450
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-131-827-8330

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      TYPE: DNA
      ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match          3.8%; Score 42.4; DB 3; Length 399;
Best Local Similarity 8.9%; Pred. No. 0.0046;
Matches 25; Conservative 142; Mismatches 113; Indels 0; Gaps 0;

QY      6 CACGCGGAGGGAGAGCCCTTCGCATGGCCTTCCATGTGCTCTTTTGCCACTCTGTG 65
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      284 SRRGTGMSVSRRAMRBSKSGGSSYYRMGYSRFRSWYSAMWRKKMTGWSGRSSW 225
        GGTCACTCCGCCGGGGAAGGGGAGCGAGGAGGAGATGGGGGTCCAGCTGTACAGCGG 125
QY      66 GGTCACTCCGCCGGGGAAGGGGAGCGAGGAGGAGATGGGGGTCCAGCTGTACAGCGG 125
       :||:~::~|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      224 GSRSTGYAMMYKKSWMCTSRKMNYKKRKRRKRCSTKTCTCYGSIYCKMAYTYKR 165
        GSRTGTAATCTTGTGGAACAGTTGGCTCACAAATTATCATGACCACAGTTGAGAATGCTT 245
QY      186 GTATTACTTGTGGAACAGTTGGCTCACAAATTATCATGACCACAGTTGAGAATGCTT 245
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      104 RYRRRWYAKAKMSKRCCTSWTCTCYCMKMKMAKCSWYMSMSMKMGSMWKMYYYYY 45
        TATGTCTTCTCCACCGAGGAGAACACTTATGAATACTG 285
QY      246 TATGTCTTCTCCACCGAGGAGAACACTTATGAATACTG 285
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      44 YMMKWSKMTYWSMMSCVARKCWRYAKTYTWMTCTWGKR 5

RESULT 9
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFLINGER, F.
; APPLICANT: PALKNER, F.G.
; TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; FAX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Pis
US-08-232-463-14

Query Match
Best Local Similarity 3.8%; Score 41.4; DB 2; Length 7218;
Matches 27; Conservative 198; Mismatches 174; Indels 0; Gaps 0;

OY      263 GAGGACACCTTTATGAATACTGACAAGAAGACAGAACAAATCCGTCAAGCCTTAAGAAG 322
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1407 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1348
OY      323 AACTCCGAAGATTCTGCCAGAGAGACACTTACATGCATAGAAGATTGAAAAGGCCA 382
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1347 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1288
OY      383 GTGGACGATTTTATGA AAAACAGACAAGGTACGACACCGCTCATCATTCCTT 442
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1287 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1228
OY      443 TGACTGATGGAACCTCATGAAGATCTTTTTCTATTCAAGAGAGGAGCTTAAGT 502
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1227 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1168
OY      503 CTGAGATCTTGATGCAATGTTTACTGTGTGTGTA AAATTTCAATGAGACAGC 562
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1167 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1108
OY      563 TGGCCGGATTTGGGACAGTAAGATCATGTGTTCCGTGAATGACGCTTTCAGGCTC 622
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1107 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1048
OY      623 TGCAGGATCATCTCACTCAATTTTGAAGAAGCTCTGCA 661
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1047 TGCAGCCAAGCTCGAATTATTTCTGAGCGATGCA 1009

RESULT 10
US-09-806-708B-22
Sequence 22, Application US//09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match
Best Local Similarity 3.7%; Score 40.6; DB 3; Length 1141;
Matches 68; Conservative 270; Mismatches 353; Indels 2; Gaps 1;

OY      226 CCACAGTTGAATGTCCTTATTTGTTTCTCACCCGAGAAACAACCTTAATGAATG 285
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      98 YHARRWMDKMTAYBMVTWKMGKTGRHRHYFWWRABBDVTHHYVYANNANNTWTGMNDK 157
OY      286 ACAGAAACAGAGAACAAATCCGTCACAGGCTTAGAAGAACTCCAGAAATGTTGCGACGA 345
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      158 DDKRTTRWWKKNNNAATGGDDTCTYHHMNNNGCBFTYVMRYRTIDRWBSKRNYGMBWK 217
```

QY 346 GGAGACACTTACATGCATGTAAGATTGAAAGGCCGATGAGACATTTATATGAAC 405
DB 218 NMSYDVTYVWVDDMKRYRVRVTRGRNRVWVMBTAHRRYNNGTBMAAYRRMT 277
QY 406 AGACAAGGCTTACAGACAGCAGCATCATCTTCTTGA--CTGATGAGAACTCCATG 463
DB 278 MNNNNNNNAKACBRKAKWGNBVBVNSTCTTWSKTTKAVTSCMANNCRAGDANKHKWM 337
QY 464 AAGATCTCTTTTCTATTCAGAGAGAGGCTTAATAGCTCTGAGATCTTGTCGCAATTG 523
DB 338 KMSAAMGVYNNNNNNNNMTYKKAHBAWMDVMVMSAKKWMANAAAHYSRKMTBYKKXTM 397
QY 524 TTTACTGTGTGGGTGTAAGATTTCATATGACACAGCTGGCCCGATGCGGACAGTA 583
DB 398 VNNNGTGTWKRMMWAMWYMKMDMBGTNNNNNGRTYGTWTKNKKMTYKMKANNCKW 457
QY 584 AGGATCATGTGTTCCCGTGAATGACGGCTTTCAGGCTTCGCAAGCATCATCCACTCA 643
DB 458 RAMDHKTCTNNNTTWMKTKTYMNNCYKSKMTNGSHBAAAVTYWMMRRYAHANNNN 517
QY 644 TTTGAAGAAGTCTGTCATCGAAATTTCTAGACAGTCAACATCCATATGTCAGAG 703
DB 518 WDYWKACTWYKYBVCCKMNNNVAAYTKSMYNTSHYRWKTNNSWRMSDTRSMGRAN 577
QY 704 AGTCATTTCAAGTTGTGTGAGAGAAACGGCTTCGACATGCCCGCAAGCTGACAGG 763
DB 578 NYARABHYGYKMTNRMBWHSHTWBRAGAHAYMBWYBAKCHCMAMWKAKKYAGAG 637
QY 764 TCCTCTCAGCTTCAGATCATGACTCGGTCACTCAATGAGAACCCCTTTCTGTGG 823
DB 638 SNNNNNNNNNNNNNNNNATCARDDYAAASRYMAAAMKYYKBAANNAAYTHANNWGC 697
QY 824 AAGACCTTATTTACTGTGTCAGCGGCTATCTTAAAGAAGTTGGCATGAAGCTGCAC 883
DB 698 MNNATDTRATWTKNNNNNNAGTWKNNNNNAKNAASAAKVAAYAAVKAAGKWRWANKWAM 757
QY 884 TCCAGTCCAGCATGAACGATGCGCTCTCTTTTA 916
DB 758 RGMWADAABRTDGRNNNGAYTKYTTNNNTYR 790

RESULT 11
US-09-949-016-16291/C
; Sequence 16291, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16291
; LENGTH: 37822
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1)...(37822)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16291

Query March 3.6%; Score 40; DB 3; Length 37822;
Best Local Similarity 51.7%; Pred. No. 0.61;

Matches 91; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 259 ACCCGAGGAACACCTTAATGAACATGACAGAAAGCAAGAAATCCGTGAGCCCTA 318
DB 8207 ATCCGAGAAACATAATTAACAAACAGACGCAAAATTAATTAATGCTGTAATAA 8148
QY 319 GAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAATGATGAGATTTGAAGG 378
DB 8147 CAAGAAACCGAGTAGGAGAAAGATCTGAGTTCTAGATATGACATATTTTAATG 8088
QY 379 GCCAGTGAAGATTTATATGAAAACAGCAAGGATACAGACAGCCAGCGTCAT 434
DB 8087 TCCAGTTTTCAGCAAAACGATATAGACACAAAGAAACGAGAAAGTATGGCTCAT 8032

RESULT 12
US-09-806-708B-22/C
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match 3.4%; Score 37.6; DB 3; Length 1141;
Best Local Similarity 10.9%; Pred. No. 0.34;
Matches 89; Conservative 281; Mismatches 443; Indels 6; Gaps 1;

QY 286 ACAGAGACAGAGAAACATCCCTCAAGCCTGAGAGAACTCCAGAAAGTTGCGCAGA 345
DB 987 AAKKMAWAGNNNNNNMTGAAGNRMGCWAATATGBWWDATAGKCNNNNNNTTIVRRMA 928
QY 346 GGAGACACTTACATGCATGTAAGATTGAAAGGCCGATGAGACATTTATGAAC 405
DB 927 MKAANNNNNAAYTTACTNRAATNNKAATMMKMTTHAGHSRRRTHTRTCKRNNNNN 868
QY 406 AGACAAGGCTTACAGACAGCAGCATCATCTTCTTGA--CTGATGAGAACTCCATGA 465
DB 867 NARTVYVYHHAARWMAWMTRTNNNNNNNNNAACRTYMAWBMKSWCNNNNNNNNN 808
QY 466 GATCTCTTTTCTATTCAGAGAGAGGCTTAATAGCTGTGAGATCTGTGCAATTGT 525
DB 807 NNNNTWCHYTTAABDCTRANNNNAARMAKTCNNYMAAVTTTHDWCYKTMWNTYWD 748
QY 526 TACTGTGTGTGTAAGATTCAATGAGACACAGCTGCGCGGATTTGCGACAGTAAG 585
DB 747 MMTTBTTRNNNTSTNNNNNNNNNNMACTNNNNNNMMAYAAHANNMGCMWNTDAR 688
QY 586 GATCATGTGTTCCCGTGAATGACGGCTTCAGGCTTCGAAAGCATCATCACTCAAT 645
DB 687 RTNNNTTVMRBRWMTNTKTRWYSTRRHYGTATNNNNNNNNNNNNNNNNNSCTCTRTMTM 628
QY 646 TTGAAGAAGTCCGCAATCGAAATTTCTAGACAGCTGAACCATCCACATATGAGAGAG 705
DB 627 RWTMKSGMTVRKKVKRDTTCTYVDWADSWWMAWMAKRCDDVYTRNTYCKSYAHS 568
QY 706 TCATTTCAAGTTGTCGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGATC 765

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Db      567 YWYWSNANMWRYSARNSMABWTRNNMWSGBWRNRWAGTWMMRHNNNNNTDTRY 508
Qy      766 CTCGACGCTTCAAGATGATGACTCGGTCACTCAATGAGAAGCCCTTTCTGTGAA 825
Db      507 WKKKRAABTTTTYDSMCNAKSKSMRGNNRRAMMMMAANNADAGAMHWTYMMGNNTMMR 448
Qy      826 GACACTTATTTACTGTGTCCAGCGCTATCTTAAAGAGTTGGACGAAGCTGCATC 885
Db      447 RAKMMNMMWCRAYCCNNNNNRACVWHK-----MMRWTKYMMKKAACNNNNKAMY 394
Qy      886 CAGGTAGCATGACATGAGCCCTCTCTTTATCTCCAGTTCTGTCTATCATCACCACAA 945
Db      393 MRVAMMMYRDTTNTMMMTSDWBMMWYVDYTMRAVNNNNNNNRBCKTSMWMD 334
Qy      946 CACTGTCTGACGAGTTCATCTCGGACATCGCCCTGTGATCTCTCTCTCTCTAGCC 1005
Db      333 HAHHTCTTGNNMTGSAVBMAAASMAAGASNBVTYWCRRMTYMGKITNNNNNNKAWY 274
Qy      1006 CTGGCTCTCTCTGTGTGTCTGGCCCTCTCTGCTGCACTGTGATTTATCAAGAGTCCCT 1065
Db      273 RFTKTVAMCNNRYYYDTAVMTBKKNYKCYAVBMYEMYGKHHMBWRABHRSNMWV 214
Qy      1066 CCACCCCTGCCGAGAGAGTGGAAATTAATAA 1104
Db      213 KCRNKYVSMHYHAMRYBKWABAAGCANNMKDMAHHW 175

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RESULT 13

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US-08-728-323A-1/c
; Sequence 1, Application US/08728323A
; Patent No. 5948676
; GENERAL INFORMATION:
; APPLICANT: Chahenzky, Yuan
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
; TITLE OF INVENTION: Encoding Same And Uses Thereof
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,323A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MSC/SKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

```

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; LOCATION: 1..3489
US-08-728-323A-1

```

```

Query Match 3.4%; Score 37.4; DB 2; Length 3489;
Best Local Similarity 50.3%; Pred. No. 0.85;
Matches 92; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

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```

Qy      883 CTCGACGTCAGATGAGATGAGCCCTCTTTATCTCCAGTTCTGTCTATCATCACCACC 942
Db      1149 CTCCTGTCATCTCTCTGTCATCTCTCCGTCATCTCTGTCATCTCTCTGTCATC 1090
Qy      943 ACACACTGTTCTGACGGTTTCATCTCGGCATCGCCCTGCTGATCTGTCTCTCTTA 1002
Db      1089 CTCCTGTCATCTCTCTGTCATCTCTCGTCATCTCTGTCATCTCTCTCTGTCATC 1030
Qy      1003 GCCCTGCTCTCTGTTGTTCTGGCCCTCTGCTGCACTGTATTCAGAGAGTCC 1062
Db      1029 CTCCTGTCCTCTATCTGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 970
Qy      1063 CCT 1065
Db      969 CTT 967

```

RESULT 14

```

US-09-298-568-1/c
; Sequence 1, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballesteras, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/298,568
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,422
; EARLIER FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

```

```

Query Match 3.4%; Score 37.4; DB 3; Length 3489;
Best Local Similarity 50.3%; Pred. No. 0.85;
Matches 92; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

```

```

Qy      883 CTCGACGTCAGATGAGATGAGCCCTCTTTATCTCCAGTTCTGTCTATCATCACCACC 942
Db      1149 CTCCTGTCATCTCTCTGTCATCTCTCCGTCATCTCTGTCATCTCTCTGTCATC 1090
Qy      943 ACACACTGTTCTGACGGTTTCATCTCGGCATCGCCCTGCTGATCTGTCTCTCTTA 1002
Db      1089 CTCCTGTCATCTCTCTGTCATCTCTCCGTCATCTCTGTCATCTCTCTCTGTCATC 1030
Qy      1003 GCCCTGCTCTCTGTTGTTCTGGCCCTCTGCTGCACTGTATTCAGAGAGTCC 1062
Db      1029 CTCCTGTCCTCTATCTGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 970
Qy      1063 CCT 1065
Db      969 CTT 967

```

RESULT 15

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US-09-410-399-1/c
; Sequence 1, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:

```

APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A. to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: Method to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ. ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

Query Match 3.4%; Score 37.4; DB 3; Length 3489;
Best Local Similarity 50.3%; Pred. No. 0.85;
Matches 92; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 883 CTCACGTCAGCATGAGCATGGCCCTCTTTATCTCCAGTCTGTGCATCATCACACC 942
1149 CTCCTGTCATCCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATC 1090
QY 943 ACACACTGTTCTGACGGTTCATCTGCGCATCGCCCTGATCTCTGTCCTCTA 1002
1089 CTCCTGTCATCCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATC 1030
QY 1003 GCCCTGGCTCTCTCTGAGGTCCTGAGCCCTCTGTCGACTGTGATTTATCAAGAGGTC 1062
1029 CTCCTGTCCTCTCTGTCATCTGTCTGTCCTCTCTCTCATCACTTATGTGATGTGATC 970
QY 1063 CCT 1065
969 CTT 967
Db

Search completed: December 17, 2005, 13:37:40
Job time : 215.822 secs

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| | | | |
|----|------|--|------|
| Db | 284 | GAATCTATTACTTGTGTGGAAAGTTGGCTCACAAATTCTATCGCCCAAGTTGAAGT | 343 |
| Qy | 241 | TCCTTTATTTGTTTTCTCCACCCGAGGAAACAACCTTAATGAAACTGACAGAAACAGAGA | 300 |
| Db | 344 | TCCTTTATTTGTTTTCTCCACCCGAGGAAACAACCTTAATGAAACTGACAGAAACAGAGA | 403 |
| Qy | 301 | CAAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG | 360 |
| Db | 404 | CAAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG | 463 |
| Qy | 361 | CATGAGGATTTGAAAGGCGCAGTGAAGCAATTTATATGAAACAGACAGGGTACAG | 420 |
| Db | 464 | CATGAGGATTTGAAAGGCGCAGTGAAGCAATTTATATGAAACAGACAGGGTACAG | 523 |
| Qy | 421 | ACAGCCAGCGTCATCATTTGCTTTGACATGATGAGAACTCCATGAAGTCTTTTCTAT | 480 |
| Db | 524 | ACAGCCAGCGTCATCATTTGCTTTGACATGATGAGAACTCCATGAAGTCTTTTCTAT | 583 |
| Qy | 481 | TCAGAGAGGGAGGCTAATAGGCTCGAGATCTTGTCGATCTGTTACTGTTGTGTGAG | 540 |
| Db | 584 | TCAGAGAGGGAGGCTAATAGGCTCGAGATCTTGTCGATCTGTTACTGTTGTGTGAG | 643 |
| Qy | 541 | AAAGATTTCAATGAGACACACAGCTGGCCCGGATTTGCGGACAGTAAGATCATGTGTTCCC | 600 |
| Db | 644 | AAAGATTTCAATGAGACACACAGCTGGCCCGGATTTGCGGACAGTAAGATCATGTGTTCCC | 703 |
| Qy | 601 | GTAATAGACGGCTTTCAGGCTCTGCAAGGCAATCATCTCAATTTTGAAGAGTCTGC | 660 |
| Db | 704 | GTAATAGACGGCTTTCAGGCTCTGCAAGGCAATCATCTCAATTTTGAAGAGTCTGC | 763 |
| Qy | 661 | ATCGAAATTTCTAGAGAGCTGAACCATTCACCATATGTGCAGAGAAAGTCATTTCAAGTTGTC | 720 |
| Db | 764 | ATCGAAATTTCTAGAGAGCTGAACCATTCACCATATGTGCAGAGAAAGTCATTTCAAGTTGTC | 823 |
| Qy | 721 | GTCGAGAGAAACGGCTTCCGACATGCCCCGACACGTGACAGGGTCTCTGACAGCTTCAAG | 780 |
| Db | 824 | GTCGAGAGAAACGGCTTCCGACATGCCCCGACACGTGACAGGGTCTCTGACAGCTTCAAG | 883 |
| Qy | 781 | ATCAATGACTGGTTCACACTCATATGAGAAAGCCCTTTTCTGTGAAAGACATTATTTACTG | 840 |
| Db | 884 | ATCAATGACTGGTTCACACTCATATGAGAAAGCCCTTTTCTGTGAAAGACATTATTTACTG | 943 |
| Qy | 841 | TGTCACAGCGCTATCTTTAAAAAGAAAGTTGGCATGAAAGCTGCACTCCAGAGTCAGCATGAAC | 900 |
| Db | 944 | TGTCACAGCGCTATCTTTAAAAAGAAAGTTGGCATGAAAGCTGCACTCCAGAGTCAGCATGAAC | 1003 |
| Qy | 901 | GATGAGCCCTCTTTTATCTCCAGTTCTGTCAATCATACACACACACACTGTTCTGAAGGT | 960 |
| Db | 1004 | GATGAGCCCTCTTTTATCTCCAGTTCTGTCAATCATACACACACACACTGTTCTGAAGGT | 1063 |
| Qy | 961 | TCATATCTGTGAGCATGCGCCCTGCTGATCCTGTTCTGTGCTCTAGAGCCCTGCTCTCTGTG | 1020 |
| Db | 1064 | TCATATCTGTGAGCATGCGCCCTGCTGATCCTGTTCTGTGCTCTAGAGCCCTGCTCTCTGTG | 1123 |
| Qy | 1021 | TGTTTCTGTGCCCCCTCTGTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG | 1080 |
| Db | 1124 | TGTTTCTGTGCCCCCTCTGTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG | 1183 |
| Qy | 1081 | GAGAGTGAAGAAATTAATAATTAATA | 1104 |
| Db | 1184 | GAGAGTGAAGAAATTAATAATTAATA | 1207 |

```

RESULT 2
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
;
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING

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: TITLE OF INVENTION:  DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
:
: TITLE OF INVENTION:  OTHER BIOLOGICAL STATES
: FILE REFERENCE:  11613.56US01
:
: CURRENT APPLICATION NUMBER:  US/10/133,937
:
: CURRENT FILING DATE:  2002-11-04
:
: NUMBER OF SEQ ID NOS:  99
:
: SOFTWARE:  PatentIn version 3.1
:
: SEQ ID NO 58
:
: LENGTH:  1454
:
: TYPE:  DNA
:
: ORGANISM:  Homo sapiens
:
: US-10-133-937-58

```

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|----------------------------|---------|--------------|-------|------------------|
| Query Match | 100.0%; | Score 1104; | DB 6; | Length 1454; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 1104; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0 |

| | | | |
|----|-----|---|-----|
| Oy | 1 | ATGCGCACGGGGAGAGCGGAGAGCCCTCGGACATCGGCTTCACAGTGGCTCTCTTTGGCCACT | 60 |
| Db | 144 | ATGGCCACGGGGAGCGGAGAGCCCTCGGACATCGGCTTCAGATGGCTCTCTTTGGCCACT | 203 |
| Oy | 61 | CTGGTGTCAATCTGGCGCCGGGCAAGGGGAGACGACAGGAGATGGGGGTTCAGCTGTCTAC | 120 |
| Db | 204 | CTGGTGTCAATCTGGCGCCGGGCAAGGGGAGACGACAGGAGATGGGGGTTCAGCTGTCTAC | 263 |
| Oy | 121 | GGCGGATTTGACCTGTACTTCAATTTTGGACAAATCAGGAAGTGTCTGCACACCTGGAAT | 180 |
| Db | 264 | GGCGGATTTGACCTGTACTTCAATTTTGGACAAATCAGGAAGTGTCTGCACACCTGGAAT | 323 |
| Oy | 181 | GAATCTATTACTTGTGTGAAACAGTGTGGCTCACAATTCATCAGCCCAAGTTGAGAAATG | 240 |
| Db | 324 | GAATCTATTACTTGTGTGAAACAGTGTGGCTCACAATTCATCAGCCCAAGTTGAGAAATG | 383 |
| Oy | 241 | TCTCTTATTTGTTTCTCCACCCGAGAACAACTTAAAGAACTGACAGGAACAGAGAA | 300 |
| Db | 384 | TCTCTTATTTGTTTCTCCACCCGAGAACAACTTAAAGAACTGACAGGAACAGAGAA | 443 |
| Oy | 301 | CAAAATCCGTCAGAGGCTGTAGAGAACTCAGAGAAAGTTCTGCCAGAGAGACACTTAACATG | 360 |
| Db | 444 | CAAAATCCGTCAGAGGCTGTAGAGAACTCAGAGAAAGTTCTGCCAGAGAGACACTTAACATG | 503 |
| Oy | 361 | CATGAAAGATTTGAAAGGGCCAGTGAGCAGATTTATATGAAAACAGACAAAGGTTACAGG | 420 |
| Db | 504 | CATGAAAGATTTGAAAGGGCCAGTGAGCAGATTTATATGAAAACAGACAAAGGTTACAGG | 563 |
| Oy | 421 | ACACCCAGCCCTCATCATTTGGCTTTCATGTGATGAGAACTCCATGAAAGATCTCTTTTTCAT | 480 |
| Db | 564 | ACACCCAGCCCTCATCATTTGGCTTTCATGTGATGAGAACTCCATGAAAGATCTCTTTTTCAT | 623 |
| Oy | 481 | TCAGAGAGGAGGCTAATAGGCTCTCGAAGATCTTGGTGCAAATTTGTTACTGTGTGGTGTG | 540 |
| Db | 624 | TCAGAGAGGAGGCTAATAGGCTCTCGAAGATCTTGGTGCAAATTTGTTACTGTGTGTGTG | 683 |
| Oy | 541 | AAAGATTTCAATGAGACACAGCTGGCCCGGATGTGGACAAGTAAGATCATGTGTTTCCC | 600 |
| Db | 684 | AAAGATTTCAATGAGACACAGCTGGCCCGGATGTGGACAAGTAAGATCATGTGTTTCCC | 743 |
| Oy | 601 | GTGAATGACGGGCTTTCAGGCTCTCGAAGAGCATATCCACTCAATTTTGAAGAAAGTCTGC | 660 |
| Db | 744 | GTGAATGACGGGCTTTCAGGCTCTCGAAGAGCATATCCACTCAATTTTGAAGAAAGTCTGC | 803 |
| Oy | 661 | ATCGAAATTTTAGACAGCTGAACCAATCCACCATATGTGTGACAGAGATCAATTCAGTGTCTC | 720 |
| Db | 804 | ATCGAAATTTTAGACAGCTGAACCAATCCACCATATGTGTGACAGAGATCAATTCAGTGTCTC | 863 |
| Oy | 721 | GTGAGAGAAACGGCTTCCGACATGCCCGCAACGTGACAAGGGTCTCTGCAAGCTTCAAG | 780 |
| Db | 864 | GTGAGAGAAACGGCTTCCGACATGCCCGCAACGTGACAAGGGTCTCTGCAAGCTTCAAG | 923 |
| Oy | 781 | ATCAATATGCTGGTGTACACTCAATAGAAAGCCCTTTTCTGTGGAAGACACTTAATTTACG | 840 |
| Db | 924 | ATCAATATGCTGGTGTACACTCAATAGAAAGCCCTTTTCTGTGGAAGACACTTAATTTACG | 983 |


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; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-176

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Query Match 98.8%; Score 1090.8; DB 3; Length 5540;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0

| | | | |
|----|------|--|------|
| OY | 1 | ATGACCAAGCGGAGAGCGGAGAGACCTCGGATATCGGCTTCAGATGGCTCTCTTTGGCACT | 60 |
| Db | 144 | ATGGCCACGGCGGAGCGGAGAGACCTCGGATATCGGCTTCAGATGGCTCTCTTTGGCACT | 203 |
| OY | 61 | CTGGTGTCTCATCTGCGCCGGGCAAGAGGGAGCGCAGGAGAGATGGGGGTCCAGCTGTCTAC | 120 |
| Db | 204 | CTGGTGTCTCATCTGGGCGCGGGCAAGAGGGAGCGCAGGAGAGATGGGGGTCCAGCTGTCTAC | 263 |
| OY | 121 | GGCGGATTTGACCTGTACTTTCAATTTTGGACAAATTCAGGAATGTGTCTGCACACTGGAAAT | 180 |
| Db | 264 | GGCGGATTTGACCTGTACTTTCAATTTTGGACAAATTCAGGAATGTGTCTGCACACTGGAAAT | 323 |
| OY | 181 | GAAATCTATTACTTTGTGGAAACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAGAAATG | 240 |
| Db | 324 | GAAATCTATTACTTTGTGGAAACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAGAAATG | 383 |
| OY | 241 | TCCTTTATTTGTTTTCTCCACCAGGAACAACTTTATGAAACTGACAGAAACAGAGAA | 300 |
| Db | 384 | TCCTTTATTTGTTTTCTCCACCAGGAACAACTTTATGAAACTGACAGAAACAGAGAA | 443 |
| OY | 301 | CAAAATCCGTCAAAGGCTTGAAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG | 360 |
| Db | 444 | CAAAATCCGTCAAAGGCTTGAAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG | 503 |
| OY | 361 | CATGAGAGATTTGAAAGGGCCAGTGAGCAGATTTATTAAGAAAACAGCAAGGGTACAGG | 420 |
| Db | 504 | CATGAGAGATTTGAAAGGGCCAGTGAGCAGATTTATTAAGAAAACAGCAAGGGTACAGG | 563 |
| OY | 421 | ACAGCCAGCGTCATCATTTGCTTTTGACTGATGAGAGAACTCCATGAAAGATCTCTTTTCTAT | 480 |
| Db | 564 | ACAGCCAGCGTCATCATTTGCTTTTGACTGATGAGAGAACTCCATGAAAGATCTCTTTTCTAT | 623 |
| OY | 481 | TCAGAGAGGAGGCTTAATAGTCTTCGAAATCTTGGTCAAATTTGTTTACTGTGTGTGTG | 540 |
| Db | 624 | TCAGAGAGGAGGCTTAATAGTCTTCGAAATCTTGGTCAAATTTGTTTACTGTGTGTGTG | 683 |
| OY | 541 | AAAGATTTCAATGAGACACAGCTGGCCGGGATTTGGCGGACAGTAAGAGATCATGTGTTTCC | 600 |
| Db | 684 | AAAGATTTCAATGAGACACAGCTGGCCGGGATTTGGCGGACAGTAAGAGATCATGTGTTTCC | 743 |
| OY | 601 | GTGAATGACGGCTTTCAGGCTCTCGCAAGGCATCATCACTCAATTTTGAAGAAAGTCCCTGC | 660 |
| Db | 744 | GTGAATGACGGCTTTCAGGCTCTCGCAAGGCATCATCACTCAATTTTGAAGAAAGTCCCTGC | 803 |
| OY | 661 | ATCGAAATTCATGACGCTGGAACCATCCACATATGTGACAGAGAGTCAATTCAGATGTCTC | 720 |
| Db | 804 | ATCGAAATTCATGACGCTGGAACCATCCACATATGTGACAGAGAGTCAATTCAGATGTCTC | 863 |
| OY | 721 | GTGAGAGAAAACGGCTTCGACATGTCCCGGACACGTGGAACAGGGTCTCTCGAGACTTCAAG | 780 |
| Db | 864 | GTGAGAGAAAACGGCTTCGACATGTCCCGGACACGTGGAACAGGGTCTCTCGAGACTTCAAG | 923 |
| OY | 781 | ATCATATGACTGGTCACTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACATTTATTAATCTG | 840 |
| Db | 924 | ATCATATGACTGGTCACTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGATTAATTTAATCTG | 983 |
| OY | 841 | TGTCAGAGGCTTATCTTAAAGAAAGTTGGCATGAAAGTGCATCTCAGGTCAGCATGAAAC | 900 |
| Db | 984 | TGTCAGAGGCTTATCTTAAAGAAAGTTGGCATGAAAGTGCATCTCAGGTCAGCATGAAAC | 1043 |
| OY | 901 | GATGGCCCTCTCTTTATATCTCCAGTCTGTCAATCATCAACACACACATCTGTTCGACGGT | 960 |
| Db | 1044 | GATGGCCCTCTCTTTATATCTCCAGTCTGTCAATCATCAACACACATCTGTTCGACGGT | 1103 |

| | | | | | | | | | | | |
|----|------|-------------|--------------|----------|-------------|-------|--------|--------|--------|--------|------|
| Qy | 961 | TCATTCCTGGC | CATGCGCCCTG | CACTCTG | ATCCTG | TCCTG | CCCTAG | CCCTGG | CCCTG | CTCTCG | 1020 |
| Db | 1104 | TCATTCCTGG | CCATGCGCCCTG | CATCTG | TCTG | TCCTG | CCCTAG | CCCTGG | CCCTCT | CTCTCG | 1153 |
| Qy | 1021 | TGCTTCGGCC | CCCTGCTG | CACTGTAT | ATCAAGAG | GGTCC | CTCCAC | CCCTG | CCGAG | 1080 | |
| Db | 1164 | TGCTTCGG | CCCCCTG | CTGCACTG | TATATCAAGAG | GGTCC | CTCCAC | CCCTG | CCGAG | 1223 | |
| Qy | 1081 | GAGAGTGAG | AAAA | 1094 | | | | | | | |
| Db | 1224 | GAGAGTGAG | GAGAGA | 1237 | | | | | | | |

RESULT 5
US-09-918-715-231

! Sequence 231, Application US/09918715
! Publication No. US20030017157A1

```

; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix

```

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; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler

```

; TITLE OF INVENTION: ENDOTHELIAL CELL
; FILE REFERENCE: 1107.00134
;

; CURRENT APPLICATION NUMBER: US/09/91
 ; CURRENT FILING DATE: 2001-08-01
 ;

PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR PUBLICATION NUMBER: 60/224,360

; PRIOR APPLICATION NUMBER: 60/282,850
 ; PRIOR FILING DATE: 2000-04-11

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; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 1.0.1

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; SEQ ID NO 231
; LENGTH: 5540
;

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; TYPE: DNA
; ORGANISM: Homo sapiens

```

US-09-918-715-231

| | | |
|-----------------------|--------|-------|
| Query Match | 98.8%; | score |
| Best Local Similarity | 99.8%; | Pred. |

Matches 1092; Conservative 0; M

1 ATGGCCACGGCGAGCGGAGAGCC

DB 144 A1GCGCAGCGAGAGCGCC

61 C T G G C C A C C G G C A A G
Dy |||||
304 C T C C T C T A T C C C C C A A C

DB 204 CCCCCC1CMLC1GCGCCGGGCAAG

121 GCGGAAIIGACCTGACIICAI
 364 CCGCCATTGACCTCTACCTTCTT

204 GGCAGAA11GACC1G1AC11CA11

281 GAAATCCTATCTTCTGCACT
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DU 329 GHSAICIAI IACIIIGISGASAG

DU 341 GHSAICIAI IACIIIGISGASAG

241 TCCCTTTATGTTTCTCCACCCGAG
DB |||||||

CU 301 CAAATCCGTCAACCCCTAGAGAAAC

444 CAAATCCCTCAACCCCTAGACAAAC

444 CATTACCGATTTGAAACGCGCACTG

| | | | |
|----|--|-----|-----------------------------|
| QY | | 504 | CATGACCAATTTCATAACCCCGCACTC |
| DB | | | |

D0 304 CAGAGGGA11GGAGAGGGCCAG1C

C0 431 AGAGGAGCGCTATCATTTGCTTATG

QY 421 AUCHCAGGICMIMCIIIGCIIIG

| | | |
|----|--|---|
| | US-09-918-715-231 | RESULT 5 |
| | / Sequence 231, Application US/09918715 | |
| | / Publication No. US20030017157A1 | |
| | / GENERAL INFORMATION: | |
| | / APPLICANT: Brad St. Croix | |
| | / APPLICANT: Bert Vogelstein | |
| | / APPLICANT: Kenneth Kinzler | |
| | / TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS | |
| | / FILE REFERENCE: 1107_00134 | |
| | / CURRENT APPLICATION NUMBER: US/09/918_715 | |
| | / CURRENT FILING DATE: 2001-08-01 | |
| | / PRIOR APPLICATION NUMBER: 60/222,599 | |
| | / PRIOR FILING DATE: 2000-08-02 | |
| | / PRIOR APPLICATION NUMBER: 60/224,360 | |
| | / PRIOR FILING DATE: 2000-08-11 | |
| | / PRIOR APPLICATION NUMBER: 60/282,850 | |
| | / PRIOR FILING DATE: 2000-04-11 | |
| | / NUMBER OF SEQ ID NOS: 358 | |
| | / SOFTWARE: FastSeq for Windows Version 3.0 | |
| | / SEQ ID NO 231 | |
| | / LENGTH: 5540 | |
| | / TYPE: DNA | |
| | / ORGANISM: Homo sapiens | |
| | US-09-918-715-231 | |
| | Query Match | 98.8%; Score 1090.8; DB 3; Length 5540; |
| | Best Local Similarity | 99.8%; Pred. No. 0; |
| | Matches 1092; Conservative | 0; Mismatches 2; Indels 0; Gaps 0; |
| QY | 1 ATGGCGACGGGAGCGGAGCCCTGGCATGGGCTTTCAGATGGCTCTTTGGCACT | 60 |
| DB | 144 ATGGCGACGGGAGCGGAGCCCTGGCATGGGCTTTCAGATGGCTCTTTGGCACT | 203 |
| QY | 61 CTGTGTCTCATCTCGCCGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCCTGTAC | 120 |
| DB | 204 CTGTGTCTCATCTCGCCGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCCTGTAC | 263 |
| QY | 121 GGCGATTGACCTGTACTTATTTTGACAATACTAGAATGTGTCTGCACCATTGAAAT | 180 |
| DB | 264 GGCGATTGACCTGTACTTATTTTGACAATACTAGAATGTGTCTGCACCATTGAAAT | 323 |
| QY | 181 GAATCTATTACTTTGTGGAACAGTGGCTCACAAATTCATCAGCCCACAGTTGAAATG | 240 |
| DB | 324 GAATCTATTACTTTGTGGAACAGTGGCTCACAAATTCATCAGCCCACAGTTGAAATG | 383 |
| QY | 241 TCTTTATTTGTTTTCTCCACCCGAGGAACAACCTTAATGAATCTGACAGAAACAGAA | 300 |
| DB | 384 TCTTTATTTGTTTTCTCCACCCGAGGAACAACCTTAATGAATCTGACAGAAACAGAA | 443 |
| QY | 301 CAATCCGTCAGGCTGAGAAGAACTCCAGAAAGTTCTGCCAGAGGAGACATTACATG | 360 |
| DB | 444 CAATCCGTCAGGCTGAGAAGAACTCCAGAAAGTTCTGCCAGAGGAGACATTACATG | 503 |
| QY | 361 CATGAGAGATTGAAAAGGCGCAGTAGACAGATTTATATGAAAACAGCAAAGGTACAGG | 420 |
| DB | 504 CATGAGAGATTGAAAAGGCGCAGTAGACAGATTTATATGAAAACAGCAAAGGTACAGG | 563 |
| QY | 421 AAGCGACGCTCATCTTGTCTTTGATCTGATGAGAACTCCATGAAGATCTCTTTTCTAT | 480 |

DB 564 ACAGCCAGCCTCATCTGCTTTGACTGAGTGGAGAACTCATBAAGTCTCTTTCTAT 623
QY 481 TCAGAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGAATGTTTACTGTGTGTG 540
DB 624 TCAGAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGAATGTTTACTGTGTGTG 683
QY 541 AAAGATTTCAATAGACACAGCTGGCCCGGATTTGGCGACGTAAGATCAATGTGTTCC 600
DB 684 AAAGATTTCAATAGACACAGCTGGCCCGGATTTGGCGACGTAAGATCAATGTGTTCC 743
QY 601 GTGAATGACGCTTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAAGCTGCG 660
DB 744 GTGAATGACGCTTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAAGCTGCG 803
QY 661 ATCGAAATTTAGACAGCTGACCAATCCACATATGTGACAGAGATCATTTCAAGTTGC 720
DB 804 ATCGAAATTTAGACAGCTGACCAATCCACATATGTGACAGAGATCATTTCAAGTTGC 863
QY 721 GTGAGAGGAAACGGCTTCCGACATGCCGCAAGTGGACAGAGGCTCTGACGCTTCAAG 780
DB 864 GTGAGAGGAAACGGCTTCCGACATGCCGCAAGTGGACAGAGGCTCTGACGCTTCAAG 923
QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGACACTTATTTACTG 840
DB 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGACACTTATTTACTG 983
QY 841 TGTCAGAGGCTTATCTTAAAGAAAGTTGGACATGAAAGCTGCACTCCAGGTCAGATGAC 900
DB 984 TGTCAGAGGCTTATCTTAAAGAAAGTTGGACATGAAAGCTGCACTCCAGGTCAGATGAC 1043
QY 901 GATGGGCTCTCTTTTATCTGCAATGTTGTATCATATCAACACACATCTTCTGAGGCT 960
DB 1044 GATGGGCTCTCTTTTATCTGCAATGTTGTATCATATCAACACACATCTTCTGAGGCT 1103
QY 961 TCATCTGAGCAATCGGCTGCTGATCTGTTCTGCTGCTGAGGCTGCTCTCTCTG 1020
DB 1104 TCATCTGAGCAATCGGCTGCTGATCTGTTCTGCTGCTGAGGCTGCTCTCTCTG 1163
QY 1021 TGGTCTGAGGCTCTGCTGCTGATGATTAATCAAGAGGTCCTTCCAGCCCTGCGAG 1080
DB 1164 TGGTCTGAGGCTCTGCTGCTGATGATTAATCAAGAGGTCCTTCCAGCCCTGCGAG 1223
QY 1081 GAGAGTAGAGAAA 1094
DB 1224 GAGAGTAGAGAAA 1237

RESULT 6
US-10-301-822-198
Sequence 198, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatekar, Shubhangt
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MEM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 198
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)...(1838)
US-10-301-822-198

Query Match 98.8%; Score 1090.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGGCGGAGAGGAGGCTTCCGATCTGCTTCAAGGCTCTTTGGGCACT 60
DB 144 ATGGCCACGGCGGAGAGGAGGCTTCCGATCTGCTTCAAGGCTCTTTGGGCACT 203
QY 61 CTGGTCTCATCTGCGCGGCGCAAGGGGAGCGCAGGAGGAGATGGGGGTCCAGCTGTAC 120
DB 204 CTGGTCTCATCTGCGCGGCGCAAGGGGAGCGCAGGAGGAGATGGGGGTCCAGCTGTAC 263
QY 121 GGGGATTTGACCTGTACTTCAATTTTGAACAAATCAGAAAGTGTGCTGACCACTGGAAT 180
DB 264 GGGGATTTGACCTGTACTTCAATTTTGAACAAATCAGAAAGTGTGCTGACCACTGGAAT 323
QY 181 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAATAAT 240
DB 324 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAATAAT 383
QY 241 TCCCTTATGTTTCTCCACCGGAGAACACTTAATGAACTGACAGAAAGAGAA 300
DB 384 TCCCTTATGTTTCTCCACCGGAGAACACTTAATGAACTGACAGAAAGAGAA 443
QY 301 CAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
DB 444 CAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
QY 361 CATGAAGATTTGAAGAGGCTGAGAGCAATGATTAATTAAGAAACAGCAAGGCTACAG 420
DB 504 CATGAAGATTTGAAGAGGCTGAGAGCAATGATTAATTAAGAAACAGCAAGGCTACAG 563
QY 421 ACAGCAGAGGCTATCATGCTTTGAGTGAATGAGAACTCATGAAGATCTCTTTCTAT 480
DB 564 ACAGCAGAGGCTATCATGCTTTGAGTGAATGAGAACTCATGAAGATCTCTTTCTAT 623
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGAATGTTTACTGTGTGTG 540
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGAATGTTTACTGTGTGTG 683
QY 541 AAAGATTTCAATAGACACAGCTGGCCCGGATTTGGCGACGTAAGATCAATGTGTTCC 600
DB 684 AAAGATTTCAATAGACACAGCTGGCCCGGATTTGGCGACGTAAGATCAATGTGTTCC 743
QY 601 GTGAATGACGCTTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAAGCTGCG 660
DB 744 GTGAATGACGCTTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAAGCTGCG 803
QY 661 ATCGAAATTTAGACAGCTGACCAATCCACATATGTGACAGAGATCATTTCAAGTTGC 720
DB 804 ATCGAAATTTAGACAGCTGACCAATCCACATATGTGACAGAGATCATTTCAAGTTGC 863
QY 721 GTGAGAGGAAACGGCTTCCGACATGCCGCAAGTGGACAGAGGCTCTGACGCTTCAAG 780
DB 864 GTGAGAGGAAACGGCTTCCGACATGCCGCAAGTGGACAGAGGCTCTGACGCTTCAAG 923
QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGACACTTATTTACTG 840
DB 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGACACTTATTTACTG 983
QY 841 TGTCAGAGGCTTATCTTAAAGAAAGTTGGACATGAAAGCTGCACTCCAGGTCAGATGAC 900

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Db      984 TGTCCAGCGCTATCTTTAAAAGAAAGTTGGCAGTGAAGAGCTGCACTCCAGGTCAGCATGAAC 1043
Qy      901 GATGCGCTCTCTTTTATCTCCAGTTCTGTATCATCATCACACACACTGTTCTGAAGT 960
Db      1044 GATGCGCTCTCTTTTATCTCCAGTTCTGTATCATCATCACACACACTGTTCTGAAGT 1103
Qy      961 TCCATCTGCGCCATCGCCCTGCTGATCTGTCTCTGCTCCAGCCCTGCTCTCTG 1020
Db      1104 TCCATCTGCGCCATCGCCCTGCTGATCTGTCTCTGCTCCAGCCCTGCTCTCTG 1163
Qy      1021 TGGTTTGGCCCTCTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1080
Db      1164 TGGTTTGGCCCTCTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1223
Qy      1081 GAGAGTGAGGAAAA 1094
Db      1224 GAGAGTGAGGAAAA 1237

RESULT 7
; US-10-474-794-176
; Sequence 176, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-474-794-176

Query Match      98.8%; Score 1090.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGGCCACGCGGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60
Db      144 ATGGCCACGCGGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 203
Qy      61 CTGGTCTCATCTGCGCCCGGGGGAAGGGGAGCGAGGAGAGATGGGGGTCCAGCTCTAC 120
Db      204 CTGGTCTCATCTGCGCCCGGGGGAAGGGGAGCGAGGAGAGATGGGGGTCCAGCTCTAC 263
Qy      121 GGGGAGTTGACCTGTACTTATTTTGGACAATTCAGAAAGTGTGTCGACCACTGGAAT 180
Db      264 GGGGAGTTGACCTGTACTTATTTTGGACAATTCAGAAAGTGTGTCGACCACTGGAAT 323
Qy      181 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCACAAATTCATCGCCCAAGTTGAGAAATG 240
Db      324 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCACAAATTCATCGCCCAAGTTGAGAAATG 383
Qy      241 TCTTTATTTGTTTCTTCCACCCGAGAACCACTTAATGAAATGACAGAAACAGAGAA 300
Db      384 TCTTTATTTGTTTCTTCCACCCGAGAACCACTTAATGAAATGACAGAAACAGAGAA 443
Qy      301 GAAATCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
Db      444 GAAATCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
Qy      361 CATGAAGATTTGAAAAGGCGCACTGAGCAGATTTATATGAAAAACAGACAAAGGTACAG 420
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Db      504 CATGAAGATTTGAAAAGGCGCACTGAGCAGATTTATATGAAAAACAGAAAGGTACAG 563
Qy      421 ACAGCAGGCTCATCTGTTTGAATGATGAGAACTCATGAAGATCTCTTTTCTAT 480
Db      564 ACAGCAGGCTCATCTGTTTGAATGATGAGAACTCATGAAGATCTCTTTTCTAT 623
Qy      481 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGATGCAATTTGTTACTGTGTGTGTG 540
Db      624 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGATGCAATTTGTTACTGTGTGTGTG 683
Qy      541 AAAAGTTTCAATGAAACACAGTGGCCCGGATTTGGGACAGTAAGATTCATGTTTCCC 600
Db      684 AAAAGTTTCAATGAAACACAGTGGCCCGGATTTGGGACAGTAAGATTCATGTTTCCC 743
Qy      601 GTGAATGACGCGCTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTG 660
Db      744 GTGAATGACGCGCTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTG 803
Qy      661 ATCGAAATTTTGAAGCTGAACCATTCACCATATGTGACAGAGATCATTTGAAGTGTG 720
Db      804 ATCGAAATTTTGAAGCTGAACCATTCACCATATGTGACAGAGATCATTTGAAGTGTG 863
Qy      721 GTGAAGAGAAAGGCTTCCGACATGCGCGCAACGTGACAGGCTCTGCAAGCTTCAAG 780
Db      864 GTGAAGAGAAAGGCTTCCGACATGCGCGCAACGTGACAGGCTCTGCAAGCTTCAAG 923
Qy      781 ATCAATGACCTGCGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGACACTAATTTACTG 840
Db      924 ATCAATGACCTGCGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGATCTTATTTACTG 983
Qy      841 TGTCCAGCGCTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGTCAAGTGAAC 900
Db      984 TGTCCAGCGCTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGTCAAGTGAAC 1043
Qy      901 GATGCGCTCTCTTTTATCTCCAGTTCTGTATCATCATCACACACACTGTTCTGAAGT 960
Db      1044 GATGCGCTCTCTTTTATCTCCAGTTCTGTATCATCATCACACACACTGTTCTGAAGT 1103
Qy      961 TCCATCTGCGCCATCGCCCTGCTGATCTGTCTCTGCTCCAGCCCTGCTCTCTG 1020
Db      1104 TCCATCTGCGCCATCGCCCTGCTGATCTGTCTCTGCTCCAGCCCTGCTCTCTG 1163
Qy      1021 TGGTTTGGCCCTCTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1080
Db      1164 TGGTTTGGCCCTCTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1223
Qy      1081 GAGAGTGAGGAAAA 1094
Db      1224 GAGAGTGAGGAAAA 1237

RESULT 8
; US-10-474-794-231
; Sequence 231, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 5540
```

TYPE: DNA
ORGANISM: Homo sapiens
US-10-474-794-231

Query Match 98.8%; Score 1090.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCAGCGGCGAGAGAGCCCTGGGATCGGCTTCCAGTGGCTCTCTTGGCCACT 60
DB 144 ATGGCCAGCGGCGAGAGAGCCCTGGGATCGGCTTCCAGTGGCTCTCTTGGCCACT 203

QY 61 CTGGTCTCATCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 204 CTGGTCTCATCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263

QY 121 GGGGATTTGACCTGTATCTTCAATTTGAGCAAAATCAGAAAGTGTCTGCACTGGAAT 180
DB 264 GGGGATTTGACCTGTATCTTCAATTTGAGCAAAATCAGAAAGTGTGTGCACTGGAAT 323

QY 181 GAAATCTATTACTTTGAGCAAGTGGCTCAAAATTCACAGCCCACTGGAATG 240
DB 324 GAAATCTATTACTTTGAGCAAGTGGCTCAAAATTCACAGCCCACTGGAATG 383

QY 241 TCCCTTATTGTTTCTCCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 384 TCCCTTATTGTTTCTCCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443

QY 301 CAAATCCGTCAAGGCTTGAAGAACTTCAGAAAGTTCGACAGAGAGAGAGAGAGAGAG 360
DB 444 CAAATCCGTCAAGGCTTGAAGAACTTCAGAAAGTTCGACAGAGAGAGAGAGAGAGAG 503

QY 361 CATGAAGAGATTGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 504 CATGAAGAGATTGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563

QY 421 ACAGCCAGGCTCATCTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 564 ACAGCCAGGCTCATCTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623

QY 481 TCAG 540
DB 624 TCAG 683

QY 541 AAGAGATTCAATGAG 600
DB 684 AAGAGATTCAATGAG 743

QY 601 GTGAATGAGAGGCTTTCAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 744 GTGAATGAGAGGCTTTCAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803

QY 661 ATGGAATTTAG 720
DB 804 ATGGAATTTAG 863

QY 721 GTGAG 780
DB 864 GTGAG 923

QY 781 ATGAATGAGAGGCTTTCAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 924 ATGAATGAGAGGCTTTCAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983

QY 841 TGTCCAGGCGCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 984 TGTCCAGGCGCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043

QY 901 GATGGGCTCTCTTTTATCTCAAGTGTGATCATCAACACACACACACACACACACAC 960
DB 1044 GATGGGCTCTCTTTTATCTCAAGTGTGATCATCAACACACACACACACACACACAC 1103

QY 961 TCATCTGAGCATCGGCTGATGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1020

DB 1104 TCATCTGAGCATCGGCTGATGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1163

QY 1021 TGCTTCCGCGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080

DB 1164 TGCTTCCGCGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223

QY 1081 GAGAGTGAAG 1094

DB 1224 GAGAGTGAAG 1237

RESULT 9
US-10-979-159-176
Sequence 176, Application US/10979159
Publication No. US20050142138A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-979-159-176

Query Match 98.8%; Score 1090.8; DB 9; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCAGCGGCGAGAGAGCCCTGGGATCGGCTTCCAGTGGCTCTCTTGGCCACT 60
DB 144 ATGGCCAGCGGCGAGAGAGCCCTGGGATCGGCTTCCAGTGGCTCTCTTGGCCACT 203

QY 61 CTGGTCTCATCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 204 CTGGTCTCATCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263

QY 121 GGGGATTTGACCTGTATCTTCAATTTGAGCAAAATCAGAAAGTGTCTGCACTGGAAT 180
DB 264 GGGGATTTGACCTGTATCTTCAATTTGAGCAAAATCAGAAAGTGTCTGCACTGGAAT 323

QY 181 GAAATCTATTACTTTGAGCAAGTGGCTCAAAATTCACAGCCCACTGGAATG 240
DB 324 GAAATCTATTACTTTGAGCAAGTGGCTCAAAATTCACAGCCCACTGGAATG 383

QY 241 TCCCTTATTGTTTCTCCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 384 TCCCTTATTGTTTCTCCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443

QY 301 CAAATCCGTCAAGGCTTGAAGAACTTCAGAAAGTTCGACAGAGAGAGAGAGAGAGAG 360
DB 444 CAAATCCGTCAAGGCTTGAAGAACTTCAGAAAGTTCGACAGAGAGAGAGAGAGAGAG 503

QY 361 CATGAAGAGATTGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 504 CATGAAGAGATTGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563

QY 421 ACAGCCAGGCTCATCTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

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|||||
Db 564 ACAGCAGGCGTCATCTGCTTTGACTGATGAGAACTCATGAAATCTCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTTAATAGGTCGTGAGATCTTTGGCAATGTTTACTGTTGGTGG 540
Db 624 TCAGAGAGGAGGAGGCTTAATAGGTCGTGAGATCTTTGGCAATGTTTACTGTTGGTGG 683
QY 541 AAAGATTTCAATGAGACACAGCTGGCCCGAATTCGAGAGTAAAGATCATGTTTCCC 600
Db 684 AAAGATTTCAATGAGACACAGCTGGCCCGAATTCGAGAGTAAAGATCATGTTTCCC 743
QY 601 GTGAATGACGCTTTTCAAGCTCTGCAAGCAATCATCACTCAATTTTGAAGAATCTTCC 660
Db 744 GTGAATGACGCTTTTCAAGCTCTGCAAGCAATCATCACTCAATTTTGAAGAATCTTCC 803
QY 661 ATCGAAATTTCTAGCAGCTGAACCATCATATATGCGAGAGATCATTTTAAAGTTTC 720
Db 804 ATCGAAATTTCTAGCAGCTGAACCATCATATATGCGAGAGATCATTTTAAAGTTTC 863
QY 721 GTGAGAGGAAACGCTTCCGACATGCGCCGCAACGTGAGAGGGTCTCTGACAGTTCAAG 780
Db 864 GTGAGAGGAAACGCTTCCGACATGCGCCGCAACGTGAGAGGGTCTCTGACAGTTCAAG 923
QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGAGAGCACTTATTACTG 840
Db 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGAGAGATCTTATTACTG 983
QY 841 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAAGCTCACTCCAGGTCGACATGAAC 900
Db 984 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAAGCTCACTCCAGGTCGACATGAAC 1043
QY 901 GATGGCTCTCTTTTATCTCAAGTTCTGTATCATATCACCACACACACTGTTCTGACGGT 960
Db 1044 GATGGCTCTCTTTTATCTCAAGTTCTGTATCATATCACCACACACACTGTTCTGACGGT 1103
QY 961 TCCATCTTGGCCATTCGCTCTGTATCTGTTCTCTCTCTGAGCCTTCTCTCTG 1020
Db 1104 TCCATCTTGGCCATTCGCTCTGTATCTGTTCTCTCTCTGAGCCTTCTCTCTG 1163
QY 1021 TGGTCTTGGCCCTCTGCTGCACTGATGATTAATCAAGAGGTCCTCCACCCCTGCGAG 1080
Db 1164 TGGTCTTGGCCCTCTGCTGCACTGATGATTAATCAAGAGGTCCTCCACCCCTGCGAG 1223
QY 1081 GAGAGTGAGAGAAA 1094
Db 1224 GAGAGTGAGAGAAA 1237

RESULT 10
US-10-979-159-231
; Sequence 231, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Beir Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-979-159-231
Query Match 98.8%; Score 1090.8; DB 9; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGGCGGAGCGGAGAGCCCTCGCATTCGGCTTCCAGTGGCTCTCTTGGCCACT 60
Db 144 ATGGCCACGGCGGAGCGGAGAGCCCTCGCATTCGGCTTCCAGTGGCTCTCTTGGCCACT 203
QY 61 CTGGGTCTATCTTGGCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 204 CTGGGTCTATCTTGGCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 263
QY 121 GCGGATTTGACCTGTACTTCAATTTTGGACAATGAGAAAGTGTCTGACCACTGGAAT 180
Db 264 GCGGATTTGACCTGTACTTCAATTTTGGACAATGAGAAAGTGTCTGACCACTGGAAT 323
QY 181 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCATGAGCCCAAGTTGAGAAATG 240
Db 324 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCATGAGCCCAAGTTGAGAAATG 383
QY 241 TCCTTTATTTGTTTCTCCACCGGAGGAACAACCTTAATGAATGTACAGAGAAACAGAGA 300
Db 384 TCCTTTATTTGTTTCTCCACCGGAGGAACAACCTTAATGAATGTACAGAGAAACAGAGA 443
QY 301 CAATCCGCTCAAGGCGCTGAAAGAACTCCGAAAGTTCTGCGAGAGAGACACTTAATG 360
Db 444 CAATCCGCTCAAGGCGCTGAAAGAACTCCGAAAGTTCTGCGAGAGAGACACTTAATG 503
QY 361 CATGAAGATTTGAAAGGCGCAAGTGAAGATTTATGAAACAGACAAAGGTTACAG 420
Db 504 CATGAAGATTTGAAAGGCGCAAGTGAAGATTTATGAAACAGACAAAGGTTACAG 563
QY 421 ACAAGCAGCTCATATTTGCTTTGATCTGATGAGAAATCCATGAAGATCTCTTTTCTAT 480
Db 564 ACAAGCAGCTCATATTTGCTTTGATCTGATGAGAAATCCATGAAGATCTCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTTAATAGGTCGTGAGATCTTGGTGCATATTTTACTGTTGGTGG 540
Db 624 TCAGAGAGGAGGCTTAATAGGTCGTGAGATCTTGGTGCATATTTTACTGTTGGTGG 683
QY 541 AAAGATTTCAATGAGACACAGCTGGCCCGAATTCGAGAGTAAAGATCATGTTTCCC 600
Db 684 AAAGATTTCAATGAGACACAGCTGGCCCGAATTCGAGAGTAAAGATCATGTTTCCC 743
QY 601 GTGAATGACGCTTTTCAAGCTCTGCAAGCAATCATCACTCAATTTTGAAGAATCTTCC 660
Db 744 GTGAATGACGCTTTTCAAGCTCTGCAAGCAATCATCACTCAATTTTGAAGAATCTTCC 803
QY 661 ATCGAAATTTCTAGCAGCTGAACCATCATATATGCGAGAGATCATTTTAAAGTTTC 720
Db 804 ATCGAAATTTCTAGCAGCTGAACCATCATATATGCGAGAGATCATTTTAAAGTTTC 863
QY 721 GTGAGAGGAAACGCTTCCGACATGCGCCGCAACGTGAGAGGGTCTCTGACAGTTCAAG 780
Db 864 GTGAGAGGAAACGCTTCCGACATGCGCCGCAACGTGAGAGGGTCTCTGACAGTTCAAG 923
QY 841 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCGACATGAAC 900
Db 984 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCGACATGAAC 1043
QY 901 GATGGCTCTCTTTTATCTCAAGTTCTGTATCATATCACCACACACACTGTTCTGACGGT 960
Db 1044 GATGGCTCTCTTTTATCTCAAGTTCTGTATCATATCACCACACACACTGTTCTGACGGT 1103
QY 961 TCCATCTTGGCCATTCGCTCTGTATCTGTTCTCTCTCTGAGCCTTCTCTCTG 1020
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Db 1104 TCCATCCTGGCCATCGCCCTGCTGATCTGTCTGCTCCTAGCCCTGCTCTCTCTG 1163
Qy 1021 TGGTTCTGGCCCTCTGCTGCTGCTGATATCAAGAGGTCCCTTCAACCCCTCTGCCAG 1080
Db 1164 TGGTTCTGGCCCTCTGCTGCTGCTGATATCAAGAGGTCCCTTCAACCCCTCTGCCAG 1223
Qy 1081 GAGAGTGAGGAAA 1094
Db 1224 GAGAGTGAGGAAA 1237

RESULT 11
US-11-047-278-5
Sequence 5, Application US/11047278
Publication No. US20050196407A1
GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: US/11/047,278
CURRENT FILING DATE: 2005-01-31
PRIOR APPLICATION NUMBER: US/09/970,076
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)..(1835)
US-11-047-278-5

Query Match 98.8%; Score 1090.8; DB 10; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60
Db 144 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTTTGGCCACT 203
Qy 61 CTGGTGTCTATCTGCGCGGCGGAGAGCGGAGAGTGGGGGTCCAGCTGCTAC 120
Db 204 CTGGTGTCTATCTGCGCGGCGGAGAGCGGAGAGTGGGGGTCCAGCTGCTAC 263
Qy 121 GCGGAGTTTGACCTGTATCTTATTTGACAAATCAGAAAGTGTCTGCACTGAGAT 180
Db 264 GCGGAGTTTGACCTGTATCTTATTTGACAAATCAGAAAGTGTCTGCACTGAGAT 323
Qy 181 GAAATCTATTAATTGTGGAAACAGTTGGCTCAAAATTCACGCCACAGTTGAGATG 240
Db 324 GAAATCTATTAATTGTGGAAACAGTTGGCTCAAAATTCACGCCACAGTTGAGATG 383
Qy 241 TCCCTTATTTGTTTCTCCACCCGAGGAAACCTTAATGAAACGACAGAGAGAGAGAA 300
Db 384 TCCCTTATTTGTTTCTCCACCCGAGGAAACCTTAATGAAACGACAGAGAGAGAGAA 443
Qy 301 CAAATCCGTCAAGGCTAGAGAACTCCAGAAAGTCTGCCAGAGAGACACTTACATG 360
Db 444 CAAATCCGTCAAGGCTAGAGAACTCCAGAAAGTCTGCCAGAGAGACACTTACATG 503
Qy 361 CATAGAGATTGAAAGGCGCAGTGAAGCATTTATTTGAAAACAGCAAGGTTACAG 420
Db 504 CATAGAGATTGAAAGGCGCAGTGAAGCATTTATTTGAAAACAGCAAGGTTACAG 563
Qy 421 ACAGCGAGGTCATCATTTGCTTTGACTGATGAGAGAACTCCAGAAAGTCTTTTTCAT 480

Db 564 ACAGCGAGGTCATCATTTGCTTTGACTGATGAGAGAACTCCAGAAAGTCTTTTTCAT 623
Qy 481 TCAGAGAGGAGGCTTAATGATGCTGAGATCTTGGGCAATTTGTTACTGTGTGGTGG 540
Db 624 TCAGAGAGGAGGCTTAATGATGCTGAGATCTTGGGCAATTTGTTACTGTGTGGTGG 683
Qy 541 AAAATTTCAATAGACACAGCTGGCCCGGATTCGAGACAGTAAGATCATGTGTTCC 600
Db 684 AAAATTTCAATAGACACAGCTGGCCCGGATTCGAGACAGTAAGATCATGTGTTCC 743
Qy 601 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTCG 660
Db 744 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTCG 803
Qy 661 ATCGAAATCTAGCAGCTTAACCATCAATATGCGAGAGATTCATTAAGTTGTC 720
Db 804 ATCGAAATCTAGCAGCTTAACCATCAATATGCGAGAGATTCATTAAGTTGTC 863
Qy 721 GTGAGAGAAAAGGCTTCCGACATGCGCCCAAGTGAAGAGGTCTCTGACGCTTCAAG 780
Db 864 GTGAGAGAAAAGGCTTCCGACATGCGCCCAAGTGAAGAGGTCTCTGACGCTTCAAG 923
Qy 781 ATCAATGACTCGGTCACTCAATGAGAAAGCTTTTCTGTGAGACACTTATTTACTG 840
Db 924 ATCAATGACTCGGTCACTCAATGAGAAAGCTTTTCTGTGAGATCTTATTTACTG 983
Qy 841 TGTCCAGCGCTATCTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGTCCAGATGAAC 900
Db 984 TGTCCAGCGCTATCTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGTCCAGATGAAC 1043
Qy 901 GATGAGCTCTCTTATCTCAAGTTGTGATCATGACACACACACTGTTTGAAGGT 960
Db 1044 GATGAGCTCTCTTATCTCAAGTTGTGATCATGACACACACACTGTTTGAAGGT 1103
Qy 961 TCCATCCTGGCCATCGCCCTGCTGATCTGTTCTGCTCTCTGACCTGCTCTCTG 1020
Db 1104 TCCATCCTGGCCATCGCCCTGCTGATCTGTTCTGCTCTCTGACCTGCTCTCTG 1163
Qy 1021 TGGTTCTGGCCCTCTGCTGCTGCTGATATCAAGAGGTCCCTTCAACCCCTGCGAG 1080
Db 1164 TGGTTCTGGCCCTCTGCTGCTGCTGATATCAAGAGGTCCCTTCAACCCCTGCGAG 1223
Qy 1081 GAGAGTGAGGAAA 1094
Db 1224 GAGAGTGAGGAAA 1237

RESULT 12
US-10-038-307-17
Sequence 17, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OKAYMAK
TITLE OF INVENTION: Judith J. HEALEY
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1674
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-17

Query Match 87.0%; Score 960.8; DB 6; Length 1674;
Best Local Similarity 99.8%; Pred. No. 5; 2e-303;
Matches 962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60


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Db      793 ATCAATGACTCGGTCACACTCAATGAGAACCCCTTTCTGTGGAAGTACTTATTTACTG 852
      841 TGTCCAGCGGCTTACTTTAAAGAAAGTTGGCATGAAAGCTGCATCCAGGTCAGCATGAAAC 900
      853 TGTCCAGCGGCTTACTTTAAAGAAAGTTGGCATGAAAGCTGCATCCAGGTCAGCATGAAAC 912
Qy      901 GATGGCCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGTCTTGACGGT 960
      913 GATGGCCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGTCTTGACGGT 972
Db      961 TCCA 964
      973 CCGA 976
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RESULT 14

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US-10-038-307-13
; Sequence 13, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Englin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-13
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Query Match 86.3%; Score 952.4; DB 6; Length 1650;

Best Local Similarity 99.4%; Pred. No. 2.9e-300;

Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      1 ATGGCCAGCGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60
      1 ATGGCCAGCGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60
Db      61 CTGTGTCTCATCTCTCGCGGCGGAGAGCGGAGAGCGGAGAGTGGGGTCCAGCTGTCTAC 120
      61 CTGTGTCTCATCTCTCGCGGCGGAGAGCGGAGAGCGGAGAGTGGGGTCCAGCTGTCTAC 120
Qy      121 GCGGAGTTTGAAGCTGTACTTCTTATTTGGACAATTCAGAAATGATGTGTGCAACACCTGGAAT 180
      121 GCGGAGTTTGAAGCTGTACTTCTTATTTGGACAATTCAGAAATGATGTGTGCAACACCTGGAAT 180
Db      121 GCGGAGTTTGAAGCTGTACTTCTTATTTGGACAATTCAGAAATGATGTGTGCAACACCTGGAAT 180
      121 GCGGAGTTTGAAGCTGTACTTCTTATTTGGACAATTCAGAAATGATGTGTGCAACACCTGGAAT 180
Qy      181 GAAATCTAATTAATTTGGAGACATGTGCTCAAAATTCAGACCCACAGTTGAGATG 240
      181 GAAATCTAATTAATTTGGAGACATGTGCTCAAAATTCAGACCCACAGTTGAGATG 240
Db      181 GAAATCTAATTAATTTGGAGACATGTGCTCAAAATTCAGACCCACAGTTGAGATG 240
      181 GAAATCTAATTAATTTGGAGACATGTGCTCAAAATTCAGACCCACAGTTGAGATG 240
Qy      241 TCCTTTATTTGTTTCTCCAGCCGAGGAAACAATTAAATGAAATGACAGAGAGAGAGAA 300
      241 TCCTTTATTTGTTTCTCCAGCCGAGGAAACAATTAAATGAAATGACAGAGAGAGAGAA 300
Db      241 TCCTTTATTTGTTTCTCCAGCCGAGGAAACAATTAAATGAAATGACAGAGAGAGAGAA 300
      241 TCCTTTATTTGTTTCTCCAGCCGAGGAAACAATTAAATGAAATGACAGAGAGAGAGAA 300
Qy      301 CAAATTCGCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
      301 CAAATTCGCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
Db      301 CAAATTCGCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
      301 CAAATTCGCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
Qy      361 CATAGAAGATTGAAAGGCGAGTGAAGATTTATTTGAAAACAGACAGGGTACAGG 420
      361 CATAGAAGATTGAAAGGCGAGTGAAGATTTATTTGAAAACAGACAGGGTACAGG 420
Db      361 CATAGAAGATTGAAAGGCGAGTGAAGATTTATTTGAAAACAGACAGGGTACAGG 420
      361 CATAGAAGATTGAAAGGCGAGTGAAGATTTATTTGAAAACAGACAGGGTACAGG 420
Qy      421 ACAGCGACGCTCATCATTTGCTTTTGAATGATGAGAGAACTCAATGAAGATCTCTTTTCTAT 480
      421 ACAGCGACGCTCATCATTTGCTTTTGAATGATGAGAGAACTCAATGAAGATCTCTTTTCTAT 480
Db      421 ACAGCGACGCTCATCATTTGCTTTTGAATGATGAGAGAACTCAATGAAGATCTCTTTTCTAT 480
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RESULT 15

US-10-038-307-15

; Sequence 15, Application US/10038307

; Publication No. US20030134786A1

; GENERAL INFORMATION:

; APPLICANT: James B. ROTTMAN

; APPLICANT: Theresa L. O'KEEFE

; APPLICANT: Englin OZKAYNAK

; APPLICANT: Judith J. HEALEY

; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

; FILE REFERENCE: 7853-253-999

; CURRENT APPLICATION NUMBER: US/10/038,307

; CURRENT FILING DATE: 2002-06-28

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 1650

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-038-307-15

Query Match 86.3%; Score 952.4; DB 6; Length 1650;

Best Local Similarity 99.4%; Pred. No. 2.9e-300;

Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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      481 TCAGAGGAGGAGCTAATAGTCTCGAGATCTTGTGCAATGTTTACTGTGTGTGTGTG 540
Db      541 AAAGATTTCAATGAGACACAGCTGCCCCGAGATTGCCAGAGTAAGATCATGTGTTCCC 600
      541 AAAGATTTCAATGAGACACAGCTGCCCCGAGATTGCCAGAGTAAGATCATGTGTTCCC 600
Qy      541 AAAGATTTCAATGAGACACAGCTGCCCCGAGATTGCCAGAGTAAGATCATGTGTTCCC 600
      541 AAAGATTTCAATGAGACACAGCTGCCCCGAGATTGCCAGAGTAAGATCATGTGTTCCC 600
Db      601 GTGAATGACGCTTTTCAAGGCTGTGCAAGGATCATCATCAATTTTGAAGAGTCTGTC 660
      601 GTGAATGACGCTTTTCAAGGCTGTGCAAGGATCATCATCAATTTTGAAGAGTCTGTC 660
Qy      601 GTGAATGACGCTTTTCAAGGCTGTGCAAGGATCATCATCAATTTTGAAGAGTCTGTC 720
      601 GTGAATGACGCTTTTCAAGGCTGTGCAAGGATCATCATCAATTTTGAAGAGTCTGTC 720
Db      661 ATGGAATTTCTACAGCTGTAACCATCAATATGTGAGAGAGTCAATTTCAAGTTGTC 780
      661 ATGGAATTTCTACAGCTGTAACCATCAATATGTGAGAGAGTCAATTTCAAGTTGTC 780
Qy      661 ATGGAATTTCTACAGCTGTAACCATCAATATGTGAGAGAGTCAATTTCAAGTTGTC 780
      661 ATGGAATTTCTACAGCTGTAACCATCAATATGTGAGAGAGTCAATTTCAAGTTGTC 780
Db      721 GTGAGAGAGAAACGCTTCCGACATGCCCCGACAGTGAACAGGCTCTGACGCTTCAAG 780
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Qy      781 ATCAATGACTCGGTCACACTCAATGAGAGCCCTTTTCTGTGGAAGACTTATTTTACTG 840
      781 ATCAATGACTCGGTCACACTCAATGAGAGCCCTTTTCTGTGGAAGACTTATTTTACTG 840
Db      841 TGTCCAGCGGCTTACTTTAAAGAAAGTTGGCATGAAAGCTGCATCCAGGTCAGCATGAAAC 900
      841 TGTCCAGCGGCTTACTTTAAAGAAAGTTGGCATGAAAGCTGCATCCAGGTCAGCATGAAAC 900
Qy      901 GATGGCCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGTCTTGACGGT 960
      901 GATGGCCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGTCTTGACGGT 960
Db      901 GATGGCCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGTCTTGACGGT 960
      901 GATGGCCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGTCTTGACGGT 960
Qy      961 TC 962
      961 TC 962
Db      961 TC 962
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OY 181 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 240
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Db 181 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 240
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|
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OY 241 TCGTTTATTTGTTTTCTCCACCCGAGAACACTTATGAAACTGACAGAGACAGAGAA 300
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Db 241 TCGTTTATTTGTTTTCTCCACCCGAGAACACTTATGAAACTGACAGAGACAGAGAA 300
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OY 301 CAAATCCGTCAGAGGCGCTAGAGAACTCCAGAAAGTCTGCCAGAGAGACACTTACATG 360
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Db 301 CAAATCCGTCAGAGGCGCTAGAGAACTCCAGAAAGTCTGCCAGAGAGACACTTACATG 360
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OY 361 CATGAAGATTGAAAGGCGCAGTGAAGAGATTTATGAAACACAGCAAGGTTACAG 420
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Db 361 CATGAAGATTGAAAGGCGCAGTGAAGAGATTTATGAAACACAGCAAGGTTACAG 420
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OY 421 ACAGCCAGCGTCATCTTGGTTGACTGATGAGAACTCCATGAGATCTTTTCTAT 480
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OY 661 ATCGAAATTTCTGACAGCTGAACCATCCACATATGTGCAAGAGATCATTTCAAGTTGTC 720
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Db 661 ATCGAAATTTCTGACAGCTGAACCATCCACATATGTGCAAGAGATCATTTCAAGTTGTC 720
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OY 721 GTGAGAGAAACGCGCTTCCGACATGCGCCGCAAGTGGACAGGCTCTGACAGCTTCAAG 780
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Db 721 GTGAGAGAAACGCGCTTCCGACATGCGCCGCAAGTGGACAGGCTCTGACAGCTTCAAG 780
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OY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACACTTATTTACTG 840
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Db 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGATCTTATTTACTG 840
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OY 841 TGTCCAGCGCCTATCTTAAAGAGTTGGATGAAAGCTCACTCCAGGTCAAGCATGAAC 900
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Db 841 TGTCCAGCGCCTATCTTAAAGAGTTGGATGAAAGCTCACTCCAGGTCAAGCATGAAC 900
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OY 901 GATGCGCTCTCTTTTATCTCAAGTTGTGCATCATCAACACACACTGTTCTGACGGT 960
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Db 901 GATGCGCTCTCTTTTATCTCAAGTTGTGCATCATCAACACACACTGTTCTCCCAAA 960
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OY 961 TC 962
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Db 961 TC 962
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Job time : 1019.43 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 13:29:40 ; Search time 200.365 Seconds
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2700.811 Million cell updates/sec

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Perfect score: 1104
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Scoring table: IDENTITY_NUC
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-----------------------|-------------------|
| 1 | 1090.8 | 98.8 | 5540 | 7 US-11-186-284-198 | Sequence 198, App |
| 2 | 61.4 | 5.6 | 2765 | 6 US-10-750-185-25275 | Sequence 25275, A |
| 3 | 36.4 | 3.3 | 201 | 6 US-10-995-561-83675 | Sequence 83675, A |
| 4 | 35.6 | 3.2 | 2368 | 6 US-10-131-826A-423 | Sequence 423, App |
| 5 | 35.2 | 3.2 | 201 | 6 US-10-995-561-83660 | Sequence 83660, A |
| 6 | 35.2 | 3.2 | 201 | 6 US-10-995-561-83669 | Sequence 83669, A |
| 7 | 35.2 | 3.2 | 201 | 6 US-10-995-561-83674 | Sequence 83674, A |
| 8 | 35.2 | 3.2 | 201 | 6 US-10-995-561-83814 | Sequence 83814, A |
| 9 | 35.2 | 3.2 | 201 | 6 US-10-995-561-83925 | Sequence 83925, A |
| 10 | 35.2 | 3.2 | 2016 | 7 US-11-029-003-7 | Sequence 7, Appl1 |
| 11 | 34.8 | 3.2 | 201 | 6 US-10-995-561-83647 | Sequence 83647, A |
| 12 | 34.8 | 3.2 | 201 | 6 US-10-995-561-83658 | Sequence 83658, A |
| 13 | 34.8 | 3.2 | 40000 | 6 US-10-995-561-13509 | Sequence 13509, A |
| 14 | 34.6 | 3.1 | 6000 | 6 US-10-750-185-21593 | Sequence 21593, A |
| 15 | 34.6 | 3.1 | 4856 | 6 US-10-750-185-43111 | Sequence 43111, A |
| 16 | 34.4 | 3.1 | 201 | 6 US-10-995-561-83654 | Sequence 83654, A |
| 17 | 34.4 | 3.1 | 153376 | 7 US-11-121-086-5 | Sequence 5, Appl1 |
| 18 | 34.2 | 3.1 | 918 | 6 US-10-750-185-62250 | Sequence 62250, A |
| 19 | 34 | 3.1 | 1449 | 6 US-10-821-234-561 | Sequence 561, App |
| 20 | 33.8 | 3.1 | 96716 | 6 US-10-995-561-13331 | Sequence 13331, A |
| 21 | 33.8 | 3.1 | 134499 | 7 US-11-117-187-192 | Sequence 192, App |
| 22 | 33.6 | 3.0 | 201 | 6 US-10-995-561-70418 | Sequence 70418, A |
| 23 | 33.6 | 3.0 | 1054 | 6 US-10-750-185-58946 | Sequence 58946, A |

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|------|------|-----|--------|-----------------------|--------------------|
| C 24 | 33.6 | 3.0 | 28499 | 6 US-10-995-561-13420 | Sequence 13420, A |
| C 25 | 32.8 | 3.0 | 154548 | 7 US-11-121-086-33 | Sequence 33, Appl1 |
| C 26 | 32.6 | 3.0 | 1838 | 6 US-10-750-185-60565 | Sequence 60565, A |
| C 27 | 32.4 | 2.9 | 1005 | 6 US-10-858-730-191 | Sequence 191, App |
| C 28 | 32.2 | 2.9 | 1841 | 6 US-10-750-185-55750 | Sequence 55750, A |
| C 29 | 32 | 2.9 | 2553 | 7 US-11-126-468-25 | Sequence 25, Appl1 |
| C 30 | 32 | 2.9 | 3010 | 6 US-10-750-185-36112 | Sequence 36112, A |
| C 31 | 32 | 2.9 | 139054 | 7 US-11-121-086-96 | Sequence 96, Appl1 |
| C 32 | 32 | 2.9 | 155989 | 7 US-11-121-086-57 | Sequence 57, Appl1 |
| C 33 | 32 | 2.9 | 193363 | 7 US-11-112-908-32 | Sequence 32, Appl1 |
| C 34 | 31.8 | 2.9 | 3388 | 6 US-10-750-185-34560 | Sequence 34560, A |
| C 35 | 31.8 | 2.9 | 176503 | 7 US-11-121-086-53 | Sequence 53, Appl1 |
| C 36 | 31.6 | 2.9 | 3040 | 6 US-10-750-185-48628 | Sequence 48628, A |
| C 37 | 31 | 2.8 | 655 | 6 US-10-750-185-29911 | Sequence 29911, A |
| C 38 | 31 | 2.8 | 187745 | 7 US-11-121-086-83 | Sequence 83, Appl1 |
| C 39 | 30.8 | 2.8 | 1785 | 6 US-10-750-185-50775 | Sequence 50775, A |
| C 40 | 30.8 | 2.8 | 3505 | 7 US-11-000-463-560 | Sequence 560, App |
| C 41 | 30.8 | 2.8 | 3551 | 7 US-11-000-463-88 | Sequence 88, Appl1 |
| C 42 | 30.6 | 2.8 | 1118 | 6 US-10-750-185-54797 | Sequence 54797, A |
| C 43 | 30.6 | 2.8 | 1371 | 7 US-11-102-240-27 | Sequence 27, Appl1 |
| C 44 | 30.6 | 2.8 | 1655 | 6 US-10-750-185-59355 | Sequence 59355, A |
| C 45 | 30.6 | 2.8 | 85682 | 7 US-11-117-187-205 | Sequence 205, App |

ALIGNMENTS

```
RESULT 1
US-11-186-284-198
; Sequence 198, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)...(1838)
US-11-186-284-198
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Query Match 98.8%; Score 1090.8; DB 7; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCAGCGCGAGCGAGAGCCCTTGGCAGTGGCTTTCAGTGGCTCTTTGGCACT 60
DB 144 ATGGCCAGCGCGAGCGAGAGCCCTTGGCAGTGGCTCTTCAGTGGCTCTTTGGCACT 203

QY 61 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGAGGGAGATGGGGGTCCAGCTGTAC 120
DB 204 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGAGGGAGATGGGGGTCCAGCTGTAC 263
QY 121 GGGGGATTTGACCTGTACTTCAATTTTGGAGAAATCGAGAAAGTGTGTGCACTGTGAAT 180
DB 264 GGGGGATTTGACCTGTACTTCAATTTTGGAGAAATCGAGAAAGTGTGTGCACTGTGAAT 323
QY 181 GAAATCTATTACTTTGGAGCAAGTTGGCTCAAAATTCATGACCCACAGTTGAGAATG 240
DB 324 GAAATCTATTACTTTGGAGCAAGTTGGCTCAAAATTCATGACCCACAGTTGAGAATG 383
QY 241 TCCTTATTGTTTTCTCCACCAGAGAAACCTTAATGAACTGACAGAGACAGAGAA 300
DB 384 TCCTTATTGTTTTCTCCACCAGAGAAACCTTAATGAACTGACAGAGACAGAGAA 443
QY 301 CAAATCCGTCAAGGCTTAGAAACCTCCAGAAAGTTCTGCAGAGAGAGACATTACATG 360
DB 444 CAAATCCGTCAAGGCTTAGAAACCTCCAGAAAGTTCTGCAGAGAGAGACATTACATG 503
QY 361 CATGAAGATTTGAAAGGCGAGTAGAGAGATTTATATGAAACAGACAGGGTACAGG 420
DB 504 CATGAAGATTTGAAAGGCGAGTAGAGAGATTTATATGAAACAGACAGGGTACAGG 563
QY 421 ACAGCAGCGTCATCATCTGCTTGTGATGAGAACTCCATGAGATCTTTTCTAT 480
DB 564 ACAGCAGCGTCATCATCTGCTTGTGATGAGAACTCCATGAGATCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGGTGCAATTTTAACTGTGTGTGTG 540
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGGTGCAATTTTAACTGTGTGTGTG 683
QY 541 AAAGATTTTCAATAGACACAGCTGCGCCGGATGGCGGACAGTAAGATCATGTGTCC 600
DB 684 AAAGATTTTCAATAGACACAGCTGCGCCGGATGGCGGACAGTAAGATCATGTGTCC 743
QY 601 GTGAATGACGCGCTTTCAGGCTTCGAAAGCATCATCTCAATTTTGAAGAAGTCTGC 660
DB 744 GTGAATGACGCGCTTTCAGGCTTCGAAAGCATCATCTCAATTTTGAAGAAGTCTGC 803
QY 661 ATGGAATTTTACAGCTGAAACATTCACCATATGTGCGAGAGAGTCAATTTCAAGTTGC 720
DB 804 ATGGAATTTTACAGCTGAAACATTCACCATATGTGCGAGAGAGTCAATTTCAAGTTGC 863
QY 721 GTGAGAGAAAGGCTTCCGACATGCGCCGCAAGGTGAGCAAGGCTCTGCAGCTTCAAG 780
DB 864 GTGAGAGAAAGGCTTCCGACATGCGCCGCAAGGTGAGCAAGGCTCTGCAGCTTCAAG 923
QY 781 ATCAATGACTCGTCACTCAATGAGAAAGCTTTTGTGTGAGAGACATTATTTACTG 840
DB 924 ATCAATGACTCGTCACTCAATGAGAAAGCTTTTGTGTGAGAGACATTATTTACTG 983
QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCAGACATGAAC 900
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCAGACATGAAC 1043
QY 901 GATGAGCTCTCTTTATCTCAGTTCATCATCAACACACACAGCTTTGAGCGGT 960
DB 1044 GATGAGCTCTCTTTATCTCAGTTCATCATCAACACACACAGCTTTGAGCGGT 1103
QY 961 TCCATCTGTGCGCATGCGCCCTGATCTGTCTGTCTGTAGCCCTGTGCTCTCTG 1020
DB 1104 TCCATCTGTGCGCATGCGCCCTGATCTGTCTGTCTGTAGCCCTGTGCTCTCTG 1163
QY 1021 TGGTTCTGCGCCCTGTGCTGCACTGTGATATCAAGAGAGTCCCTGACCCCTGCCGAG 1080
DB 1164 TGGTTCTGCGCCCTGTGCTGCACTGTGATATCAAGAGAGTCCCTGACCCCTGCCGAG 1223
QY 1081 GAGAGTGAGGAAAA 1094
DB 1224 GAGAGTGAGGAAAA 1237

RESULT 2
US-10-185-25275/c
; Sequence 25275, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MVI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent version 3.1
; SEQ ID NO 25275
; LENGTH: 2765
; TYPE: DNA
; ORGANISM: Bovine 19866881163262
US-10-750-185-25275

Query Match 5.6%; Score 61.4; DB 6; Length 2765;
Best Local Similarity 77.9%; Pred. No. 1.9e-09;
Matches 74; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CATCATCCACATCAATTTGAGAAAGTCTGCATCGAAATTTAGACGCTGAACATCCAC 689
DB 211 CCTTCCTCTCATGATATTTGAGAAATCCTGCATCGAAATTTAGACGCTGAACATCCAC 152
QY 690 CATATGTGAGAGAGTCAATTTCAAGTGTCTGA 724
DB 151 CATATGTGAGAGAGTCAATTTGAACTAAGTGTTA 117

RESULT 3
US-10-995-561-83675
; Sequence 83675, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83675
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83675

Query Match 3.3%; Score 36.4; DB 6; Length 201;
Best Local Similarity 62.5%; Pred. No. 0.059;
Matches 55; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 928 GTATCATACACACACACACATGTTCTGACGGTTCATCTGCGCATGCGCCGCTGATC 987
DB 69 GTATCATACACACACACACATGTTCTGACGGTTCATCTGCGCATGCGCCGCTGATC 128
QY 988 CTGTTCTGTCTCTGACCTGCTGCTCC 1015
DB 129 CTGACACACCGCTGCTCTCACTGACC 156

RESULT 4

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US-10-131-826A-423/C
; Sequence 423. Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanyoyers, Luc
; APPLICANT: Elivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerilleen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matarabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P333ORC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 423
; LENGTH: 2368
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-423

Query Match      3.2%; Score 35.6; DB 6; Length 2368;
Best Local Similarity 50.6%; Pred. 0.54;
Matches 86; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      884   TCACAGTCAGCATGAACAATGCGCTCTTTTATCTCCAGTTCGTCAATCAACCACCA    943
          |||||
DB      1002   TCACACACGACGCCAACGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA    943
          |||||

QY      944   CACACTGTTCAGCGATTTCATCTCAGGCATCGCGCCCTGGTGATTCCTGTTCGTCTCTAG    1003
          |||||
DB      942   AGATCTTCTTCTCTCTCTCTCTCATCATCTACAAAGCGTCTTTTCTTCTCTTCAATTGA    883
          |||||

QY      1004  CCTGAGCTCTCTCTGTGAGTTCGTGAGCCCTCTGCTGCACGTGTATATC    1053
          |||||
DB      882   TCATCTTTTCTCTCTCTCCGCACTCGCAACTGTTCAGCTCTATGAGCCTC    833
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RESULT 5
US-10-995-561-83660
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; Sequence 83660, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83660
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83660

Query Match      3.2%; Score 35.2; DB 6; Length 201;
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0

QY      928  GTCAATCATCACCAACACACTGTTCTGACGGTTCCATCTGGCCATGCGCCTGCTGATC 987
      |||||
DB      44  GTCAATCATCCCGACGACGTAAGTCCCGGGACACCAACACGACATGCGGCTGCTGAC 103
      |||||

QY      988  CTGTTCTGCTCTTCAAGCCCTGGCTCTCC 1015
      |||||
DB      104  CTGCACCAAGCCCGGTGTTCTTCACTGACC 131
      |||||

RESULT 6
US-10-995-561-83669
; Sequence 83669, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83669
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83669

Query Match      3.2%; Score 35.2; DB 6; Length 201;
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0

QY      928  GTCAATCATCACCAACACACTGTTCTGACGGTTCCATCTGGCCATGCGCCTGCTGATC 987
      |||||
DB      29  GTCAATCATCCCGACGACGTAAGTCCCGGGACACCAACACGACATGCGGCTGCTGAC 88
      |||||

QY      988  CTGTTCTGCTCTTCAAGCCCTGGCTCTCC 1015
      |||||
DB      89  CTGCACCAAGCCCGGTGTTCTTCACTGACC 116
      |||||

RESULT 7
US-10-995-561-83674
; Sequence 83674, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83674
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83674

Query Match      3.2%; Score 35.2; DB 6; Length 201;
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0

QY      928  GTCAATCATCACCAACACACTGTTCTGACGGTTCCATCTGGCCATGCGCCTGCTGATC 987
      |||||
DB      29  GTCAATCATCCCGACGACGTAAGTCCCGGGACACCAACACGACATGCGGCTGCTGAC 88
      |||||

QY      988  CTGTTCTGCTCTTCAAGCCCTGGCTCTCC 1015
      |||||
DB      89  CTGCACCAAGCCCGGTGTTCTTCACTGACC 116
      |||||

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/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 83674
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-83674

Query Match
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACACACACACACTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 79 GTCATCATCCCGACGACGATCGMCCGGGACACACACACGACATCGCGCTGCTCCGC 138

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 139 CTGCACACAGCCCGTGTGCTCTCACTGACC 166

RESULT 8
US-10-995-561-83814
/ Sequence 83814, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 83814
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-83814

Query Match
Best Local Similarity 3.2%; Score 35.2; DB 6; Length 201;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACACACACACACTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 43 GTCATCATCCCGACGACGATCGMCCGGGACACACACACGACATCGCGCTGCTCCGC 102

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 103 CTGCACACAGCCCGTGTGCTCTCACTGACC 130

RESULT 9
US-10-995-561-83925
/ Sequence 83925, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 83925
/ LENGTH: 201
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/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-83925

Query Match
Best Local Similarity 3.2%; Score 35.2; DB 6; Length 201;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACACACACACACTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 112 GTCATCATCCCGACGACGATCGMCCGGGACACACACACGACATCGCGCTGCTCCGC 171

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 172 CTGCACACAGCCCGTGTGCTCTCACTGACC 199

RESULT 10
US-11-029-003-7
/ Sequence 7, Application US/11029003
/ Publication No. US20050260194A1
/ GENERAL INFORMATION:
/ APPLICANT: PETERS, ROBERT T.
/ APPLICANT: MEZO, ADAM R.
/ APPLICANT: RIVERA, DANIEL S.
/ APPLICANT: BITONTI, ALAN J.
/ APPLICANT: STATTEL, JAMES
/ TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
/ FILE REFERENCE: 08945.0007-01000
/ CURRENT APPLICATION NUMBER: US/11/029,003
/ CURRENT FILING DATE: 2005-01-05
/ PRIOR APPLICATION NUMBER: 60/539,207
/ PRIOR FILING DATE: 2004-01-26
/ PRIOR APPLICATION NUMBER: 60/487,964
/ PRIOR FILING DATE: 2003-07-17
/ PRIOR APPLICATION NUMBER: 60/469,600
/ PRIOR FILING DATE: 2003-05-06
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 7
/ LENGTH: 2016
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-029-003-7

Query Match
Best Local Similarity 3.2%; Score 35.2; DB 7; Length 2016;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACACACACACACTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 796 GTCATCATCCCGACGACGATCGMCCGGGACACACACACGACATCGCGCTGCTCCGC 855

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 856 CTGCACACAGCCCGTGTGCTCTCACTGACC 883

RESULT 11
US-10-995-561-83647
/ Sequence 83647, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
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; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83647
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83647

Query Match
Best Local Similarity 61.4%; Pred. No. 0.2;
Matches 54; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTGATCATCACCAACACACTGTTCTGAGGTTCCATCTGGCCATCGCCCTGCTGATC 987
Db 52 GTGATCATCCCCAGCAGTACGTCCTCCGGGACCAACCAACGACATCGTGTCTCCG 111

QY 988 CTGTTCTGCTCTAGCCCTGCTGCTCC 1015
Db 112 CTGCACCAAGCCCGTGTCTCCTCCTGACC 139

RESULT 12
US-10-995-561-83658
; Sequence 83658, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83658
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83658

Query Match
Best Local Similarity 61.4%; Pred. No. 0.2;
Matches 54; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTGATCATCACCAACACACTGTTCTGAGGTTCCATCTGGCCATCGCCCTGCTGATC 987
Db 53 GTGATCATCCCCAGCAGTACGTCCTCCGGGACCAACCAACGACATCGGCTGCTCCG 112

QY 988 CTGTTCTGCTCTAGCCCTGCTGCTCC 1015
Db 113 CTGCACCAAGCCCGTGTCTCCTCCTGACC 140

RESULT 13
US-10-995-561-13509
; Sequence 13509, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13509
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13509

Query Match
Best Local Similarity 59.1%; Pred. No. 6.4;
Matches 52; Conservative 4; Mismatches 32; Indels 0; Gaps 0;

QY 928 GTGATCATCACCAACACACTGTTCTGAGGTTCCATCTGGCCATCGCCCTGCTGATC 987
Db 33430 GTGATCATCCCCAGCAGTACGTCCTCCGGGACCAACCAACGACATCGTGTCTCC 33489

QY 988 CTGTTCTGCTCTAGCCCTGCTGCTCC 1015
Db 33490 CTGCACCAAGCCCGTGTCTCCTCCTGACC 33517

RESULT 14
US-10-750-185-21593
; Sequence 21593, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21593
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-21593

Query Match
Best Local Similarity 48.6%; Pred. No. 0.47;
Matches 85; Conservative 3; Mismatches 87; Indels 0; Gaps 0;

QY 195 TGTGAACAGTTGGCTCACAAATTCAATGAGCCACAGTTGAGAAATGCTTATTGTTT 254
Db 398 TATGTTGATTTTCTCAGGATCTCTTCAATTGAAATTACAGTGTGAGGGGAACGTA 457

QY 255 CTCACCCGAGGAACCTTAATGAATGACGAAGACAGAACTTCCGTCAGG 314
Db 458 YAGTRAGAGGGCGACCAACGAAGAAAGAAAGACCACTTAATAGCGAGTAGT 517

QY 315 CTTAGAAAGAACTTCCAGAACTTCTCCAGGAGAGACCTTACATGCTAAGGA 369
Db 518 CTGAAGGACAGCTAGCAACTCTGAAGGAGAGAGACTTACTTGAAGGTGAGA 572

RESULT 15
US-10-750-185-43111
; Sequence 43111, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
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/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43111
/ LENGTH: 4856
/ TYPE: DNA
/ ORGANISM: Bovine 1986680415951
US-10-750-185-43111

Query Match 3.1%; Score 34.6; DB 6; Length 4856;
Best Local Similarity 50.3%; Pred. No. 1.9;
Matches 85; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 886 CAGGTGAGCATGAAAGATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCACCACACA 945
DB 3707 CTGTACACATGCTGTGGCCGCTTCAAGATGATGCTACTTCTCATCATCTCAAC 3766
QY 946 CACTGTTTGAGCGGTTCATCTGGGCATGCGCCCTGCTGATCTCTGTTCTGCTCTAGCC 1005
DB 3767 CACATGCTCTCCCTTCATGATCACCCCTGAGCTGCCCATCTTCATCTCTGATCC 3826
QY 1006 CTGGCTCTCCTCTGATGATCTGGCCCTCTGCTGCACTGTGATATCA 1054
DB 3827 ATGCTGTCCATCCCTGCGCCACAGGCACTTCTGATGATGAGCATCA 3875

Search completed: December 17, 2005, 18:54:55
Job time : 203.369 secs

us-09-970-076-1 copy_104_1207.rai

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RESULT 1
US-10-104-047-263
; Sequence 2639
; Patent No. 694
; GENERAL INFORMATION
; APPLICANT: HEIT

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/ FILE REFERENCE
/
/ CURRENT APPLIC
/ CURRENT FILING
/ PRIOR APPLICAT
/ PRIOR FILING I
/
/ NUMBER OF SEQ
/
/ SOFTWARE: Paten
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; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens

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1

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Alignment Scores
Pred. No.:
Score:
Percent Similarity
Best Local Similarity
Query Match:
DB:
US-09-970-076-1_
QY 10 GCC
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Db 3 Al
QY 70 ATTC
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ALIGN=15
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Alignment Scores:

| Pred. No.: | Description |
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| Percent Similarity | |
| Best Local Similida | |
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| | Sequence 46, Appl |

US-09-970-076-1 0

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| nuence 46, | Appl | | QY | 10 Gcc |
| nuence 46, | Appl | | | |
| nuence 46, | Appl | | | |
| nuence 46, | Appl | | Db | 3 Alpc |
| nuence 46, | Appl | | | |
| nuence 53, | Appl | | QY | 70 Atnc |
| nuence 53, | Appl | | | ::: |

Db 23 ValIeuSerGlyProGlyLeuLeuAaXgAlaInGluInProSerCySaAaGAla 42

Qy 127 TTGACCTGCTACTTCACTTTTGGACAAATCAAGAAAGTGTGTGTGACCACTGGAATGAAATC 186

Db 43 PheAapLeuTyPheValLeuAapLysSerGlySerValAlaAaasnPrIleGluIle 62

Qy 187 TATTACTTGTGGAACAGTTGGCTGCAAAATTCATCAGGCCACAGTTGAGTAATGTCTTT 246

Db 63 TyrAapPheValGInGInLeuAlaGluAapPheValSerProGluMetAaGlySerPhe 82

Qy 247 ATTGTTTTCGCCACCCGGAACCAACCTTAATGAACTGACAGAGAACAGAGAACAATC 306

Db 83 IleValPheSerSerGlnAlaThrIleIleLeuProLeuThrGlyAapGlyLysIle 102

Qy 307 CGTCAAGGCTTGAAGAATCTCCAGAAAGTTCTGCCAGAGAGAACACTTTCATGCTATGA 366

Db 103 SerLysGlyLeuGlnAapLysPheLysValSerProValGlyGluThrTyrlleHsGlu 122

Qy 367 GGATTGTGAAGGGCCGAGTGGAGATTTATTAAGAAACAGAACAGGGGTACAGAGACGCC 426

Db 123 GlyLeuLysLeuAlaMetGluInIle-----GlnLysAlaGlyLeuLysTrpSer 140

Qy 427 AGCGTCATCATTTGCTTGACTGATGAGAACCTCCATGAAGATCTTTTCTATTCCAGAG 486

Db 141 SerIleIleIleAlaLeuThrAapGlyLysLeuAapGlyLeuValProSerTyrlaGlu 160

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Db 161 LysGlnAlaLysIleSerAaPserLeuGlyAlaSerValTyrcySaValGlyValLeuAap 180

Qy 547 TTCATATGACACAGCTGGCCGGATTTGGGGAACAGTAAGATCATGATGTTCCCGAAT 606

Db 181 PheGluGlnAlaGlnLeuGluAaTrgIleAlaAapSerLysGluGlnAlaPheProValLys 200

Qy 607 GACGCGCTTCAGGCTCTGCAGAGCATATCATCTCAATTTTGAAGAAGTCTCCATCGAA 666

Db 201 GLyGlyPheGlnAlaLeuLysGlyIleIleAaSerIleLeuAlaGlnSerCySthrGlu 220

Qy 667 ATTCTAGACGTGAACCATCCACCATATGTGCAGAGAGTCAATTTCAAAGTTGTGTGAGA 726

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Qy 727 GGAAACGGCTTCGCAATGCCGCCAACGTGCAAGGTCCTCTGCGACCTTCAGATCAAT 786

Db 241 GlyAaGlyPheMetLeuGlySerAaGanglySerValLeuCySthrTyrlThrValAsn 260

Qy 787 GACTCGGTACACTCATGAGAAGACCCCTTTCTGTGGAGAACAATTATTACTGTGTCGA 846

Db 261 GlnThrTyrlThrThrSerValLysProValSerValGlnLeuAaasnMetLeuCyPro 280

Qy 847 GCGCTATCTTAAGAAGCTGGCATGAAAGCTGCACTCCAGGTCAAGCATGAACATGATGC 906

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Qy 907 CTCTCTTTATCTCCAGTCTGTGCATCATCAACAACAACAAGTTCAGAGGTTCCATC 966

Db 301 LysSerValIleSerLysLeuIleValThrAlaThrGluCySeraaanglyIleAla 320

Qy 967 CTGGCAGTGCCTCTGTGATCCGTTCTGCTGCTCTAGCCCTGGCTCTCCCTGGTGGTTC 1026

Db 321 AlaIleIleValIleLeuValLeuLeuLeuLeuLeuGlyIleGlyLeuMetTrpTrpPhe 340

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Db 341 TrpProLeuCyecyAlaLysValValIleLysAapProProProProAlaProAlaPro 360

Qy 1078 ---GAGGAGAGTGAAGAA 1092

Db 361 LysGluGluGluGluGlu 366

RESULT 2

US-08-286-889-46

i Sequence 46, Application US/08286889

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; Patent No.5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Macker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0., Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-889-46

Alignment Scores:
Pred. No.:      2.9e+09          length:    1155
Score:         166.00           Matches:   66
Percent Similarity: 46.15%     Conservative: 42
Best Local Similarity: 28.21%   Mismatches: 96
Query Match:    8.29%          Indels:    30
DB:             1              Gaps:       12
US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-286-889-46 (1-1155)

QY      CCAGCGCTGTCACGGC--GGAATTGACTGTACTTCAATTTTGACAATAATCCAGAAGTGTG 1655
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QY      166 ---CTGCACCACTGSAAATGAATCTATTACTTTGTTCGGAACAGTGGCTCACAAATTCATC 2222
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QY      AGCCACAGTTGAGATGTCCTTTATTGTTTTCTCCACCAGAGAACCAACTTAATGAAA 2822
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Db      184 SerThrSerThrSerPheSerLeuMetgIntyrSeAsnilleuleulysthrrhspeThr 2033
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QY      CTGCAGAGACAGCAGA-----GAACAATCCGTCAAGGCCCTTAGAAGAACTC 3277
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Db      204 PhethrIgluphelNylSerSerLeuSerProginSerLeuvalAspalatlevalgIntlu 2233
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QY      CAGAAAGTTCTGCCAGAGAGAGACACTTACATGCATGAAGATTGAAAAAGGCCCACTGAG 3877
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Db      224 Glu-----GlyLeuthryTrhrAlaseGlylleGINYSVALVALLYS 2388
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QY      CAGATTATTATGAABAACGACMAAGGTCACAGAGACGC---AGCGTCATCATTTGCTTTG 4444
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Db 239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLysIleLeuIleValIle 258
Qy 445 ACTGATGAGAACTCCATGAGATCTCTTTTATTATTCAGAG-----AGGAGGCTAAT 498
Db 259 ThrAspGlyGlnLysPheArgAspProLeuGluTyrArgHisValIleProGluAlaGlu 278
Qy 499 AGGTCGAGATCTTGTGCAATGTTTACTGTGTGGGTGGAAGAT---TTCATGAG 555
Db 279 LysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAspAlaPheArgGlu 295
Qy 556 ---ACACAGCTGGCCCGGATT-----GCGACAGTAAGATCATGTGTT 597
Db 296 ProThrAlaLeuGlnGluLeuAsnThrIleGlySerAlaProSerGlnPheHisValPhe 315
Qy 598 CCCGTGAATGACGGCTTTACAGCTCTGCAAGGATCATCATCATTTTGAAGAAGTCC 657
Db 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGluLys--- 333
Qy 658 TGCATGGAATTTCACAGCTGCAACATCCACATATGTGCAGAGAGTCAATTCAAGTT 717
Db 334 -----IlePheAlaIleGlnGlyThrGluSerArgSerSerSerPheGlnHis 350
Qy 718 GTCGTAGAGAAACGGCTTCCGACATGCCCGCAGAGTGGAC 759
Db 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 3
US-08-485-618-46
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-485-618-46
Alignment Scores:
Pred. No.: 2.9e-09
Score: 166.00
Percent Similarity: 46.15%
Best Local Similarity: 28.21%
Query Match: 8.29%
DB: 1
Gaps: 12

US-09-970-076-1_copy_104_1207 (1-1104) x US-08-485-618-46 (1-1155)
Qy 109 CCAGCTGCTACGGC---GGATTGACCTGATCTTCAATTTTGACAAATGAGAGTGG 165
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Qy 166 ---CTGCACACTGGAATGAAATCTATTATCTTTGTGCAACAGTGGCTCACAATTCATC 222
Db 164 AspGlnSerAspPheThrGlnMetLysAspPheValIleAlaLeuMetGlyGlnLeuAla 183
Qy 223 AGCCACAGTGAAGATGCTTATTTATTTCTCCACCCGAGAACACACTTAATGAA 282
Db 184 SerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeuLysThrHisPheThr 203
Qy 283 CTGCACAGACAGACA-----GAACAAATCCGTCAAGCCTAGAGAACTC 327
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Qy 328 CAGAAAGTTCTGCACAGAGAGACACTTACATGATGAAAGATTGAAAGGCCAGTGG 387
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Qy 388 CAGATTATTTGAAACACAGACAGAGTACAGACAGCC---AGCCTCATTTGCTTGG 444
Db 239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLysIleLeuIleValIle 258
Qy 445 ACTGATGAGAACTCCATGAGATCTTTTCTATTATTCAGAG-----AGGAGGCTAAT 498
Db 259 ThrAspGlyGlnLysPheArgAspProLeuGluTyrArgHisValIleProGluAlaGlu 278
Qy 499 AGGTCGAGATCTTGTGCAATGTTTACTGTGTGGGTGGAAGAT---TTCATGAG 555
Db 279 LysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAspAlaPheArgGlu 295
Qy 556 ---ACACAGCTGGCCCGGATT-----GCGACAGTAAGATCATGTGTT 597
Db 296 ProThrAlaLeuGlnGluLeuAsnThrIleGlySerAlaProSerGlnPheHisValPhe 315
Qy 598 CCCGTGAATGACGGCTTTACAGCTCTGCAAGGATCATCATCATTTTGAAGAAGTCC 657
Db 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGluLys--- 333
Qy 658 TGCATGGAATTTCACAGCTGCAACATCCACATATGTGCAGAGAGTCAATTCAAGTT 717
Db 334 -----IlePheAlaIleGlnGlyThrGluSerArgSerSerSerPheGlnHis 350
Qy 718 GTCGTAGAGAAACGGCTTCCGACATGCCCGCAGAGTGGAC 759
Db 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 4
US-08-362-652-46
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower

```

: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/362,652
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,869
: FILING DATE: 5-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32391
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1155 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-362-652-46

Alignment Scores:
Pred. No.: 2.9e-09 Length: 1155
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
Gaps: 12

US-09-970-076-1_COBY_104_1207 (1-1104) x US-08-362-652-46 (1-1155)
QY 109 CGAGCTGTGTAAGGC---GGATTGACCTGTACTTGAATTTGGCAAAATGAGAGTGTG 165
Db 144 PROGLNCGYBPGLGNGLNWETABPTLEALAPHEULELNAEPGLYSEGLYSE 163
QY 166 ---CTGCACACCTGAGATGAATCTATTACTTGTGTGGAACAGTGTGGCTCAAAATTCATC 222
Db 164 AEPGLNSETAPRPHETHRGLNCTLYSAPRPHVALLYALALEUWETGLYGLNLEUALA 183
QY 223 AGCCCAAGTTGAGAAATGTCCTTTATGTTTCTCCACCCGAGAAACACTTAATGAAA 282
Db 184 SETRTTSETTSETRPHSETRLEUWETGLNLYSEYASMLLEULEYSTRNHSRPHETHR 203
QY 283 CTGACAGAGACAGA-----GAACAAACTCGTCAAGGCCCTAGAAAGACTC 327
Db 204 PHEHTGLPHEUYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEY 223
QY 328 CAGAAAATTTCTGCAAGAGACAGACACTTATCATGATGAAGATTGAAAGGCCAGTGA 387
Db 224 GLN-----GLYLEUTHRTYRTHALASECYLLLEGLNLYSEYVALLYLSE 238
QY 388 CAGATTTATTAATAAACAAGACAGAGGTACAGACAGCC---AGCGTATCATTCCTTTG 444
Db 239 GTLEUPHEHIESERTLYSANGLYALARGLYSEYVALYSEYSEYSEYSEYSEYSEY 258
QY 445 ACTGATGGAAGATTCATGAAGATCTCTTTTCTATTTCAGAG-----AGGAGAGCTAAT 498
Db 259 TTTAPRGLYGLNLYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEYSEY 278

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| | | | |
|-------------------|--|---|--------------|
| QY | 499 | AGGTTCCAGAACTCTGGAGCAATTTCTTACTGTGTGGTGTGTAAGAAT---TTCAATGAG | 555 |
| DB | 279 | LYSALA-----GLYILEILEARGTRYRALALEGLYVALGLYASPLAPHEARGLU | 295 |
| QY | 556 | ---ACACAGCTGGCCCGGATT-----GCCGACGATGAAGCATCATGTGTT | 597 |
| DB | 296 | PROTHRALLEUGLNLGLULDEUAMNTHRIILEGLYSERIALAPROSERGLINAPHSIVALPHE | 315 |
| QY | 598 | CCCGTGATGACGCGTTTTCAGGCTCTGCAGGCAATTCACACTCAATTTTGAAGAAGTCC | 657 |
| DB | 316 | LYSVALGLYASN--PHEVALALALEUARGSERILEGLINARGLNLGLINGLUYS--- | 333 |
| QY | 658 | TGCATCAAAATTTCTGAGCTGACCTACCAATCCACATATGTCAGAGAGATTCATTTCAAGTT | 717 |
| DB | 334 | -----LLEPHALALEGLULGLYTHRGLUSERARGSERSERPHEGINHLS | 350 |
| QY | 718 | GTCGTGAGAGGAAACGCGCTTCGCAGATGCCCGCAACGTGAC | 759 |
| DB | 351 | GLUWETSERGLNGLUGLYPHEUSERSERIALAUSERMETASP | 364 |
| RESULT 5 | | | |
| | US-08-605-672-46 | | |
| | Sequence 46, Application US/08605672 | | |
| | Patent No. 5817515 | | |
| | GENERAL INFORMATION: | | |
| | APPLICANT: Gallatin, W. Michael | | |
| | APPLICANT: Van der Vieren, Monica | | |
| | TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit | | |
| | NUMBER OF SEQUENCES: 103 | | |
| | CORRESPONDENCE ADDRESS: | | |
| | ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun | | |
| | STREET: 233 South Wacker Drive, 6300 Sear Tower | | |
| | CITY: Chicago | | |
| | STATE: Illinois | | |
| | COUNTRY: United States | | |
| | ZIP: 60606-6402 | | |
| | COMPUTER READABLE FORM: | | |
| | MEDIUM TYPE: Floppy disk | | |
| | COMPUTER: IBM PC compatible | | |
| | OPERATING SYSTEM: PC-DOS/MS-DOS | | |
| | SOFTWARE: Patent Release #1.0, Version #1.25 | | |
| | CURRENT APPLICATION DATA: | | |
| | APPLICATION NUMBER: US/08/605,672 | | |
| | FILING DATE: | | |
| | CLASSIFICATION: 530 | | |
| | PRIOR APPLICATION DATA: | | |
| | APPLICATION NUMBER: US 08/173,497 | | |
| | FILING DATE: 23-DEC-1993 | | |
| | PRIOR APPLICATION DATA: | | |
| | APPLICATION NUMBER: US 08/286,889 | | |
| | FILING DATE: 5-AUG-1994 | | |
| | PRIOR APPLICATION DATA: | | |
| | APPLICATION NUMBER: US 08/362,652 | | |
| | FILING DATE: 21-DEC-1994 | | |
| | ATTORNEY/AGENT INFORMATION: | | |
| | NAME: Williams Jr., Joseph A. | | |
| | REGISTRATION NUMBER: 38,659 | | |
| | REFERENCE/DOCKET NUMBER: 27866/32684 | | |
| | TELECOMMUNICATION INFORMATION: | | |
| | TELEPHONE: 312-474-6300 | | |
| | TELEFAX: 312-474-0448 | | |
| | TELEX: 25-3856 | | |
| | INFORMATION FOR SEQ ID NO: 46: | | |
| | SEQUENCE CHARACTERISTICS: | | |
| | LENGTH: 1155 amino acids | | |
| | TYPE: amino acid | | |
| | TOPOLOGY: linear | | |
| | MOLECULE TYPE: protein | | |
| | US-08-605-672-46 | | |
| Alignment Scores: | | | |
| | Pred. No.: | 2.9e-09 | Length: 1155 |
| | Score: | 166.00 | Matches: 66 |


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; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-193-043-46

Alignment Scores:
Pred. No.: 2.9e-09      Length: 1155
Score: 166.00          Matches: 66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%    Mismatches: 96
Query Match: 8.29%             Indels: 30
DB: 2                      Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-193-043-46 (1-1155)
OY 109 CCAGCTGCTACGGC---GGATTGACCTGTACTTCTTATTTGGACAATTCAGAAAGTGTG 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 Proglucyberolylnglumetabp1lealpheuleleapglserglyserlle 163
OY 166 ---CTGCACCACTGGAATGAAATCTATTACTTTGGACAGTTGGCTCAAAATTCATC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 AepglserapherhrglmetyAepPheVallyalaleumetglylnleuAla 183
OY 223 AGCCACAGTTGGAATGTCCTTATTTCTTCCACCGAGAAACAACCTTAATGAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 SerThSerThSerPheSerleuMetGlnTySerAsnilleuLystrHlsPheThr 203
OY 283 CTGACAGAAAGACAG-----GAACAAATCCGTCAAGGCTTGAAGAATCTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 PheThrdluphelyserSerleuSerProglInservuAlaPheAlaIleValGlnleu 223
OY 328 CAGAAAGTTCTGCACAGAGAGACACTTACATGATGAAAGATTGAAAGGCCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 224 Gln-----GlyLeuthrTyThrAlaserglylleglnlysvAllyls 238
OY 388 CAAATTTATATGAAAAACAGCAAGGTACAGACAGCC---AGCGTCATCATTCCTTG 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 239 GluleuPheHlsSerlysaenglyAlaArglySerAlaLylylsIleleuIleValIle 258
OY 445 ACTGATGAGAGACTCCATGAAAGATCTCTTTTCTTATTCAGAG-----AGGAGGCTAAT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 259 ThrAspIlyGlnlysaPheArgAspProleuGlnTytrArgHlsValIleProgluAlaGln 278
OY 499 AGGCTCGAGACTTGGTGCAATTTGTTACTGTGTGGTGGAAGAT---TTCATGAG 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 LyAla-----GlyIleIleArgTyAlaIleGlyValGlyAspAlaPheArgGln 295
OY 556 ---ACACAGCTGGCCCGGATT-----GCGGACGTAAGATCATGTGTTT 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 ProThralaleuGlnGlnleuAenThrIleGlySerAlaProSerGlnAspHlsValPhe 315
OY 598 CCGGTGAATACGGCTTTCAGGCTCTGCAAGGCTCATCCATCAATTTGAAAGATGCC 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 LyvalaIlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGlnlyls--- 333
OY 658 TGCAATGAAATTTAGACAGTGAACCATCATATATGTGCAGAGAGATTCATTCAAGTT 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 334 -----IlePheAlaIleGlnGlyThrGlnSerArgSerSerSerPheGlnHls 350
OY 718 GTCTGTAGAGAAAAGGCTTCCGACATGCCCGCAACGTGAC 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 351 GlumetserGlnGlnGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 9
US-09-688-307A-46
; Sequence 46; Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
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; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46

Alignment Scores:
Pred. No.: 2.9e-09      Length: 1155
Score: 166.00          Matches: 66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%    Mismatches: 96
Query Match: 8.29%             Indels: 30
DB: 2                      Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-688-307A-46 (1-1155)
OY 109 CCAGCTGCTACGGC---GGATTGACCTGTACTTCTTATTTGGACAATTCAGAAAGTGTG 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 Proglucyberolylnglumetabp1lealpheuleleapglserglyserlle 163
OY 166 ---CTGCACCACTGGAATGAAATCTATTACTTTGGACAGTTGGCTCAAAATTCATC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 AepglserapherhrglmetyAepPheVallyalaleumetglylnleuAla 183
OY 223 AGCCACAGTTGGAATGTCCTTATTTCTTCCACCGAGAAACAACCTTAATGAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 SerThSerThSerPheSerleuMetGlnTySerAsnilleuLystrHlsPheThr 203
OY 283 CTGACAGAAAGACAG-----GAACAAATCCGTCAAGGCTTGAAGAATCTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 PheThrdluphelyserSerleuSerProglInservuAlaPheAlaIleValGlnleu 223
OY 328 CAGAAAGTTCTGCACAGAGAGACACTTACATGATGAAAGATTGAAAGGCCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 224 Gln-----GlyLeuthrTyThrAlaserglylleglnlysvAllyls 238
OY 388 CAAATTTATATGAAAAACAGCAAGGTACAGACAGCC---AGCGTCATCATTCCTTG 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 239 GluleuPheHlsSerlysaenglyAlaArglySerAlaLylylsIleleuIleValIle 258
OY 445 ACTGATGAGAGACTCCATGAAAGATCTCTTTTCTTATTCAGAG-----AGGAGGCTAAT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 259 ThrAspIlyGlnlysaPheArgAspProleuGlnTytrArgHlsValIleProgluAlaGln 278
OY 499 AGGCTCGAGACTTGGTGCAATTTGTTACTGTGTGGTGGAAGAT---TTCATGAG 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 LyAla-----GlyIleIleArgTyAlaIleGlyValGlyAspAlaPheArgGln 295
OY 556 ---ACACAGCTGGCCCGGATT-----GCGGACGTAAGATCATGTGTTT 597
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DB 296 ProThralaleuGlnGlnleuAenThrIleGlySerAlaProSerGlnAspHlsValPhe 315
OY 598 CCGGTGAATACGGCTTTCAGGCTCTGCAAGGCTCATCCATCAATTTGAAAGATGCC 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 LyvalaIlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGlnlyls--- 333
OY 658 TGCAATGAAATTTAGACAGTGAACCATCATATATGTGCAGAGAGATTCATTCAAGTT 717
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Db      334 -----|||phenAlaIleeluglyThrGlnSerArgSerSerSerPheGlnHis 350
Qy      718 GTCTGAGAGAAACGGCTTCGACATGCCCGCAACGTGAAC 759
      ::::|||||
Db      351 GlnMetSerGlnGlnGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 10
US-09-350-259-46
; Sequence 46, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/123,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/266,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-259-46

Alignment Scores:
Pred. No.:      2.9e-09      Length:      1155
Score:          166.00      Matches:      66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%      Mismatches: 96
Query Match:      8.29%      Indels:      30
DB:                2      Gaps:      12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-350-259-46 (1-1155)
Qy      109 CGAGCGCTGTACGGC---GGATTGACCTGTACTTCACTTTGGACAATAAGAGAGTGTG 165
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      144 ProGluCySPProGluYngluMetAspIleAlaPheleuIleSpGlySerGlySerIle 163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      166 ---CTGCACCACTGTGAATGAATACTTACTTTGTGGAAACAGTTGGCTCAAAATTCATC 222
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      164 ArgGlnSerAspPheThrGlnMetLysAspPheValLysAlaLeuMetGlnLeuAla 163
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      223 AGCCCACTGTGAAGATGTCCTTATTGTTTCTCCACCCGAGAAACACTTAATGAAGA 282
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      184 SerThrSerThrSerPheSerLeuMetGlnTySerAsnIleLeuYSerThrHisPheThr 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      283 CTGCACGAAGACAGA-----GAACAATCCGTCAAGGCTCAGAAAGAACTC 327
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      204 PheThrGlnPheIleSerLysSerLeuSerProGlnSerLeuValAlaPheAlaIleValGlnLeu 223
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      328 CAGAAAGTTCTGCGCAGAGAGACACTTACATCATGAAGATTGTAAGAGGCCACGTGAG 387
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      224 Gln-----GlyLeuThrTyThrAlaSerGlyIleGlnLysValValLys 238
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      388 CAGATTATTATGAAAAACAGACAAGGGTACAGACAGCC---AGCTCATCATGCTTGTG 444
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      239 GlnLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLysIleLeuIleValIle 258
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      445 ACTGATGAGAGAACTCATGAAGATCTCTTTTCTATTCAAG-----AGGAGGCTTAAT 498
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      259 ThrAspGlyGlnLysPheArgAspProLeuGlnTyArgHisValIleProGlnLysGln 278
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QY 499 AGGCTGCAAGATCTTGGTGCATATCTTTACTGTGTGGTGTGAAGAT---TTCATGTAG 555
Db lysala-----GlyIleIleArgTyrAlaIleGlyValGlyAhpAlaPheArgGlu 295
QY 556 --ACACAGCTGGCCCCGATT-----GCCGACAGTAAGATCATGTGTT 597
Db ProThrAlaIleuGlnGluLeuAsnThrIleGlySerAlaProSerGlnPheHisValPhe 315
QY 598 CCCGTAATGACGGCTTTCAGGCTCTTGCAGAGCATCATCACTCAATTTTGAAGAAGTCC 657
Db 316 LysValGlyAen---PheValAlaLeuArgSerIleGlnArgGlnIleGlnIleGlyuys--- 333
QY 658 TGCATCGAAATTTCTGACGCTGACACCATCCACATATGACGAGAGATCATTTTCAAGTT 717
Db 334 -----IlePheAlaIleGluGlyIhrGluSerArgSerSerSerPheGlnHis 350
QY 718 GTCGTGAGAGAAACGCTTCCGACATGCCCGCAACGTGAC 759
Db 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 11
US-08-485-618-53
; Sequence 53, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-618-53

Alignment Scores: 2.91e-09 Length: 1161
Pted. No.:

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Score: 166.00
Percent Similarity: 46.15%
Best Local Similarity: 28.21%
Query Match: 8.29%
DB: 1
Matches: 66
Conservative: 42
Mismatch: 96
Indels: 30
Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-485-618-53 (1-1161)

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QY 109 CCAAGCTGCTAAGC--GGATTGACCTGCTACTTATTTGGACAAATCAGGAAGTGTG 165
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DB 144 Proglucybrproglucinglumetaspilaleaephenuileapgliserysile 163
QY 166 ---CTGACACACGGAATGAATCTATTACTTTGTGACAGTGGCTCAAAATTCATC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 AspGlnserasphehrGlnmetLysasphevalLysalaLeuwerGlyGlnLeuAla 183
QY 223 AGCCACAGTTGGAATGCTCTTATTTGTTTCACCCGAGAACACCTTAATGAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 SerThrserrThrserrPheSerleuMetGlnTySeranlleuLysrthHAspethr 203
QY 283 CTGACAGACAGACA-----GAACAAATCCGTCAGAGCCTTAAGAAATCTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 PheThrcIuhelySerSerleuSerProGlnSerleuValaspalailevalGlnLeu 223
QY 328 CAGAAAGTCTGCCAGAGACACTTACATGATGATGAAGATTGAAGGCCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 224 Gln-----GlyLeuThrTyThralaserGlyileGlnLysvalValLys 238
QY 388 CAGATTATTATGAAAAACACAAAGGTCACAGACAGC--AGCCTCATTCATGCTTTG 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 239 GluLeuphehiserLysaenglyAlaXylserserlalyblybilleleuilevalile 256
QY 445 ACTGATGAGAACTCCATGAAGATCTTTTCTATTCAAG-----AGGAGGCTPAAT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 259 ThrAspGlyGlnLysPheArgaspProleuGlnTyArgHlsvalileProgluAlaGln 278
QY 499 AGGCTCGAATCTTGTCATTTACTGTCGTGGTGAAGAT---TTCATGAG 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 LysAla-----GlyleileargTyAlaileGlyAlaGlyaspalaPheargGln 295
QY 556 ---ACACAGCTGGCCCGGATT-----CGGACAGTAAGATCATGTGTTT 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 ProThralaLeuGlnGlnLeuAenThrileGlySerlalyProserGlnaPheAlaPhe 315
QY 598 CCCGTGAATGACGGCTTCAGGCTTCGCAAGGATCATTCATCAATTTGAAGATCC 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 LysValaGlyAen--PheValaLalaLeuArgserileGlnArgGlnileGlnLys--- 333
QY 658 TGCATGCAATTTCTAGAGCTGAACCATCCACCATATGTGACAGAGATCATTTCAAGTT 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 334 -----IlePheAlaileGlnGlyThrcIuSerArgSerSerSerPheGlnHis 350
QY 718 GTCGTGAGAGAAAGCGCTTCGACATGCCGACAGCTGAGAC 759
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DB 351 GluMetserGlnGlnGlyPheSerSerlalyLeuSerMetasp 364

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RESULT 12
US-08-362-652-53
Sequence 53: Application US/08362652
Patent No. 5766850

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-362-652-53

Alignment Scores:

Pred. No.: 2,91e-09 Length: 1161
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-362-652-53 (1-1161)

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QY 109 CCAAGCTGCTAAGC--GGATTGACCTGCTACTTATTTGGACAAATCAGGAAGTGTG 165
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DB 144 Proglucybrproglucinglumetaspilaleaephenuileapgliserysile 163
QY 166 ---CTGACACACGGAATGAATCTATTACTTTGTGACAGTGGCTCAAAATTCATC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 AspGlnserasphehrGlnmetLysasphevalLysalaLeuwerGlyGlnLeuAla 183
QY 223 AGCCACAGTTGGAATGCTCTTATTTGTTTCACCCGAGAACACCTTAATGAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 SerThrserrThrserrPheSerleuMetGlnTySeranlleuLysrthHAspethr 203
QY 283 CTGACAGACAGACA-----GAACAAATCCGTCAGAGCCTTAAGAAATCTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 PheThrcIuhelySerSerleuSerProGlnSerleuValaspalailevalGlnLeu 223
QY 328 CAGAAAGTCTGCCAGAGACACTTACATGATGATGAAGATTGAAGGCCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 224 Gln-----GlyLeuThrTyThralaserGlyileGlnLysvalValLys 238
QY 388 CAGATTATTATGAAAAACACAAAGGTCACAGACAGC--AGCCTCATTCATGCTTTG 444
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DB 239 GluLeuphehiserLysaenglyAlaXylserserlalyblybilleleuilevalile 256
QY 445 ACTGATGAGAACTCCATGAAGATCTTTTCTATTCAAG-----AGGAGGCTPAAT 498
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DB 259 ThrAspGlyGlnLysPheArgaspProleuGlnTyArgHlsvalileProgluAlaGln 278
QY 499 AGGCTCGAATCTTGTCATTTACTGTCGTGGTGAAGAT---TTCATGAG 555
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QY 556 ---ACACAGCTGGCCCGGATT-----CGGACAGTAAGATCATGTGTTT 597

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Db 296 ProthAlaLeuGlnIleuValenThrIleGlySerAlaProSerGlnAspHisValPhe 315
QY 598 CCCGTAATGAGCGGCTTCAGGCTCGCAAGCATCATCATTTTGAAGAGTCC 657
Db 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGlyAsn--- 333
QY 658 TGCATCGAAATTCAGCTGAGTGAACCATCCATATGTGCAGAGAGTCAATTCAGATT 717
Db 334 -----IlePheAlaIleGlnGlyThrGlnSerArgSerSerSerPheGlnHis 350
QY 718 GTCGTGAGAGAAAGCGCTTCGACATGCCCGCAAGTGGAC 759
Db 351 GluMetSerGlnGlnGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 13
US-08-605-672-53
Sequence 53, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-53

Alignment Scores:
Pred. No.: 2,91e-09 Length: 1161
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-605-672-53 (1-1161)
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Db 144 ProGluCyArgProGlyGlnGlnMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
QY 166 ---CTGCACCACTGGAAATGAAATCTATTACTTTGTGGAAACAGTGGCTCACAATTCATC 222
Db 164 AspGlnSerAspPheThrGlnMetCysAspPheValValLeuMetGlyGlnLeuAla 183
QY 223 AGCCCAAGTTGAGAAATGTCCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAA 282
Db 184 SerThrSerThrSerPheSerLeuMetGlnIlySerAsnIleLeuLysThrIlePheThr 203
QY 283 CTGACAGAAAGACAGA-----GAACAATTCCTCAAGCGCTGAGAAACATC 327
Db 204 PheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
QY 328 CAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGAAAGGCCAGTGA 387
Db 224 Gln-----GlyLeuThrTyrrThrAlaSerGlyIleGlnIleValValLys 238
QY 388 CAGATTATATGAAAAACAGACAGAGGTACAGACAGC---AGCCTCATCTGCTTG 444
Db 239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysAlaLysIleLeuIleVal 258
QY 445 ACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTTCAGAG-----AGGAGGCTAAT 498
Db 259 ThrAspGlyGlnLysPheArgAspProLeuGluTyrrArgHisValIleProGluAlaGln 278
QY 499 AGGCTCGAGATCTTGGTGAATTTGTTACTGTGTGGTGGAAGAT---TTCAATGAG 555
Db 279 LysAla-----GlyIleIleArgTyrrAlaIleGlyValGlyAspAlaPheArgGln 295
QY 556 ---ACACAGCTGGCCCGGAT-----GGCGAAGTAAAGATCATGTGTT 597
Db 296 ProthAlaLeuGlnIleuValenThrIleGlySerAlaProSerGlnAspHisValPhe 315
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QY 658 TGCATCGAAATTCAGCTGAGTGAACCATCCATATGTGCAGAGAGTCAATTCAGATT 717
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QY 718 GTCGTGAGAGAAAGCGCTTCGACATGCCCGCAAGTGGAC 759
Db 351 GluMetSerGlnGlnGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 14
US-08-482-293A-53
Sequence 53, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A

FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA: 27866/32684
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION: NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-53

Alignment Scores:

Pred. No.: 2,91e-09 Length: 1161
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-482-293A-53 (1-1161)

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DB 144 ProglucyberoligluinlumeAspIleAlaPheleuleaserglySerIle 163
QY 166 ---CTGACACCATGGAATCTATTCTTGTGGACAGTGGCTCAAAATTCATC 222
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DB 184 SerThrSerThrSerPheSerIleuMetGlnIyrSerAnIleuLysThrIlePheThr 203
QY 283 CTGACAGACAGACA-----GAAACAAATCCGTCAAGCCCTAAGAAATCTC 327
DB 204 PheThrIlePheLysSerSerIleuSerProGlnSerIleuValAspAlaIleValGlnLeu 223
QY 328 CAGAAGTTTGGCAGAGAGACACTTACATGATGAAAGATTGAAAGGCCAGTGA 387
DB 224 Gln-----GlyLeuThrIleThrAlaSerGlyIleGlnLysValValLys 238
QY 388 CAGATTATTATGAAAACAGACAGGTCAGACAGCC--AGCGTCATCATGCTTGG 444
DB 239 GluleuPheIleSerLysAnGlyAlaIleGlySerIleLysIleLeuIleValIle 258
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QY 499 AGGCTTCGAGATCTTGTGCAATGTTTACTGTGTGGTGAAGAT---TTCATGAG 555
DB 279 LysAla-----GlyIleIleArgIleAlaIleGlyValGlyAspAlaPheArgLys 295
QY 556 ---ACACAGCTGGCCCGCGATT-----CGGACAGTAAAGATCATGTGTT 597
DB 296 ProThrIleLeuGlnGlnLysLeuAenThrIleGlySerIleAlaProSerGlnAspIleValPhe 315

QY 598 CCAGTGAATGAGCGCTTTCAGGCTGTGACAGCATCATCAATTTTGAAGAATGCC 657
DB 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnLys---- 333
QY 658 TGCATGAAATTTCTAGACAGTGAACCATCCACCATATGTGACGAGAGATTCATTAAGTT 717
DB 334 -----IlePheAlaIleGlnGlnIleGlnLysArgSerSerSerPheGlnIle 350
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DB 351 GluMetSerGlnGlnLysPheSerSerAlaLeuSerMetAsp 364

RESULT 15

US-08-943-363-53
Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OR INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Alignment Scores:

Pred. No.: 2,91e-09 Length: 1161
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-943-363-53 (1-1161)

QY 109 CCAGCTGCTAAGCGC--GGATTGACCTGTACTTCTTGGACAAATCAGGAAGTGTG 165

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Search completed: December 14, 2005, 12:02:48
Job time : 51.8908 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 14, 2005, 11:59:14 ; Search time 165.732 Seconds
(without alignments)
5566.636 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207
Perfect score: 2003
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPTCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human0.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEARSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA_Main:.*
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2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:.*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:.*
4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:.*
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6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1914 | 95.6 | 368 | 6 | US-11-047-278-2 |
| 2 | 1894 | 94.6 | 564 | 3 | US-09-918-715-187 |
| 3 | 1894 | 94.6 | 564 | 3 | US-09-918-715-187 |
| 4 | 1894 | 94.6 | 564 | 3 | US-09-918-715-187 |
| 5 | 1894 | 94.6 | 564 | 4 | US-10-301-822-199 |
| 6 | 1894 | 94.6 | 564 | 4 | US-10-408-765A-1823 |
| 7 | 1894 | 94.6 | 564 | 4 | US-10-474-794-187 |
| 8 | 1894 | 94.6 | 564 | 4 | US-10-474-794-187 |
| 9 | 1894 | 94.6 | 564 | 5 | US-10-979-159-187 |
| 10 | 1894 | 94.6 | 564 | 6 | US-10-979-159-232 |
| 11 | 1889 | 94.3 | 403 | 3 | US-09-833-245-621 |
| 12 | 1870 | 93.4 | 403 | 3 | US-09-833-245-620 |

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|----|--------|------|-----|---|-------------------|-------------------|
| 13 | 1793 | 89.5 | 562 | 3 | US-09-918-715-194 | Sequence 194, App |
| 14 | 1793 | 89.5 | 562 | 3 | US-09-918-715-301 | Sequence 301, App |
| 15 | 1793 | 89.5 | 562 | 4 | US-10-474-794-194 | Sequence 194, App |
| 16 | 1793 | 89.5 | 562 | 4 | US-10-474-794-301 | Sequence 301, App |
| 17 | 1793 | 89.5 | 562 | 5 | US-10-979-159-194 | Sequence 194, App |
| 18 | 1793 | 89.5 | 562 | 5 | US-10-979-159-301 | Sequence 301, App |
| 19 | 1670 | 83.4 | 551 | 4 | US-10-038-307-18 | Sequence 18, App1 |
| 20 | 1670 | 83.4 | 551 | 4 | US-10-201-292-18 | Sequence 18, App1 |
| 21 | 1654.5 | 82.6 | 564 | 4 | US-10-038-307-20 | Sequence 20, App1 |
| 22 | 1654.5 | 82.6 | 564 | 4 | US-10-201-292-20 | Sequence 20, App1 |
| 23 | 1649 | 82.3 | 333 | 3 | US-09-796-753-12 | Sequence 12, App1 |
| 24 | 1649 | 82.3 | 333 | 4 | US-10-038-307-2 | Sequence 2, App11 |
| 25 | 1649 | 82.3 | 333 | 4 | US-10-201-292-2 | Sequence 2, App11 |
| 26 | 1649 | 82.3 | 333 | 6 | US-11-047-278-8 | Sequence 8, App11 |
| 27 | 1649 | 82.3 | 345 | 4 | US-10-038-307-24 | Sequence 24, App1 |
| 28 | 1649 | 82.3 | 345 | 4 | US-10-201-292-24 | Sequence 24, App1 |
| 29 | 1636 | 81.7 | 328 | 4 | US-10-038-307-26 | Sequence 26, App1 |
| 30 | 1636 | 81.7 | 328 | 4 | US-10-201-292-26 | Sequence 26, App1 |
| 31 | 1636 | 81.7 | 543 | 4 | US-10-038-307-14 | Sequence 14, App1 |
| 32 | 1636 | 81.7 | 543 | 4 | US-10-201-292-14 | Sequence 14, App1 |
| 33 | 1634.5 | 81.6 | 342 | 4 | US-10-038-307-22 | Sequence 22, App1 |
| 34 | 1634.5 | 81.6 | 342 | 4 | US-10-201-292-22 | Sequence 22, App1 |
| 35 | 1633 | 81.5 | 543 | 4 | US-10-038-307-16 | Sequence 16, App1 |
| 36 | 1633 | 81.5 | 543 | 4 | US-10-201-292-16 | Sequence 16, App1 |
| 37 | 1626 | 81.2 | 543 | 4 | US-10-038-307-10 | Sequence 10, App1 |
| 38 | 1626 | 81.2 | 529 | 4 | US-10-201-292-10 | Sequence 10, App1 |
| 39 | 1555 | 77.6 | 534 | 4 | US-10-038-307-12 | Sequence 12, App1 |
| 40 | 1495 | 74.6 | 534 | 4 | US-10-201-292-12 | Sequence 12, App1 |
| 41 | 1495 | 74.6 | 504 | 4 | US-10-201-292-34 | Sequence 34, App1 |
| 42 | 1434.5 | 71.6 | 504 | 4 | US-10-201-292-34 | Sequence 34, App1 |
| 43 | 1307 | 65.3 | 479 | 4 | US-10-201-292-32 | Sequence 32, App1 |
| 44 | 1193 | 59.6 | 460 | 4 | US-10-201-292-28 | Sequence 28, App1 |
| 45 | 1183 | 59.1 | 460 | 4 | US-10-201-292-30 | Sequence 30, App1 |

ALIGNMENTS

RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, Kenneth A.
; APPLICANT: Bradley, John A.T.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Alignment Scores:
Pred. No.: 2,766-182
Score: 1914.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 95.56%
DB: 6
Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-047-278-2 (1-368)
QY 1 ATGGCACCAGCGAGCGAGAGCCTCGGCATCGCTCCAGTGCCTCTTTGGCCACT 60

Db 1 MetAlaThrAlaGluArgAlaLeuGlyLeGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 61 CTGGTGGCTATCTGCGCCGGGCAAGGGGACCGAGGAGAGATGGGGGTCCAGCTGGCTAC 120
Db 21 LeuValLeuIleValaGlyValaGlyGlnGlyArgAlaGlyLysProAlaCysTrp 40
QY 121 GCGGATTTGACCTGACTTCAATTTTGGACAAATCGAAGAGTGTGTGACCACTGGAAAT 180
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn 60
QY 181 GAAATCTATTACTTGTGTGAAACGTTGGCTCACAAATTCATCAAGCCCAAGTTGAGATG 240
Db 61 GluIleTrpTrpPheValaGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 241 TCCCTTATTTGTTTTTCCACCCGAGAGAACACCTTAATGAATCTGACAAAGACAGAGAA 300
Db 81 SerPheIleValaPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
QY 301 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
Db 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 361 CATGAAGATTGAAAAGGCGCAGTGAAGACAGATTATTATGAAAACAGACAGGGTACAG 420
Db 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140
QY 421 AACAGCAGGCTCATCTATGCTTTGACTGATGGAATCTCCATGAAATCTCTTTTCTAT 480
Db 141 ThrAlaSerValIleIleAlaLeuTrnAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160
QY 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGTGCAATTGTTTACTGTGTGTGTG 540
Db 161 SerGluArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleValLysCysValGlyVal 180
QY 541 AAAGATTTCAATGACACACAGCTGGCCCGGATTGGCGACAGTAAAGATCATGTGTTCCC 600
Db 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTGAATGAGGCGCTTGAAGCTCGAAGGCTCATCACTCATCAATTTTGAAGAAGCTCTGC 660
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 661 ATCGAATTTCTAGCAGCTGAACCATCCACCATATGTGCAAGAGAGTCAATTTCAAGTTGTC 720
Db 221 IleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY 721 GTGAGAGAAAAGGCTTCCGACATGCCCGACACGTGACAGGGTCTCTGACAGCTTCAAG 780
Db 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 781 ATCAATGACTCCGGTCAACATCAATGAGAGCCCTTTTGTGTGAGACACTTATTTAATCG 840
Db 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGlnAspThrTrpLeuLeu 280
QY 841 TGTCCAGCGCCTATCTTAAAGAAGTGGCATGAAAGCTGCACTCCAGGTCAAGCATGAAC 900
Db 281 CysProAlaProIleLeuLysGlnValaGlyMetLysAlaAlaLeuGlnAlaSerMetAsn 300
QY 901 GATGCGCTCTCTTTTATCTCCAGTTCTGTGATCATCAACACACACACTGTTTGAAGGT 960
Db 301 AspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrHisCysSerAspGly 320
QY 961 TCCATCTGGCCATTCGCCCTGATGATCCGTTCTGTCTCTTACCGCTGGCTCCCTCG 1020
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1021 TGTGTTGCGCCCTCTGTGCTGCACTGTGATATCAAGAAGGTCCCTCAACCCCTGCGGAG 1080
Db 341 TrpPheTrpProLeuLysCysSerThrValIleIleIleGlyValaProProProAlaGlu 360
QY 1081 GAGAGTGAGGAAAATAAATAA 1104
|||||

Db 361 GluSerGlnGluAsnLysIleLeuLys 368
RESULT 2
US-09-918-715-187
/ Sequence 187, Application US/09918715
/ Publication No. US20030017157A1
/ GENERAL INFORMATION:
/ APPLICANT: Brad St. Croix
/ APPLICANT: Bert Vogelstein
/ APPLICANT: Kenneth Kinzler
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00134
/ CURRENT APPLICATION NUMBER: US/09/918,715
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 187
/ LENGTH: 564
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-918-715-187
Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-918-715-187 (1-564)
QY 1 ATGGCCACGCGCGAGAGCGAGAGCCCTCGCATCGGCTTCCAGTGGCTCTTTTGGCCACT 60
Db 1 MetAlaThrAlaGluArgAlaLeuGlyLeGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 61 CTGGTGGCTATCTGCGCCGGGCAAGGGGACCGAGGAGAGATGGGGGTCCAGCTGGCTAC 120
Db 21 LeuValLeuIleValaGlyValaGlyGlnGlyArgAlaGlyLysProAlaCysTrp 40
QY 121 GCGGATTTGACCTGACTTCAATTTTGGACAAATCGAAGAGTGTGTGACCACTGGAAAT 180
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn 60
QY 181 GAAATCTATTACTTGTGTGAAACGTTGGCTCACAAATTCATCAAGCCCAAGTTGAGATG 240
Db 61 GluIleTrpTrpPheValaGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 241 TCCCTTATTTGTTTTTCCACCCGAGAGAACACCTTAATGAATCTGACAAAGACAGAGAA 300
Db 81 SerPheIleValaPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
QY 301 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
Db 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 361 CATGAAGATTGAAAAGGCGCAGTGAAGACAGATTATTATGAAAACAGACAGGGTACAG 420
Db 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140
QY 421 AACAGCAGGCTCATCTATGCTTTGACTGATGGAATCTCCATGAAATCTCTTTTCTAT 480
Db 141 ThrAlaSerValIleIleAlaLeuTrnAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160
QY 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGTGCAATTGTTTACTGTGTGTGTG 540
Db 161 SerGluArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleValLysCysValGlyVal 180

QY 541 AAGATTTCATGAGACACAGCTGGCCCGATTCCGACAGTACATGTTTCCC 600
DB 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPhePro 200
QY 601 GTCAATGACGGCTTTGAGGCTGTGCAAGGATCATCCATTTTGAAGAGTCTGCG 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIlySylSerCys 220
QY 661 ATCGAAATTTAGCAGCTGAACCATCCACCATATGTGACAGAGATCATTTCAAGTTGTC 720
DB 221 IleGlnIleLeuAlaIleGlnProSerThrIleCysAlaGlyGlnSerPheGlnValVal 240
QY 721 GTGAGAGGAAACGGCTTCCGACATGCCCCGACAGTGACAGGCTCTCTGACCTTCAAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheIys 260
QY 781 ATCAATGACTGGGCACTCAATGAGAGAGCCCTTTCTGTGAGAGACATTTATTAATG 840
DB 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGlnAspThrTyrLeuLeu 280
QY 841 TGTCACAGCCCTATCTTAAAGAGTTGGCATGAAAGCTGCACATCCAGTCAAGCATGAC 900
DB 281 CysProAlaProIleLeuIySGlnValGlyMetIysAlaIleuGlnValIserMetAsn 300
QY 901 GATGGCTCTCTTTATCTCCAGTTCGTATCATCATCACACACACATCTTTGACGGT 960
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCATCTGGGCACTGGCCCTGCTGATCTGTCTCTGCTGAGCCCTGCTCTCTG 1020
DB 321 SerIleLeuAlaIleAlaLeuIleLeuPheLeuLeuAlaLeuAlaLeuIleTyr 340
QY 1021 TGGTTCTGGCCCTCTGCTGCACTGTGATTAATCAAGAGGTCCCTCCACCCCTGCGAG 1080
DB 341 TrpPheThrProLeuCysCysThrValIleIleIySGlnValPropProProAlaGln 360
QY 1081 GAGAGTAGGAA 1092
DB 361 GluSerGlnGln 364

RESULT 3

US-09-918-715-232
Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-232

Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0

DB: 3 Gaps: 0
US-09-970-076-1_copy_104_1207 (1-1104) x US-09-918-715-232 (1-564)
QY 1 ATGGCCAGCGGAGCGAGAGAGCCCTGGCATGCGCTTCCAGTGGCTCTTTGGGCACT 60
DB 1 MetAlaThrAlaGlnArgArgAlaLeuGlyIleGlyPheGlnThrPheSerLeuAlaThr 20
QY 61 CTGGGCTCATGTCGCGCCGGGAGACCCAGGAGAGAGGGGGTCTGAGCTGCTAG 120
DB 21 LeuValLeuIleCysAlaGlyGlnGlyIyArgArgGlnAspGlyGlyProAlaCysTyr 40
QY 121 GGGGATTTGACCTGATCTTCAATTTTGAACAATCAGAAAGTGCTGACACCATGGAAT 180
DB 41 GlyGlyPheAspLeuThrPheIleLeuAspIySerValLeuHisStrPan 60
QY 181 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCAAAATTCATGACCCCACTTGAGATG 240
DB 61 GlnIleTyrTyrPheValGlnGlnLeuAlaHisIlyPheIleSerProGlnLeuArgMet 80
QY 241 TCGTTATATGTTTTCCTCCACCGGAGAGAACCTTAATGAACCTGACAGAGACAGAGA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGlnAspArgGln 100
QY 301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGACATTAATG 360
DB 101 GlnIleArgGlnGlyLeuGlnGlnLeuGlnIyValLeuProGlyGlyAspThrTyrMet 120
QY 361 CATGAAGATTGAAAGGCGCATGAGACAGATTATTAATGAACAAGAGGTACAG 420
DB 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrGlnAsnArgGlnGlyTyrArg 140
QY 421 ACGACAGGCTCATCTTCCTTGAATGAGAGAACTCCATGAATGCTCTTTCTAT 480
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyIyLeuHisGlnAspLeuPheThr 160
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGGTGTG 540
DB 161 SerGlnArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
QY 541 AAGATTTCATGAGACACAGCTGGCCCGATTCCGACAGTACATGTTTCCC 600
DB 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPhePro 200
QY 601 GTCAATGACGGCTTTGAGGCTGTGCAAGGATCATCCATTTTGAAGAGTCTGCG 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIlySylSerCys 220
QY 661 ATCGAAATTTAGCAGCTGAACCATCCACCATATGTGACAGAGTCAATTTCAAGTTGTC 720
DB 221 IleGlnIleLeuAlaIleGlnProSerThrIleCysAlaGlyGlnSerPheGlnValVal 240
QY 721 GTGAGAGGAAACGGCTTCCGACATGCCCCGACAGTGACAGGCTCTCTGACCTTCAAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheIys 260
QY 781 ATCAATGACTGGGCACTCAATGAGAGAGCCCTTTCTGTGAGAGACATTTATTAATG 840
DB 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGlnAspThrTyrLeuLeu 280
QY 841 TGTCACAGCCCTATCTTAAAGAGTTGGCATGAAAGCTGCACATCCAGTCAAGCATGAC 900
DB 281 CysProAlaProIleLeuIySGlnValGlyMetIysAlaIleuGlnValIserMetAsn 300
QY 901 GATGGCTCTCTTTATCTCCAGTTCGTATCATCATCACACACACATCTTTGACGGT 960
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCATCTGGGCACTGGCCCTGCTGATCTGTCTCTGCTGAGCCCTGCTCTCTG 1020
DB 321 SerIleLeuAlaIleAlaLeuIleLeuPheLeuLeuAlaLeuAlaLeuIleTyr 340
QY 1021 TGGTTCTGGCCCTCTGCTGCACTGTGATTAATCAAGAGGTCCCTCCACCCCTGCGAG 1080

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|||||
Db      341 TrpPheTrpProLeuCyScyThrValIleIleIleValProProProProIaGlu 360
QY      1081 GAGAGTGAGGAA 1092
Db      361 GluSerGluGlu 364

RESULT 4
US-10-301-822-199
/ Sequence 199, Application US/10301822
/ Publication No. US20030148410A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamackar, Shubhangi
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Thibodeau, Stephen N.
/ APPLICANT: Burgart, Lawrence J.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF COLON CANCER
/ FILE REFERENCE: MPM01-029P2RNM
/ CURRENT APPLICATION NUMBER: US/10/301,822
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 199
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
/ US-10-301-822-199

Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-301-822-199 (1-564)
QY      1 ATGGCCACGGCGGAGGAGAGCCCTCGGCGCTTCAGAGGCTCTTTGGCCACT 60
Db      1 MetAlIthraIaGluIuIaGlaIaIaGluIyIleGlyPheGlnItrpIeuSerIleuAlaIthr 20
QY      61 CTGGCTCTCATCTCGCGCGGCGGAGGAGGAGCGCAGGAGAGATGGGGCTCCAGCTCTAC 120
Db      21 LeuValIleuIleCySaIaIaGlyIaGlyIaGlyArgArgGluuSpGlyIaProIaCySerY 40
QY      121 GCGGATTTGACCTGTACTTCAATTTTGGACAATTCAGGAAGTGTCTGCAACCTGGAAT 180
Db      41 GlyGlyPheAspIeuYrPheIleIleuAspIySerGlySerValIleuHsIstPasn 60
QY      181 GAATCATATCACTTGTGGAAAGAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAATG 240
Db      61 GluIleIyTyIryrPheValGluGluIleuAlaHsIlyPheIleSerProGluIleuArgMet 80
QY      241 TCTTTATTTGTTTCTCCACCGAGGAACAACCTTAATGAATGACAGAAAGACAGAA 300
Db      81 SerPheIleValIaHesSerIthrArgIyThrThIleuMetIySerIthrGluuAspArgGlu 100
QY      301 CAATCGCTCAGGCGCTAGAAAGATTCAGAAAGTTCTGCCAGAGAGACACTTAACATG 360
Db      101 GlnIleArgGlnIaGlyIeuGluGluIleuGlnIyValIleuProGlyIaSpThrTyMet 120
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QY      361 CATGAAGATTGAAAGGCGCAGTGAAGATTTATGAAACAGACAAAGGTAACAG 420
Db      121 HisGluGlyPheGluIaArgIaSerGluGlnIleTyTyTyGluuAsnArgGlnIyIzArg 140
QY      421 ACAGCCAGCGTCATCATTTGCTTGACTGATGGAAATTCACGAAGATCTTTTCTAT 480
Db      141 ThrIaSerValIleIleIleIleuThrAspGlyIuIeIuHsIleGluAspIeuPhePheTy 160
QY      481 TCAGAGAGGAGGAGCTAAATAGTCTGAGATCTGTGGCAATTTGATCTGTGGTGG 540
Db      161 SerGluuArgGluIaAsnArgSerArgAspIeuGlyAlaIleValTyCyValGlyVal 180
QY      541 AAAGATTTCAATGACACACAGCTGGCCGGATTTGGGACAGTAAGATCATGTGTTCCC 600
Db      181 IySaSpPheAsnGlnIthrGlnIleuAlaArgIleAlaAspSerIyAspIstIaIaPhePro 200
QY      601 GTGAATGACGGCTTTCAAGCTCTGCAAGGCATCATCTCAATTTTGAAGAATCTTGC 660
Db      201 ValIaAsnAspGlyPheGlnIaIeGluIaGlyIleIleHsSerIleuIyAspSerCyS 220
QY      661 ATCGAAATCTGACAGCTGGAACCATCCACATATGTCAGAGAGATTCATTAAGTTC 720
Db      221 IleGluIleIleuAlaIaGluIuProSerThrIleCySaIaGlyGluSerPheGlnVal 240
QY      721 GTGAGAGGAAACGGCTTCGACATGCCCCGCAACGTGACAGGGTCTCTGACGTTCAAG 780
Db      241 ValaArgGlyAsnGlyPheArgHsIaIaArgAsnValaAspArgValIleuCySerPheIyS 260
QY      781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAAGACCTTATTTACTG 840
Db      261 IleAsnAspSerValIthrIeuAsnGluIySPropIeSerValGluAspThrTyIreIeu 280
QY      841 TGTCCAGGCGCTATCTTAAAGAAGTGGCAAGAAAGCGACTCCAGTCCAGCATGANC 900
Db      281 CySProIaAspIleuIeuIyGluIaGlyMetIySaIaIaIeGlnIaIaSerIleuAsn 300
QY      901 GATGCGCTCTCTTTATCTCCAGTCTGATCATCATCACCCACACACACTGTTCTGACGT 960
Db      301 AspGlyIeuSerPheIleSerSerSerValIleIleIthrThrThIeIySerAspGly 320
QY      961 TCCATCTCGGCGCATGCGCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTCTG 1020
Db      321 SerIleIeuAlaIleAlaIeIeuIleuIleuPheIleuIleuAlaIeIeuIuTrp 340
QY      1021 TGGTCTGGCGCCCTCGTGGCACTGTGATTCAGAGAGGTCCTCCACCCCTGCCGAG 1080
Db      341 TrpPheTrpProLeuCyScyThrValIleIleIyGluValIuProProProProIaGlu 360

QY      1081 GAGAGTGAGGAA 1092
Db      361 GluSerGluGlu 364

RESULT 5
US-10-408-765A-1823
/ Sequence 1823, Application US/10408765A
/ Publication No. US20040101874A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Fahy, Boi D.
/ APPLICANT: Zhang, Bing
/ APPLICANT: Gibson, Bradford W.
/ APPLICANT: Taylor, Steven W.
/ APPLICANT: Glenn, Gary M.
/ APPLICANT: Warnock, Dale E.
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
/ TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
/ FILE REFERENCE: 660088.465
/ CURRENT APPLICATION NUMBER: US/10/408,765A
/ CURRENT FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 3077
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1823
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; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

Alignment Scores:
Prod. No.: 3 24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-408-765A-1823 (1-564)

QY 1 ATGGCCAGCGCGAGCGAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 1 MetAlathrlagluwargalaleuGlyileGlypheGlnTrpleuSerleuAlathr 20

QY 61 CTGGTGTCTATTCGCGCGGCGAGGCGAGGAGAGATGGGGTCCAGCTGTCTAC 120
DB 21 LeuValleuileuCybalaglynglyGlyArgArgGluuApglyGlyProAlaCystr 40

QY 121 GGGGATTGACCTGTACTTCATTTTGACAAATCAGAAAGTGCTGACCACTGGAAT 180
DB 41 GlyGlypheApeuTyrrheileuApslySerGlySerValleuHishlstrpAsn 60

QY 181 GAATCTATTACTTTGTGAAACAGTTGGCTCACAAATTCACAGCCCACTTGAGATG 240
DB 61 GluileTyrrheValleuGluGlnleuAlahleuSerheleSerProGlnleuArgMet 80

QY 241 TCTCTTATTTGTTTCTCCACCCGAGGAAACACTTATGAAACTGACAGAAAGACAGAA 300
DB 81 SerpheileValPheSerThrArgGlyThrThreuleuTySerleuTrGluApgArgGlu 100

QY 301 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAATTCGCGAGGAGAGACACTTACATG 360
DB 101 GlnlleArgGlnGlyleuGlnleuGlnleuValleuProGlyGlyApgThrTyMet 120

QY 361 CATGAGAGATTGTAAGGCGCAGTGAAGATTTATTATGAAAACAGACAGGCTACAGG 420
DB 121 HieGluGlypheGluwargalaleuSerGluGlnleuTyrrGluuApgArgGlnGlyTyArg 140

QY 421 ACAGCCAGCTCATCATTTGCTTGTGATGATGGAACCTCCATGAAATCTCTTTTCTAT 480
DB 141 ThrleuSerValleuileuAlaLeuThrApgGlyGluuApglySerleuPhePheTyrr 160

QY 481 TCAGAGAGGAGGCTAATAGGCTCGAGATCTTGTCGAATGTTTCTGCTGGTGGTGTG 540
DB 161 SerGluwargGluuAlaApgSerArgApgleuGlyAlaileValTyrrCyValGlyVal 180

QY 541 AAAGATTTCATGAGACACAGCTGCGCGAGTTGCGGACAGTAAAGATCATGTGTTCCC 600
DB 181 LysApghehApgGlnuTrngInleuAlaArglleAlaApgSerTyrrApgHleValPhePro 200

QY 601 GTGAATACGAGCTTCAGGCTCTCGAAGGACATCATCCACTGAATTTTGAAGAGTCCCTGC 660
DB 201 ValApgApgGlypheGlnAlaLeuGlnGlyllelleuSerlleuLeuTyrrCyValGlyVal 220

QY 661 ATGCAATTTCTAGAGACAGTGAACATCCACCATATGTGAGAGAGATCATTTCAAGTTGTC 720
DB 221 lleGluileuAlaApgInuProSerThrleuCybalaglyGlyuSerPheGlnAlaVal 240

QY 721 GTGAGAGAAACGAGCTTCGACATGCCGCAACGTGACAGAGTCTCTGACGCTTCAG 780
DB 241 ValArgGlyApgGlnuTrngInleuAlaArgHishlApgApgValleuCySerPheTyrr 260

QY 781 ATCAATGACTCGGTACACATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 261 lleApgApgSerValThrleuApgGlnuTyrrProPheSerValGluuApgThrTyrrleu 280

QY 841 TGTCAGGCGCTATCTTAAAGAGAGTGGCATGAAGTGCATCCAGGTCCAGATGAAC 900
DB 841 TGTCAGGCGCTATCTTAAAGAGAGTGGCATGAAGTGCATCCAGGTCCAGATGAAC 900
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DB 281 CysProAlaProilleuTySerGluValGlyMetTyrrAlaAlaLeuGlnValSerMetAen 300
QY 901 GATGGCTCTCTTTATCTCCAGTTCTGTCATCATCACCACACACACTGTTCTGACGGT 960
DB 301 ApgGlyLeuSerPheleuSerSerValleuThrThrThrHishlstrpAspGly 320

QY 961 TCCATCTGGGCAATCGCGCTGTGATCTGTTCTGCTGCTGACCCCTGGCTCTCTGTG 1020
DB 321 SerilleuAlaAlaileuAlaLeuLeuileuPheleuLeuAlaLeuAlaLeuTrp 340

QY 1021 TGGTGTGAGCCCTCTGCTGTCACGTGATTAACAGAGAGTCCCTGACCCCTGGCGAG 1080
DB 341 TrpPheTrpProleuTySerCystrValleuileuTySerGluValProProProAlaGlu 360

QY 1081 GAGAGTGAAGAA 1092
DB 361 GluSerGluGlu 364

RESULT 6
US-10-474-794-187
; Sequence 187, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107,00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-187

Alignment Scores:
Prod. No.: 3 24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-474-794-187 (1-564)

QY 1 ATGGCCAGCGCGAGCGAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 1 MetAlathrlagluwargalaleuGlyileGlypheGlnTrpleuSerleuAlathr 20

QY 61 CTGGTGTCTATTCGCGCGGCGAGGCGAGGAGAGATGGGGTCCAGCTGTCTAC 120
DB 21 LeuValleuileuCybalaglynglyGlyArgArgGluuApglyGlyProAlaCystr 40

QY 121 GGGGATTGACCTGTACTTCATTTTGACAAATCAGAAAGTGCTGACCACTGGAAT 180
DB 41 GlyGlypheApeuTyrrheileuApslySerGlySerValleuHishlstrpAsn 60

QY 181 GAATCTATTACTTTGTGAAACAGTTGGCTCACAAATTCACAGCCCACTTGAGATG 240
DB 61 GluileTyrrheValleuGluGlnleuAlahleuSerheleSerProGlnleuArgMet 80

QY 241 TCTCTTATTTGTTTCTCCACCCGAGGAAACACTTATGAAACTGACAGAAAGACAGAA 300
DB 81 SerpheileValPheSerThrArgGlyThrThreuleuTySerleuTrGluApgArgGlu 100
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QY 301 CAAATCCGTCAAGCCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACATTACATG 360
| | | | |
Db 101 GlnIleArgGlnGlnIleuGlnIleuGlnIleuValIleuProGlyIleuPheThrTyrMet 120
| | | | |
QY 361 CATGAAGATTGAAAGGCGCCAGTGCAGATTATTATTAAGAAACGACAGAGGTACAG 420
| | | | |
Db 121 HIsGlnGlyPheGlnArgIleAsnSerGlnGlnIleTyrGlnuAsnArgGlnGlyTyrArg 140
| | | | |
QY 421 ACAGCAGAGGCTCATCTTGTGCTTGAAGTGAAGAACTCCATGAATCTCTTTTCTAT 480
| | | | |
Db 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyIleuUhiSerGlnuAsnLeuPhePheTyr 160
| | | | |
QY 481 TCAGAGAGGAGGCTTAATAGTCTCGAATCTTGGAATCTTGCAATTTACTGTGTGTGTG 540
| | | | |
Db 161 SerGlnuArgGlnuIleAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValGlyVal 180
| | | | |
QY 541 AAAGATTTCATATGACACACAGCTGGCCCGATTTGGCGACATGAGATCATGTGTTCCC 600
| | | | |
Db 181 LysAspPheAsnGlnuThrGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro 200
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QY 601 GTGAATGAGCGCTTTGAGGCTCGCAAGGATCATCATCATCTTTTGAAGAGTCTGCG 660
| | | | |
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuGlyLysSerCys 220
| | | | |
QY 661 ATCGAATTTCTAGCAGCTGAACCATCCATATGTGACAGAGATCATTTCAAGTTGTC 720
| | | | |
Db 221 IleGlnIleuAlaIleuAlaGlnuProSerThrIleCysAlaGlyGlnuSerPheGlnVal 240
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QY 721 GTGAGAGGAAACGGCTTCGACATGCCCCGACAGTGGACAGGGTCTTGACAGCTCAAG 780
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Db 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPheLys 260
| | | | |
QY 781 ATCAATGACTCGGTCACTCATATGAGAGAGCCCTTTGTGTGAGAGACATTATTACAG 840
| | | | |
Db 261 IleAsnAspSerValThrIleuAsnGlnuLysProPheSerValGlnuAspThrLysLeu 280
| | | | |
QY 841 TGTCCAGCGCTTACTTAAGAAAGTGGCATGGAAGCTGCATCCAGTCCAGTCAAGTAAAC 900
| | | | |
Db 281 CysProAlaProIleuGlnuValGlnuMetLysAlaIleuGlnuValSerMetAsn 300
| | | | |
QY 901 GATGCGCTCTTTTATCTTCAAGTTCTGTCATCATCACACACACATGTTTGACGGT 960
| | | | |
Db 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
| | | | |
QY 961 TCCATCTGGCCATCGCCCTGATCGCTGCTCTGCTCTAGCCCTGCTCCCTCG 1020
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Db 321 SerIleuAlaIleAlaIleuLeuIleuPheLeuLeuAlaIleuAlaIleuLeuTyr 340
| | | | |
QY 1021 TGGTCTGGCCCTCTGCTGCATCTGATATTATCAGAGAGGTCCCTCCAGCCCTGCGAG 1080
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Db 341 TrpPheTrpProIleuGlnuValIleIleValIleValIleValIleValIleValIleVal 360
| | | | |
QY 1081 GAGAGTGAGGAA 1092
| | | | |
Db 361 GlnuSerGlnu 364
| | | | |
RESULT 7
US-10-474-794-232
; Sequence 232, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107,00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-232
Alignment Scores:
Pred. No.: 3,246-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 4 Gaps: 0
US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-474-794-232 (1-564)
QY 1 ATGGCCAGCGCGGAGCGAGAGAGCCCTCGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60
| | | | |
Db 1 MetLatThrAlaGlnuArgAlaArgAlaIleuGlyIleGlyPheGlnuTrpLeuSerIleuAlaThr 20
| | | | |
QY 61 CTGGTGCTCATGTGCGCGCGGAGGAGGAGCCAGGAGAGATGGGGGTCCACCTGCTTC 120
| | | | |
Db 21 LeuValIleuIleCysAlaGlyGlnGlyArgArgGlnuAspGlyGlyProAlaCysTyr 40
| | | | |
QY 121 GCGGATTTGACCTGCTTCACTTCTTGGCAAAATCAGAGAGTGTGTCACACATGGAAT 180
| | | | |
Db 41 GlyGlyPheAspLeuTyrPheIleuGlnuLysSerGlySerValIleuHisIleuStrpAsn 60
| | | | |
QY 181 GAAATCTATTACTTTGTGGAAACAGTTGGCTCAAAATTCATCAGGCCCAAGTTGAGAAATG 240
| | | | |
Db 61 GlnuIleTyrTyrPheValGlnuGlnuIleuAlaHisLysPheIleSerProGlnuLeuArgMet 80
| | | | |
QY 241 TCTTTTATTTGTTTCTCCACCGGAGAGAACCTTAATGAACCTGACAGAAACAGAGAA 300
| | | | |
Db 81 SerPheIleValaPheSerThrArgGlyThrThrIleuMetLysLeuThrGlnuAspArgGln 100
| | | | |
QY 301 CAAATCCGTCAAGGCTTGAAGAACTCCGAAAGTTGTCGCGAGAGAGACACTTACATG 360
| | | | |
Db 101 GlnIleArgGlnGlnIleuGlnuIleuGlnuValIleuProGlyGlyAspThrTyrMet 120
| | | | |
QY 361 CATGAAGATTGAAAGGCGCCAGTGCAGATTATTATTAAGAAACGACAGAGGTACAG 420
| | | | |
Db 121 HIsGlnGlyPheGlnuArgAlaSerGlnuIleTyrTyrGlnuAsnArgGlnGlyTyrArg 140
| | | | |
QY 421 ACAGCAGCGCTATCATGCTTGTGACTGATGAGAACTCAGAAAGATCTCTTTTCTAT 480
| | | | |
Db 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnuLeuHisGlnuAspLeuPhePheTyr 160
| | | | |
QY 481 TCAGAGAGGAGGCTTAATAGTCTCGAATCTTGGAATCTTGCAATTTACTGTGTGTGTG 540
| | | | |
Db 161 SerGlnuArgGlnuIleAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValGlyVal 180
| | | | |
QY 541 AAAGATTTCATATGACACACAGCTGGCCCGATTTGGCGACATGAGATCATGTGTTCCC 600
| | | | |
Db 181 LysAspPheAsnGlnuThrGlnuAlaArgIleAlaAspSerLysAspHisValPhePro 200
| | | | |
QY 601 GTGAATGAGCGCTTTGAGGCTCGCAAGGATCATCATCATCTTTTGAAGAGTCTGCG 660
| | | | |
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuGlyLysSerCys 220
| | | | |
QY 661 ATCGAATTTCTAGCAGCTGAACCATCCATATGTCAGAGAGGATCATTTCAAGTTGTC 720
| | | | |
Db 221 IleGlnIleuAlaIleAlaGlnuProSerThrIleCysAlaGlyGlnuSerPheGlnuVal 240
| | | | |
QY 721 GTGAGAGGAAACGGCTTCGACATGCCCCGACAGTGGACAGGGTCTTGACAGCTCAAG 780
| | | | |
Db 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPheLys 260
| | | | |
QY 781 ATCAATGACTCGGTCACTCATATGAGAGAGCCCTTTGTGTGAGAGACATTATTACAG 840
| | | | |
Db 261 IleAsnAspSerValThrIleuAsnGlnuLysProPheSerValGlnuAspThrTyrIleu 280
| | | | |

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QY      841 TGTCCAGCGCTATTCTTAAAGAGTTGGATGAGTGAAGCTGCACTCCAGCTCAGCATGAAC 900
DB      281 CysProAlaProIleuLeuLysGluValGlyMetCysAlaIleuGluValSerMetAsn 300
QY      901 GATGGCCTCTCTTTTATCTCAGATTCTGTCATATCACACACACACTTTCTGACGT 960
DB      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrIleCysSerAspGly 320
QY      961 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTCTGG 1020
DB      321 SerIleuAlaIleAlaIleuLeuIleLeuPheLeuLeuAlaIleuAlaLeuLeuTrp 340
QY      1021 TGGTTCTGGCCCTCTGCTGCTGATGATATATCAAGAGAGTCCCTCCACCCCTGCCGAG 1080
DB      341 TrpPheTrpProLeuCysCysThrValIleIleLeuGluValProProProAlaGlu 360
QY      1081 GAGAGTGAGGAA 1092
DB      361 GluSerGluGlu 364

RESULT 8
US-10-979-159-187
; Sequence 187, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PaSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-187

Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 5 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-979-159-187 (1-564)
QY      1 ATGGCCAGCGGCGAGCGAGAGCCCTGCGCATCGGCTTCCAGGCTCTTTGGCCACT 60
DB      1 MetAlaThrAlaGluuArgAlaGluValIleGlyPheGlnTrpLeuSerIleuAlaThr 20
QY      61 CTGGTGTCTCATCTCGCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTTAC 120
DB      21 LeuValIleuIleCysAlaGlyGlnGlyLysArgArgGluuArgGlyProAlaCysTrp 40
QY      121 GCGGGAATTGACCTGTACTTATTTTGGACAATAATGAGGAATGTGCTGCACACTGGAAT 180
DB      41 GlyLysPheAspLeuLysPheIleLeuAspLysSerGlySerValIleuHisIleTrpAsn 60
QY      181 GAATTCATTACTTTGTGGACAGTGGCTCAAAATTCACAGCCCAAGTGAATG 240
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DB      61 GluIleTrpTrpPheValGluGluIleuAlaHisLysPheIleSerProGluLeuArgMet 80
QY      241 TCCTTTATGTTTTTCCACCCGAGGAGACACCTTATGAAATGACAGAGACAGAGAA 300
DB      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluuAspArgGlu 100
QY      301 CAATCCGTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTACATG 360
DB      101 GlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY      361 CATGAAGATTGAAAGGCGCAGTGCAGCATTTATTAAGAAACAGACAGAGGTACAGG 420
DB      121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpCysuAsnArgGlnGlyTrpArg 140
QY      421 ACAGCCAGGTCATCATTTGCTTGTGATGATGAGAACTCCATGAAATGCTCTTTTCTAT 480
DB      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluuAspLeuPhePheTrp 160
QY      481 TCAGAGAGGAGGCTATAGTCTCGAGATCTTGTCATTTGTTTACTGTGTGTGTG 540
DB      161 SerGluArgGluuAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValGlyVal 180
QY      541 AAGATTTCATGAGACACAGCTGCGCCGAGATTGCCAGACGTAAGATCATGTTGTTCCC 600
DB      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY      601 GTGAATGACGCGCTTTCAAGCTCTGCAAGGATATGATCATCTCATTTTGAAGATCCTCG 660
DB      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysLysSerCys 220
QY      661 ATGAAATTCTACAGCTGCAACCATCCACATATGTGTCAGAGAGTCAATTTCAAGTTGTC 720
DB      221 IleGluIleuAlaIleAlaGluProSerThrIleCysAlaGlyLysLeuPheGlnValVal 240
QY      721 GTGAGAGGAAACGCGCTTCCGACATGCCCGCAACGTGAGACAGGTCCTCTGACCTTCAAG 780
DB      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPheLys 260
QY      781 ATCAATGACTCGGTTCACATCAATGAGAACCCCTTTCTGTGAAGACACTTATTTTACG 840
DB      261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluuAspThrTrpLeuLeu 280
QY      841 TGTCCAGCGCTTATCTTAAAGAGTTGGATGAGTGAAGCTGCACTCCAGCTCAGCATGAAC 900
DB      281 CysProAlaProIleuLeuLysGluValGlyMetLysAlaIleuGlnValSerMetAsn 300
QY      901 GATGGCCTCTCTTTTATCTCAGATTCTGTCATATCACACACACTTTCTGACGT 960
DB      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrIleCysSerAspGly 320
QY      961 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTCTGG 1020
DB      321 SerIleuAlaIleAlaIleuLeuIleLeuPheLeuLeuAlaIleuAlaLeuLeuTrp 340
QY      1021 TGGTTCTGGCCCTCTGCTGCTGATGATATATCAAGAGAGTCCCTCCACCCCTGCCGAG 1080
DB      341 TrpPheTrpProLeuCysCysThrValIleIleLeuGluValProProProAlaGlu 360
QY      1081 GAGAGTGAGGAA 1092
DB      361 GluSerGluGlu 364

RESULT 9
US-10-979-159-232
; Sequence 232, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
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/ CURRENT FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US/09/918,715
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FASTSEQ for windows Version 3.0
/ SEQ ID NO 232
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-979-159-232

Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 5 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-979-159-232 (1-564)

QY 1 ATGGCCAGCGGAGGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 61 CTGGCTCATCTGCGCCGCGGCAAGGGGAGCGAGGAGGATGGGGTCCAGCCTCTAC 120
DB 21 LeuValLeuIleCysAlaGlyGlnGlyArgAlaGluAspGlyGlyProAlaCysTrp 40
QY 121 GCGGATTTGACCTGTGATCTTATTTGGACAATTCAGGAAGTGTGCTGCACCTGGAAT 180
DB 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValIleuHisTrpAsn 60
QY 181 GAAATCTATTACTTGTGGAGAACGTTGGCTCACAATTCATCGCCCAAGGTTGAGAATG 240
DB 61 GlnIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 241 TCCTTATTGTTTCTCCACCAGGAAACACTTAATGAACCTGACAGAGACAGAGAA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAspArgGlu 100
QY 301 CAAATCGTCAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAATG 360
DB 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 361 CATGAGAGATTGAAGGGCCAGTGAAGCATTTATTATGAAGACAGACAGGTTACAG 420
DB 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTrpGlyIleuAsnArgGlnGlyTrpArg 140
QY 421 ACAGCAGCGCTCATCTTGAAGTGAAGTGAAGAACTCCATGAAGATCTTTTCTAT 480
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160
QY 481 TCAGAGAGGAGCTTAATAGCTTCGAGATCTTGGTGCATTTGTTTACGTGTGGTGG 540
DB 161 SerGlnArgGlnIleAsnArgSerArgAspLeuGlyValIleValTrpCysValGlyVal 180
QY 541 AAAGATTTCAATGACACAGCGTGGCCGAGTTCGGAGCATGAAGATCATGTGTTTCC 600
DB 181 LysAspPheAsnGlnTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTGAATGACGCGCTTCAGGCTCTGCAAGGATCATCATCAATTTGAAGAAGTCTGCG 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 661 ATCGAAATTTAGACGCTGAACCATTCACCATATGTGCAGAGAGTCAATTTCAAGTTGTC 720
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DB 221 IleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
QY 721 GTGAGAGGAAAGCGCTTCGACATGCCCGCAACGTGACAGGGGTCCTTCAGCTTCAAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValIleAspArgValLeuCysSerPheLys 260
QY 781 ATCAATGACTCGGTGCACACTCAATGAGAACCCCTTTCTGTGGAAGACACTTATTACTG 840
DB 261 IleAsnAspSerValThrIleuAsnGlnLysProPheSerValGluAspThrTrpLeuLeu 280
QY 841 TGTCCAGCGCCCTATCTTAAAGAACTTGACATGAAGCTGCACCTCAGCTCAGCTGAAC 900
DB 281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaAlaLeuGlnValIleSerMetAsn 300
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DB 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCCATCTGGCCATCGCCCTGCTGATCCTGTTCTGCTTCAGCCCTGCTCTCTGCG 1020
DB 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTrp 340
QY 1021 TGGTTCGCGCCCTCTGCTGCACTGTGATTAACAGAGGTCCCTCCACCCCTGCGAG 1080
DB 341 TrpPheTrpProLeuCysCysThrValIleIleLysGlnValProProProAlaGln 360
QY 1081 GAGGTGAGGAA 1092
DB 361 GluSerGlnGlu 364
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RESULT 10

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US-11-047-278-6
/ Sequence 6, Application US/11047278
/ Publication No. US20050196407A1
/ GENERAL INFORMATION:
/ APPLICANT: Young, John A.T.
/ APPLICANT: Bradley, Kenneth A.
/ APPLICANT: Collier, Robert J.
/ APPLICANT: Mogridge, Jeremy S.
/ TITLE OF INVENTION: Anthrax Toxin Receptor
/ FILE REFERENCE: 960296, 97745
/ CURRENT APPLICATION NUMBER: US/11/047,278
/ CURRENT FILING DATE: 2005-01-31
/ PRIOR APPLICATION NUMBER: US/09/970,076
/ PRIOR FILING DATE: 2001-10-03
/ PRIOR APPLICATION NUMBER: 60/251,481
/ PRIOR FILING DATE: 2000-12-05
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-047-278-6
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Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-047-278-6 (1-564)
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DB 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 61 CTGGCTCATCTGCGCCGCGGCAAGGGGAGCGAGGAGGATGGGGTCCAGCCTCTAC 120
DB 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTrp 40
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121  GGGGATTTCACCGTCACTTCATTTGGACAAATCAGAAAGTGGCGACCACTGGAAAT 180
Db  41  G1G1yPheNapbLeuTyPheIleLeuNapbYsSerGlySerValLeuH1sh1tPshn 60
Qy  181  GAAATCATTAATCTTTGGAAACACTTGGCTTCACAAATTCACTCAGCCCAAGTTGAGAAATG 240
Db  61  GluIleTyTyrrPheValGluGlnLeuAlaH1bYsPheIleSerProGlnLeuArgMet 80
Qy  241  TCCTTTATATGTTTCTCCACCCGAGAAACAACCTTAATGAATCTGACAGAAAGACAGAA 300
Db  81  SerPheIleValPheSerThrArgGlyThrThreLeuMetYsLeuThrGluNapArgGlu 100
Qy  301  CAATCCGTCGAAGCCCTGAAGAACTCCAGAAACTTTCGCCAGAGAGACACTTACATG 360
Db  101  GlnIleArgGlnGlyLeuGlnGlnLeuGlnIlySerValLeuProGlyGlyNapThrTyMet 120
Qy  361  CATGAGAGATTGTAAGAGCCAGTGAGAGACAGATTATTAATGAAGAAACAGCAAGGTTACAG 420
Db  121  HisGlnGlyPheGlnIuArgAlaSerGluGlnIleTyTyrrGluNapNapGlnGlyTyArg 140
Qy  421  ACAGCCAGCGCTCATCTTGCTTTGATCTGATGAGAACTCCATGAAGATCTCTTTTCTAT 480
Db  141  ThrAlaSerValIleIleAlaLeuThrNapIlyGlnLeuHisGluNapLeuPhePheTyx 160
Qy  481  TCAGAGAGGAGGCGTAATAGTCTTCGAGATCTTGCGTGAATTTGTTACTGTGTGTGTG 540
Db  161  SerIuArgGlyAlaNapNapArgSerArgNapPheGlyAlaIleValTyCySerValGlyVal 180
Qy  541  AAGATTTCAATGAGACACACAGTGGCCCGGATTTGGCGGACAGTAAGATCATGTGTTCCC 600
Db  181  LysNapPheNapGlnThrGlnLeuAlaArgIleAlaNapSerTybNapHisValPhePro 200
Qy  601  GTGAATGACGGCTTTCAGGCTCTGTCAAGGACATCATCCATCAATTTTGAAGAAAGTCTCTG 660
Db  201  ValNapNapGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYsYsSerCyS 220
Qy  661  ATCGAAATTCATGACAGCTGAACCATCCACCATATGTGTGAGAGAGATCTTTCAAGTTGTC 720
Db  221  IleGlnIleLeuAlaAlaGluProSerThrIleCybAlaGlyGluSerPheGlnValVal 240
Qy  721  GTGAGAGAGAAACGGCTTCGACATGCGCCGCAACGCGGACAGGGTCCCTCGACGTTCAAG 780
Db  241  ValArgGlyNapGlyPheArgHisAlaArgNapValaNapArgValLeuCySerPheYs 260
Qy  781  ATCATATGACTGGTCACACTAATGAGAGCCCTTTCTGTGGAAGACACTTAATTTACTG 840
Db  261  IleNapNapSerValThrLeuNapGlnIlySerProPheSerValGluNapThrTyLeuLeu 280
Qy  841  TGTCCAGCGCTTATTTAAAGAGTTGGCATGAAGCTGCACTTCAGCTCAGCATGAAC 900
Db  281  CysProAlaProIleLeuYsGluValGlyMetCysValaAlaLeuGlnValSerMetNap 300
Qy  901  GATGGCCCTCTTTTATCTCCAGTTCTGTCAATCATCACACACACACTATGTTGAGCGGT 960
Db  301  AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
Qy  961  TCCATCTCTGGCCATGCGCCCTGTGATCTCTGTTCCGTCTTACGCTGGCTGCTCTCTG 1020
Db  321  SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuThr 340
Qy  1021  TGGTTCTGGCCCTCTGCTGCACTGTGATTTATCAAGAGAGTCCCTCCACCCCTGCGAG 1080
Db  341  TrpPheTrpProLeuCySerThrValIleIleYsGluValProProProProAlaGlu 360
Qy  1081  GAGAGCTGAGGAA 1092
Db  361  GluSerGlnGlu 364

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1  APPLICANT: Human Genome Sciences, Inc.
2  TITLE OF INVENTION: Albumin Fusion Proteins
3  FILE REFERENCE: PF546PCT
4  CURRENT APPLICATION NUMBER: US/09/833,245
5  CURRENT FILING DATE: 2001-04-12
6  PRIOR APPLICATION NUMBER: 60/259, 358
7  PRIOR FILING DATE: 2000-04-12
8  PRIOR APPLICATION NUMBER: 60/256, 931
9  PRIOR FILING DATE: 2000-12-21
10 PRIOR APPLICATION NUMBER: 60/199, 384
11 PRIOR FILING DATE: 2000-04-25
12 NUMBER OF SEQ ID NOS: 2267
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO: 621
15 LENGTH: 403
16 TYPE: prt
17 ORGANISM: Homo sapiens
18 US-09-833-245-621

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Alignment Scores:

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|------------------------|-----------|---------------|-----|
| Pred. No.: | 9,11e-180 | Length: | 403 |
| Score: | 1889.00 | Matches: | 360 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 94.31% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-09-970-076-1_COPY_104_1207 (1-1104) X US-09-833-245-621 (1-403)

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| OY | 1 | ATGGCAGAGGGAGAGGAGAGACCTCGGCATCGGCTTCAGATGGCTCTGTTGGGCACCT | 60 |
| Db | 1 | MetAlaIethAlaGluArgAlaArgAlaLeuGlyIleGlyPheGlnIrrPheSerLeuAlaIthr | 20 |
| OY | 61 | CTGTATCTCATCTGCACCCTGGGAGCAGGGAGCGCAGAGGAGATGGAGGGCTTCACGCTGTAC | 120 |
| Db | 21 | LeuValLeuIleGlyAlaGlyIleGlnGlyIleArgAlaGluAspGlyIleProAlaCysTyr | 40 |
| OY | 121 | GGCGGATTGACCTGTACTTCATTTTGGCAAAATCAGAAAGTGTGCTGCACCACTGGAAAT | 180 |
| Db | 41 | GIlyGIlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIleTPAsn | 60 |
| OY | 181 | GAATCTATTAATCTGTGGAGACAGTGGGTCAAAATTCATCAGCCCAAGTTAGAAATG | 240 |
| Db | 61 | GluIleTyrTyrPheValGlnGlnIleuAlaHisIleAspIleSerProGlnIleuAspMet | 80 |
| OY | 241 | TCTCTTATGTGTTTTCACCCGAGAAACAACCTTAATGAATGACAGAAAGACAGAA | 300 |
| Db | 81 | SerPheIleValPheSerThrArgGlyIleThrIleuMetLysLeuThrGluAspArgGlu | 100 |
| OY | 301 | CAATCGGTCAAGGCTTAGAAGATCTCCAGAAAGTTCTGCCAGAGAGAGACCTTAATG | 360 |
| Db | 101 | GlnIleArgGlnGlyLeuGlnGluIleuGlnLysValLeuProGlyGlyAspThrTyrMet | 120 |
| OY | 361 | CATGAAGATTTTAAAGGGCCAGTAGAGCAGATTTTATGAAAACAGACAGGGTACAGG | 420 |
| Db | 121 | HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGluAsnAspGlnGlyTyrArg | 140 |
| OY | 421 | ACAGCCAGCGTCATCTTCCTTGAATGATGAGAACTCCATGAAGATCTTTTCTAT | 480 |
| Db | 141 | ThrAlaSerValIleIleAlaLeuThrAspGlyGlyIleuHisGlnAspLeuPhePheTyr | 160 |
| OY | 481 | TTCAGAGGGAGGCTTAAGATCTGAGATCTTGGTGAATGGTTTACTGTGGTGGAGTG | 540 |
| Db | 161 | SerGlnArgGlnLysAsnAspSerAspArgPheLeuGlyAlaIleValTyrCysValGlyVal | 180 |
| OY | 541 | AAAGATTTCAATAGACACAGACGTGGCCCGGATTTGGGACAGTAAGAGATGATGTGTTCCC | 600 |
| Db | 181 | LysAspPheAsnGlnIrrGlnIleuAlaArgIleAlaAspSerLysAspHisValIrrPhePro | 200 |
| OY | 601 | GTGAATGACGGCTTTCAAGCTCTGCAGGACATCAACCTCAATTTGAAAGAACTCCTGC | 660 |
| Db | 201 | ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysValLysSerCys | 220 |

QY 661 ATCGAAATCTACACGTGAACCATCCACCATATGTGCAGAGAGTTCATTCAATGTTGTC 720
DB 221 IIEGLUIIELEUHLAIAAGIUPROSETHRIIECYALAGIYGIUSERPHEGINVALVAL 240
QY 721 GTGAGAGAAACGGCTTCCGACATGCCCCGACAGTGGACAGGGTCTCTGACAGTTCAAG 780
DB 241 VALARGGLYASNGIYPHEARGHISALARGASNAVALASPARGYALLEUCYSSERPHELYS 260
QY 781 ATCAATGACTCGGTCACTCAATGAGAGAACCCCTTTCTGTGAGAGACATTATTACTAG 840
DB 261 IIEASHPSESRVALTHRIEUSANGIULYSPROPHESERVALGILUSPHTHYRLEUEN 280
QY 841 TGTCCAGCCCTATCTTAAAGAAGTTGGCATAAGAGCTGCACAGTCAGTCAGATGAAC 900
DB 281 CYSPTOLAPROLIEULEUYSGLIUALGIMETLYBALALEUGINVALSERMETAN 300
QY 901 GATGGCTCTCTTTATCTTCAGATTCTGCATCATACCCACACACTGTTTGAAGGT 960
DB 301 ASPGIYLEUSERPHEHIESESRSERVALLEIETHRTHRTHRSYSSERAPGLY 320
QY 961 TCCATCTGGCCATCGCCCTGTGATCTGTTCTGTGCTGACCCCTGAGTCTCTG 1020
DB 321 SEIIELEUHLAIALEUHLAIEULEUHLIELEUPHEULEUHLAIEUHLAIEULEUTIP 340
QY 1021 TGGTTCTGGCCCTGTGCTGCTGACATGTGATTATCAAGAGAGTCCCTCCACCCCTGCGAG 1080
DB 341 TRPHEHTRPROLEUCYCSYTHRVALLEIIELEUGIULVALPROPPTOPROLAAGLU 360
QY 1081 GAGAGTGAG 1089
DB 361 GLUSERGLU 363

RESULT 12

US-09-833-245-620
Sequence 620, Application US/09833245
Publication No. US20040101341
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PPS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 620
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (330)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (368)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Alignment Scores:

Pred. No.: 7,29e-178 Length: 403
Score: 1870.00 Matches: 360
Percent Similarity: 99.17% Conservative: 0

Best Local Similarity: 99.17% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-1_copy_104_1207 (1-1104) x US-09-833-245-620 (1-403)

QY 1 ATGGCCACGGCGGAGACCGGAGAGCCCTCGCATCGCTTCAGTGGCTCTTTGGCCACT 60
DB 1 METALATHRALAGIULARGYRGLALEUGIYIIEGLYPHEGINTRPHEUSERLEUALTHR 20
QY 61 CTGTCGCTCATCTGGCCCGGCGAAGGGGACCCAGAGAGGAGGGGCTCCACCTGCTAC 120
DB 21 LEUVALLEULIECYALAGIYINGIYIYAGARGIULASPGIYGLYPTOLACYSYR 40
QY 121 GCGGATTTGACCTTACTTCTTATTTGCAATGAGAAAGTGTCTGCACACCTGGAAT 180
DB 41 GYGLYIPHEASPLEUDTYRPHIELEUASPLYSSERGIYSERVALLEUHLISHISTRAPH 60
QY 181 GAAATCTATTACTTTGTGGACAGTTGGCTCAAAATTCATGACCCACAGTTGAGATG 240
DB 61 GIUIETRYRYPHEVALGILUGINLEUHLAHLISLYSPHEIIESETRPGLINLEUARGMET 80
QY 241 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAAATGACAGAAAGAGAGA 300
DB 81 SERPHEILEVALPHESERTHRARGLYTHRINLEUMELYSLEUTHRGILUSPARGLIU 100
QY 301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTTCCSCAGAGAGACACTTACATG 360
DB 101 GINIEHARGINGIYLEUGIULIUEUGINLYSVALLEUPROGLYGLYASPTHTRYMET 120
QY 361 CATGAGAGATTGAAAAGGCGCAGTGAAGCATTTATATGAAAACAGACAGGATCAGAG 420
DB 121 HISGLUGIYPHEGLIULARGYALASERGIULGINIETRYRGLIULASARGINGIYTRARG 140
QY 421 AAGCCAGGTCATCATTTGCTTTGACATGAGAGAACTCCAGAGAGATCTCTTTTCTAT 480
DB 141 THRILASERVALLEIIELEUHLAIEUTHRSPRGYGLULEUHLISGLIUSPREUHEPHELYR 160
QY 481 TCAGAGAGGAGGCTTAATGAGTCTCGAGATCTTGTGCAATTTACTGTGTGGTGTG 540
DB 161 SERGIULARGIULALASHPRGSERARGASPLEUGIYALALIE***TYRCYSVALGILYVAL 180
QY 541 AAAGATTTCAATGAGACACAGCTGSCCGGATGCGGACAGTGAAGATCATGTGTTCCC 600
DB 181 LYSAPRPHASNGIUTHRGILINLEUHLAARGIIEALASPSERYALASPIVALPREPRO 200
QY 601 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCACTCAATTTTGAAGAAGCTCTG 660
DB 201 VALASHPGLYPHEGLINALEUGINGIYIIEHLISSETRILEUULYSSESYCS 220
QY 661 ATCGAAATCTGACAGCTGAACCATCCACCATATGTGCAGAGAGTTCATTCAATGTTGTC 720
DB 221 IIEGLUIIELEUHLAIAAGIUPROSETHRIIECYALAGIYGIUSERPHEGINVALVAL 240
QY 721 GTGAGAGAAACGGCTTCCGACATGCCCCGACAGTGGACAGGGTCTCTGACAGTTCAAG 780
DB 241 VALARGGLYASNGIYPHEARGHISALARGASNAVALASPARGYALLEUCYSSERPHELYS 260
QY 781 ATCAATGACTCGGTCACTCAATGAGAGAACCCCTTTCTGTGAGAGACATTATTACTAG 840
DB 261 IIEASHPSESRVALTHRIEUSANGIULYSPROPHESERVALGILUSPHTHYRLEUEN 280
QY 841 TGTCCAGCCCTATCTTAAAGAAGTTGGCATAAGAGCTGCACAGTCAGTCAGATGAAC 900
DB 281 CYSPTOLAPROLIEULEUYSGLIUALGIMETLYBALALEUGINVALSERMETAN 300
QY 901 GATGGCTCTCTTTATCTTCAGATTCTGCATCATACCCACACACTGTTTGAAGGT 960
DB 301 ASPGIYLEUSERPHEHIESESRSERVALLEIETHRTHRTHRSYSSERAP*** 320
QY 961 TCCATCTGGCCATCGCCCTGTGATCTGTTCTGTGCTGACCCCTGAGTCTCTCTG 1020
DB 321 SEIIELEUHLAIALEUHLAIEULEUHLIELEUPHEULEUHLAIEUHLAIEULEUTIP 340

Percent Similarity: 97.75% Conservative: 6
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 89.52% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-918-715-301 (1-562)

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DB 7 LeuGlyAlaGlyLeuKArgGlyLeuCyValAlaAlaLeuValLeuValCyAlaGlyHis 26
QY 85 GGGGGACGCGAGGAGATGGGGCTCAAGCTCTACGGCGGATTTGAATTAATTCATT 144
DB 27 GlyGlyArgArgGlyLeuArgGlyProAlaCyGlyGlyPheAspLeuTyrPheIle 46
QY 145 TTGGCAAAATCAGAAAGTGCTGCAACCACTGGAATGAATCAATTAATTTGGGAACG 204
DB 47 LeuAspLysSerIysSerValLeuHisHisIlePheAspGlnIleTyrTyrPheValGluGln 66
QY 205 TTGGCTCACAAATTCATCAGCCCAAGTTGAGATGCTCTTTATGTTTCTCCACCGA 264
DB 67 LeuAlaHisArgPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 86
QY 265 GGAACAACCTTAATGAAGTGAACAAGACAGAAACAATCCGTCAAGGCTTAAGAA 324
DB 87 GlyThrThrLeuMetLysLeuThrGlnAspArgGlnIleArgGlnGlyLeuGlnGln 106
QY 325 CTCGCAAAAGTTTGGCAGAGAGACACTTAATCAATGAAGATTTGAAGGGCGAGT 384
DB 107 LeuGlnLysValLeuProGlyGlyAspPheThrMetHisIleGlnIlePheGlnArgAlaSer 126
QY 385 GAGCAGATTATATGAAAAACAGACAGGCTACAGGACCGCTCATTCATTGCTTG 444
DB 127 GluGlnIleIleTyrGlyLeuAsnSerGlnGlyTyrArgThrAlaSerValIleIleAlaLeu 146
QY 445 ACTGATGAGAACTCCATGAAGATCTCTTTTCTATTGAGAGGGAGGCTTAATAGTCT 504
DB 147 ThrAspGlyGlyLeuHisIleGlnAspLeuPhePheTyrSerGlnArgIleAlaAsnArgSer 166
QY 505 CGAGATCTTGGTGCATTTGTTTCTGTGTTGGTGAAGAAATTTCAATGAGACAGCGT 564
DB 167 ArgAspLeuGlyAlaIleValIleTyrCyValGlyValLysAspPheAsnGlnIleThrGlnLeu 186
QY 565 GCCCGATTCGCGACAGTAAGATCATGTGTTCCGCGATGACGGCTTTCAGGCTCTG 624
DB 187 AlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeu 206
QY 625 CAAGCATCATCCATCAATTTGMAAGAGTCTGCAATGGAATTTCAAGAGCTGAACA 684
DB 207 GlnGlyIleIleHisSerIleLeuLysLysSerCysIleGlnIleLeuAlaIleGlnPro 226
QY 685 TCCACATATGTCAGAGAGTGCATTTCAAGTGTGTGAGAGAAACGGCTTCCGACAT 744
DB 227 SerThrIleCyAlaGlyLeuSerPheGlnValValValArgIleAsnGlyPheAlaGlyHis 246
QY 745 GCCCGAACGTCGACAGGCTCTCTGCAAGCTTCAAGATCAATGATCCGCTCACACTCAAT 804
DB 247 AlaArgAsnValAspArgValLeuCySerPheLysIleHisAspSerValIleThrLeuAsn 266
QY 805 GAGAACCCCTTTCTGTGAAACACTTATTTACTGTCTCAGCGCCCTATCTTAAAGAA 864
DB 267 GluLysProPheAlaValGlnAspPheTyrLeuLeuCyAspProAlaIleLeuLysGln 286
QY 865 GTTGGATGAAGTCAAGTCCAGGTCAGATGAAGTGAAGTGGCTCTTTATTCACAGT 924
DB 287 ValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSerSer 306
QY 925 TCTGTATCATCAACCAACACACTGTTCTGACGGTTCATCTGCGCATCGCCCTGTG 984
DB 307 SerValIleIleThrThrThrHisCysSerAspGlySerIleLeuAlaIleAlaLeuLeu 326
QY 985 ATCTGTCTCTGCTCTAGCCCTGAGCTCTCTGTGAGTGTGGCCCTCTGCTGCACT 1044
DB 1044
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DB 327 ValLeuPheLeuLeuLeuAlaLeuAlaLeuTyrTrpPheTrpProLeuCyCysThr 346
QY 1045 GTGATTATCAAGAGATCCCTCCACCCCTGCGGACGAGAGTGAAGAA 1092
DB 347 ValIleIleLysGlnValProProProProValGlnGlnSerGlnGln 362
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RESULT 15

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US-10-474-794-194
; Sequence 194, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107 00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 562
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-474-794-194
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Alignment Scores:

| Pred. No.: | 4,24e-170 | Length: | 562 |
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| Score: | 1793.00 | Matches: | 342 |
| Percent Similarity: | 97.75% | Conservative: | 6 |
| Best Local Similarity: | 96.07% | Mismatches: | 8 |
| Query Match: | 89.52% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-474-794-194 (1-562)

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QY 25 CTCGGATCGGGCTTCAGATGGCTCTCTTTGGCCACTGTGGTCTCATCTGCGCCGGGCA 84
DB 7 LeuGlyAlaGlyLeuKArgGlyLeuCyValAlaAlaLeuValLeuValCyAlaGlyHis 26
QY 85 GGGGGACGCGAGGAGATGGGGCTCAGCTGCTACGGCGGATTTGAATTAATTCATTGCTTG 144
DB 27 GlyGlyArgArgGlyLeuArgGlyProAlaCyGlyGlyPheAspLeuTyrPheIle 46
QY 145 TTGGCAAAATCAGAAAGTGCTGCAACCACTGGAATGAATCAATTAATTTGGGAACG 204
DB 47 LeuAspLysSerIysSerValLeuHisHisIlePheAspGlnIleTyrTyrPheValGluGln 66
QY 205 TTGGCTCACAAATTCATCAGCCCAAGTTGAGATGCTCTTTATGTTTCTCCACCGA 264
DB 227 SerThrIleCyAlaGlyLeuSerPheGlnValValValArgIleAsnGlyPheAlaGlyHis 246
QY 265 GGAACAACCTTAATGAAGTGAACAAGTGCAGAAACAATCCGTCAAGGCTTAAGAA 324
DB 287 ValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSerSer 306
QY 325 CTCGCAAAAGTTTGGCAGAGAGACACTTAATCAATGAGATTTGAAGGGCGAGT 384
DB 107 LeuGlnLysValLeuProGlyGlyAspPheThrMetHisIleGlnIlePheGlnArgAlaSer 126
QY 385 GAGCAGATTATATGAAAAACAGACAGGCTTACAGGACGCGCTCATCTGCTTG 444
DB 127 GluGlnIleIleTyrGlyLeuAsnSerGlnGlyTyrArgThrAlaSerValIleIleAlaLeu 146
QY 445 ACTGATGAGAACTCCATGAAGATCTCTTTTCTATTGAGAGGGAGCTAATAGTCT 504
DB 147 ThrAspGlyGlyLeuHisIleGlnAspLeuPhePheTyrSerGlnArgIleAlaAsnArgSer 166
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QY 505 CGAGATCTTGTCATTTGTTTACTGTGTGTGTGAAAGATTTCATGAGACAGACTG 564
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Db 167 ArgAspLeuGlyAlaIleValIYrCyValGlyValIYasPheAsnGluThrGlnLeu 186
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QY 565 GCCCGAATTGCGGACAGTAAGATCATGTGTTTCCCGTAATGACGGCTTTCAGGCTCTG 624
    |||
Db 187 AlaArgIleAlaAspSerIYbAspHisValPheProValAsnAspGlyPheGlnAlaLeu 206
    |||
QY 625 CAAGGCATCATCCATCAATTGTAAGAAGTCTGTCATCGAAATTCAGACGCTGAACCA 684
    |||
Db 207 GlnGlyIleIleHisSerIleLeuIYbSerCyIleGluIleLeuAlaIleGluPro 226
    |||
QY 685 TCCACCATATGTGAGAGAGTCAATTCAAGTTGTGTGAGAGAAACGGCTTCCGACAT 744
    |||
Db 227 SerThrIleCyAlaGlyIYbSerPheGlnValValArgGlyAsnGlyPheArgHis 246
    |||
QY 745 GCCCGCAACGTGACAGAGGTCTCTGACGCTTCAAGATCAATGACTCGATCAGACTCAAT 804
    |||
Db 247 AlaArgAsnValAspArgValIleuCySerPheIYbSerValIThrLeuAsn 266
    |||
QY 805 GAGAAAGCCCTTTCTGTGAAAGACATTATTACTGTGTCCAGCGCTATCTTAAAGAA 864
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Db 267 GluIYbSerPheAlaValGluAspThrTYrLeuLeuCySerProAlaProIleLeuIYbGlu 286
    |||
QY 865 GTTGGCATGAAAGCTGACTCCAGGTGACATGAAAGATGGCTCTTTATCTCCAGT 924
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Db 287 ValGlyMetIYbAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSerSer 306
    |||
QY 925 TCTGTCAATCAACCAACACACTGTTTGACCGGTTCCATCTGAGCCATCGCCCTGCTG 984
    |||
Db 307 SerValIleIleThrThrThrHisCySerAspGlySerIleLeuAlaIleAlaLeuLeu 326
    |||
QY 985 ATCTGTCTCTGCTCTAGCCCTGGGCTCTCTCTGTGTGTGTGCCCCCTCTGCTGCACT 1044
    |||
Db 327 ValIleuPheLeuLeuAlaLeuAlaLeuAlaLeuLeuTrpPheTrpProLeuCySerThr 346
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QY 1045 GTGATTATCAAGGAGGTCCCTCCACCCCTGCCGAGAGAGAGTGAAGAA 1092
    |||
Db 347 ValIleIleIYbGluValProProProValGluGlnSerGluGln 362
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Job time : 176.732 secs

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Alignment Scores:

Pred. No.: 4,18e-175 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 7 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-186-264-199 (1-564)

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QY 61 CTGGTCTCATCTGCGCCGGGCGAAGGGGAGCGAGGAGGATGGGGGTCACGCTCTCC 120
DB 21 LeuValLeuIleCysAlaGlyIngIyGlyAxxArgGluAspIlyGlyProAlaCysTyr 40
QY 121 GCGGATTTGACCTGTATCTTCATTTTGGACAAATCAGAAAGTGTGCTGCACATCGAAT 180
DB 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrPhe 60
QY 181 GAAATGTATTACTTTGTGGAAAGTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 240
DB 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIleLysPheIleSerProGlnLeuArgMet 80
QY 241 TCGTTATTGTTTTCCTCCACCGAGGAAACAACTTAATGAAATGACAGAAAGACAGAA 300
DB 81 SerPheIleValPheSerThrArgIyThrThleuMetLysLeuThrGluAspArgIy 100
QY 301 CAATCCGTCAAGCGCTAGAAAGACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
DB 101 GlnIleArgGlnIlyLeuGlnGluLeuGlnIlyValLeuProIyGlyAspThrTyrMet 120
QY 361 CATGAAGATTGAAAAGGCGCACTGAGACAGATTATTATGAAAACAGACAGGTTACAG 420
DB 121 HisGlnGlyPheGlnIuArgAlaSerGlnIlyGlnIleTyrGlnIuAspArgIngIyAxx 140
QY 421 AAGCCAGGCTCATCTTGTGACGTAGAGAGAACTCCATGAATCATCTTTCTTCTAT 480
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPheTyr 160
QY 481 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGTGCAATTGTTACTGTGTGGTGG 540
DB 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIyrcysValGlyVal 180
QY 541 AAGATTTTCATAGACACACAGCTGGCCCGGATTCGCGACGTAAGATCATGTGTTCCC 600
DB 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTGATGAGCGGCTTTCAGGCTCGCAAGGATCATCATCATCTTTTGAAGAGTCTCG 660
DB 201 ValAsnAspIlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 661 ATCGAAATTTCTACAGCTGAACCATCCATCATATGTGCAAGAGAGTCAATTCAGTTGTC 720
DB 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValIle 240
QY 721 GTGAGAGGAAAAGGCTTCCGACATGCCCGCAACGTGGACAGGGTCTCTGCGACTTCAAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 781 ATGAATGACTCGGCTGCACATCATAGAGAGCCCTTTTCTGTGAAGACCTTTATTAACG 840
DB 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTyrIleLeuLeu 280
QY 841 TGTCCAGCGCTATTCTTAAAGAAGTTGGCATGAAGAGTCACTCCAGGTCACATGAAC 900
DB 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIleAlaLeuGlnValIleSerMetAsn 300
QY 901 GATGCGCTCTCTTTTATCTCCAGTTCTGTCAATCAACCAACACACTGTTCTGACGGT 960
DB 901 GATGCGCTCTCTTTTATCTCCAGTTCTGTCAATCAACCAACACACTGTTCTGACGGT 960
```

```
DB 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCCATCTGGGACATGCGCCCTGTGATCTGTTCTGTCTGATGAGCCCTGCTCTGCG 1020
DB 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaIleAlaLeuLeuTrp 340
QY 1021 TGGTTCGCGCCCTGTGCTGCATGTGATTAACAAGAGTCCCTCCAGCCCTGCGCAG 1080
DB 341 TrpPheTrpProLeuCysCysThrValIleIleLysGluValProProProAlaGlu 360
QY 1081 GAGAGTGAGGAA 1092
DB 361 GluSerGluGlu 364
```

RESULT 2

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US-11-080-026-4
/ Sequence 4, Application US/11080026
/ Publication No. US20050260192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shimooka, Motomu
/ APPLICANT: Lu, Chafren
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
/ FILE REFERENCE: CFBP-P02-021
/ CURRENT FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: US/11/080,026
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1152
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-080-026-4
```

Alignment Scores:

Pred. No.: 1,94e-06 Length: 1152
Score: 145.50 Matches: 60
Percent Similarity: 45.85% Conservative: 45
Best Local Similarity: 26.20% Mismatches: 81
Query Match: 7.26% Indels: 43
DB: 7 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-080-026-4 (1-1152)

```
QY 130 GACCTGTACTTCATTTTGGACAATCAGAGAGTGTGCTG---CACCACTGAATGAATC 186
DB 150 AspIleAlaPheLeuIleAspIlySerGlySerIleIleProHisAspPheArgMet 169
QY 187 TATTACTTTGTGGAACAGTGTGCTCAAAATTCATCAGCCCACTGTGGAATGTCTCTT 246
DB 170 LysGluProValaSerThr-----ValMetGluGlnLeuLysLysSerLys 184
QY 247 ATTGTTTTCACACCGGAGGAAACACTTAATGAATCAGAGAGAC----- 294
DB 185 ThrLeuPheSer-----LeuMetGlnTyrSerGluGluPheArgIleHis 199
QY 295 -----AGAGAAACAATCCGTCAAGGCGCTAGAGAACTCCAG 330
DB 200 PheThrPheLysGluPheGlnAsnAsnProAsnProArgSerLeuValLysProIleThr 219
QY 331 AAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGAAAAGGCGCTGAGCAG 390
DB 220 GlnLeuLeu-----GlyArgThrHisThrAlaThrGlyIleArgSerValArgGln 237
QY 391 ATTATTATGAAGAAACAGCAAGGTTACAGAGACGC---AGGTCATCATGCTTGGACT 447
DB 238 LeuPheAsnIleThrAsnGlyAlaArgLysAsnAlaPheLysIleLeuValValIleThr 257
```

[illegible]

```

RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: prt
; ORGANISM: Homo Sapiens
US-11-186-284-26

Alignment Scores:
Pred. No.: 2,94e-05 Length: 3063
Score: 134.50 Matches: 81
Percent Similarity: 43.10% Conservative: 44
Best Local Similarity: 27.93% Mismatches: 123
Query Match: 6.71% Indels: 42
DB: 7 Gaps: 17

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-186-284-26 (1-3063)
QY 130 GACCTGTACTTATTGTCAGCAATCAGAGTGTG---CTGCACCACTGATGATGATC 186
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 AaPlIeVaIphNuEuVaIaMpOlySeRrYSeRrIleGyIiIaIaSnPhEuVaIySvaI 459

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| | | | | |
|----|--|-----|--|-----|
| OY | | 187 | TATTACTCTGGGAACAGTGTGCTCAAAATTC---ATCAGGCCA---CAGTTGGAAAG | 240 |
| Dd | | 460 | ArgAlaPheLeuGIValIeUValLysSerPheGIULeSerProAsnArgAlaGlnIle | 479 |
| OY | | 241 | TCCTTTATGTTTTCTCCACC-----CGAGAACAACCTTAATAACTGCACAGA | 291 |
| Dd | | 480 | SerLeuValGIInTySerArgAspProHisThrGluPheThrLeuLysValSyrPheThrLys | 499 |
| OY | | 292 | GACAGAGAACAAATCCGTCAGAGCCTTAGAAGAACTCCAGAAAGTTCTGCCA-----GGA | 345 |
| Dd | | 500 | ValGIuaPheIlelle-----GIuaIaIIeaSnThrPheProTyArgGIly | 514 |
| OY | | 346 | CGAGACACTCATCATGAAAGATTTTGAAAGGCGCAGTGCAGACAGATTATTATGAAAAC | 405 |
| Dd | | 515 | GIySerThrAenThrGILyLysAlaMetThrTyValArgGILySerIlePheValProSer | 534 |
| OY | | 406 | AGACAGAGGTACAGACA-----GCCAGCTCATCTTGGCTTTGACTGTATGAGAAATC | 459 |
| Dd | | 535 | Lys---GIySerArgSerAsnValProLySValMetIleLeuIleThrAspGIlys-- | 552 |
| OY | | 460 | CATGAAGATCTCTTTTCTATTCAGAGAGGAGGCGTAATAGGCTCGAATCTGTGTCA | 519 |
| Dd | | 553 | SerSerAspAlaPhe-----ArgAspProAlaIleLysLeuArgAsnSerAspVal | 565 |
| OY | | 520 | AATGTTTCTGTGTGTGTGAAGATTTTCATGAGACAAGCTGGCCCGAGTTGCGAC | 579 |
| Dd | | 570 | GIUIePheAlaValGIyValLysAspAlaValArgSerGIuLeuGIuaIleAlaIser | 589 |
| OY | | 580 | -----AGTAAGATCATGTGTGTTCCCGTGAAATGACGCGTTTCAGCGCTTCGAAGCATC | 633 |
| Dd | | 590 | ProProAlaGIInTyHHisIvalAlaPheThrValGIuaPhe---PheAspAlaPheGIuaAgIle | 608 |
| OY | | 634 | ATCCACTCAATTTTGAAGAAAGTCGTCAGCAAAATTCAGAGCTAACCATCCACCAT | 693 |
| Dd | | 609 | SerPheGIuLeuThrGIuSerIleCySLeuAglile-----GIUGInGIuLeuAla | 625 |
| OY | | 694 | TGTGACAGAGACTCATTTTCAGTGTGTGTAAGAGAAACGCGTTCCGACATGCCCCGAC | 753 |
| Dd | | 626 | AlaIleLysLysLysAlaIalTyAlProProLySAspLeuSerPheSerGIuaIalThnSer | 645 |
| OY | | 754 | GTCGACAGAGGTCCTTCGACAGCTTCACAAGATCATGACTCGSTCACACTCATAGMAAGCCC | 813 |
| Dd | | 646 | Tyr-----GIyPheLysThrAenTrpSer---ProAlaGIyGIuaEnVal | 659 |
| OY | | 814 | TTTTCTGTGGAGACACTTATTACTGTGTGTCAGAGCCTATCTTAAGAAGTTGGCATG | 873 |
| Dd | | 660 | PheSerTyArgHisIleThrTyr-----LysGIuaIaIaGIly | 671 |
| OY | | 874 | AAAGTGCACCTCCAGATGCAGATGAAGATGCGCTCTCTTTATCTCCAGTTGTGCATC | 933 |
| Dd | | 672 | AspAspGIuaIalThnVal---ValGIuPro-AlaSerSerThrSerValIalLeuSerSe | 690 |
| OY | | 934 | ATCACCAACCACACACTGTTTCTGACGTT | 961 |
| Dd | | 690 | IleuLysProGIuThrLeuTyLeuVal | 699 |

```

RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
;

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```
/ PRIOR APPLICATION NUMBER: 60/636,239
/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 2
/ LENGTH: 739
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-11-057-047-2

Alignment Scores:
Pred. No.: 0.00208 Length: 739
Score: 113.50 Matches: 66
Percent Similarity: 38.28% Conservative: 63
Best Local Similarity: 19.58% Mismatches: 109
Query Match: 5.67% Indels: 99
DB: Gaps: 17

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-057-047-2 (1-739)

QY 82 CAAAGGCGACGCGAGGAGTGCG---GGTCCAGCC----- 114
   |||||
Db 218 GIUGLYVALAEPALAGIUNBPGIYHISGLYPROGLUGINGLNLYSARGLYSILEVAL 237
   |||||
QY 115 -----TGTACGGCGGATTTGACCTGATCTTATTTTGACAAATCAGGAAGTGCG--- 165
   |||||
Db 238 LEUAPPROSERGLYSERMECHANIETYRLEUVALLEUAPBGLYSERAPSERILEGLY 257
   |||||
QY 166 -----CTGCACACCTGGAATGGAATCTATTACTTTGTGACAGTGGCTCAC 213
   |||||
Db 258 ALASERAPNHERHETHRGYLALEYSLYSCYLEUVALASMLEUILEGIUNYVALALASER 277
   |||||
QY 214 AATTATCATGACCCACAGTTGAGAAATGCTTATTGTTTCTCCACCCGAGGAACAACC 273
   |||||
Db 278 TYRGLYVALYLEPRO-----ARGTYRGLYLEUVALTHYRXLATHYRPROLYSILE 295
   |||||
QY 274 TTAATGAACTGACAGAA-----GACAGAAACAATCCGTCAAGGCTTAGAA 321
   |||||
Db 296 TTPVALLYVALSERGLIUNAPBSESERAPNALASPTRYVALTHRYSGINLEUASAN 315
   |||||
QY 322 GAATC-----CAGAAAGTTCTGCAGAGGACGACATTCATGACATGAAGA 369
   |||||
Db 316 GIULIASENTYRGLUNBPHISLEYBLEUYSERGLYTHRASPHR----- 330
   |||||
QY 370 TTGAAAAGGCGCGATGACAGATTATTATGAATAACA----- 408
   |||||
Db 331 ---LYLEYSHLALEUGINLAVALITYRSEMERMETSETRPROASPHYVALPROPRO 349
   |||||
QY 409 CAAGGCTAC---AGGACAGCCAGCGATCATGCTTGTGCTGATGGA----- 453
   |||||
Db 350 GIUGLYTRPASNARGTHIRARHISVALILEILEUWMECHIRAPBGLYSEUHSIASENME 369
   |||||
QY 454 -----GAATCCATGAGATCTCTTTTCTATTGATTCAGAG 486
   |||||
Db 370 GLYGLYASPPROLLETHRVALLIEAPSGIULILEARISPLEUENURYRILEGLYLSAP 389
   |||||
QY 487 AGGAGCGCTAATVGTCTCGAGATCTTGTCGCAATTGTTTACTGTGTGCT-----GTG 540
   |||||
Db 390 ARGLYASBPPOARGLIUNBPHYRILEUASPHYVALYPHEGLYVALGILYPROLEUVAL 409
   |||||
QY 541 AAGGATTTCAATGACACACAGCTGGCCCGGATTCGGACAGTAAAGTCACTGTGTTCC 600
   |||||
Db 410 AENGLIVALASNTLEASNALALEUVALASERLYLYSPASNGIUGINHSVALIPHELYS 429
   |||||
QY 601 GTGAATGACGCGCTTTGAGCTTCGACAGGCGATCATCATCTTTTGAAGAAGTCTCG 660
   |||||
Db 430 VALLYASBP---METGIUNLEUIGIUNAPVALPHECYRGLINMETCILEASPGIUNSER 447
   |||||
QY 661 ATCGAAATTTAGACAGCTGAACCATTCACCATATGTGCGAGAGATCATTTCAAGTTGTC 720
   |||||
Db 448 -----GINSETRLEUSERLEUCY----- 453
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QY 721 GTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGGCTCTGACAGTTCAAG 780
   |||||
Db 454 -----GIYMETVALTRPGLINHISARGLYSGLYTHRAP----- 464
   |||||
QY 781 ATCAATGACTCGGTCAACCTCAATGAGAAAGCCCTTTCTGTGGAAGACATTTACTG 840
   |||||
Db 465 -----TYRHISLYSGINPROTRPGINLALEYISLESERVAL----- 476
   |||||
QY 841 TGTCCAGGCGCTATCTTAAAGAAAGTTGSCATGAAGAAGTCACTCCAGSTCAGCATGAC 900
   |||||
Db 477 -----LEAPPROSERLYSGIYHISGLYSERAPSERILEGLY----- 488
   |||||
QY 901 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCACACCACTGTT 951
   |||||
Db 489 -----ALAVVALSERGLIUNYRPHREVALLEUTHRALALAHIECY 502
   |||||

RESULT 5
US-11-057-047-1
/ Sequence 1, Application US/11057047
/ Publication No. US20050260198A1
/ GENERAL INFORMATION:
/ APPLICANT: Holers, Vernon
/ APPLICANT: Thaurman, Joshua
/ APPLICANT: Taube, Christian
/ APPLICANT: Gelfand, Erwin
/ APPLICANT: Gilkeson, Gary
/ TITLE OF INVENTION: Inhibition of Factor B. The Alternative Complement Pathway and
/ TITLE OF INVENTION: Methods Related Thereto
/ FILE REFERENCE: 2848-66
/ CURRENT APPLICATION NUMBER: US/11/057,047
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,594
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: 60/636,239
/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 764
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-11-057-047-1

Alignment Scores:
Pred. No.: 0.0021 Length: 764
Score: 113.50 Matches: 66
Percent Similarity: 38.28% Conservative: 63
Best Local Similarity: 19.58% Mismatches: 109
Query Match: 5.67% Indels: 99
DB: Gaps: 17

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-057-047-1 (1-764)

QY 82 CAAAGGCGACGCGAGGAGTGCG---GGTCCAGCC----- 114
   |||||
Db 243 GIUGLYVALAEPALAGIUNBPGIYHISGLYPROGLUGINGLNLYSARGLYSILEVAL 262
   |||||
QY 115 -----TGTACGGCGGATTTGACCTGATCTTATTTTGACAAATCAGGAAGTGCG--- 165
   |||||
Db 263 LEUAPPROSERGLYSERMECHANIETYRLEUVALLEUAPBGLYSERAPSERILEGLY 282
   |||||
QY 166 -----CTGCACACCTGGAATGGAATCTATTACTTTGTGAAACAGTTGGCTCAC 213
   |||||
Db 283 ALASERAPNHERHETHRGYLALEYSLYSCYLEUVALASMLEUILEGIUNYVALALASER 302
   |||||
QY 214 AATTATCATGACCCACAGTTGAGAAATGCTTATTGTTTCTCCACCCGAGGAACAACC 273
   |||||
Db 303 TYRGLYVALYLEPRO-----ARGTYRGLYLEUVALTHYRXLATHYRPROLYSILE 320
   |||||
QY 274 TTAATGAACTGACAGAA-----GACAGAGAAACAATCCGTCAAGGCTTAGAA 321
```

```

Dh 321 TPrVAllyvAlserGlu1laerSerSerSema1aBerTPrVAlThLyvGlnLeuAsn 340
      ::|||:::|||||:::  :::  :::  :::  :::  |||
Qy 322 GAATC-----SAGAAAGTTCTGCAGAGAGACATTAATCATCATGAAGA 368
      |||:::  |||:::  |||
Db 341 Glu1leAenLyrgLyuBnrlvlyvLeuLyvSerGlyLThlnAntln----- 355
      |||
Qy 370 TTTGAAGGGCCAGTACAGCATTTATTAAGAAACAG----- 408
      ::|||:::  :::  :::  |||
Db 356 ---LyvleAlaLeuGlnAlaValLySerSemetSetTPrProAerAerValProPro 374
      |||
Qy 409 CAAGAGTAC---AGACAGCCAGCCGATCATCTGCTTGAAGTGAAG----- 455
      ::|||:::  |||
Db 375 GluGlyTPrAenLyrgLThrghlvAllelleLeuMetThAerGlyLeuNlAvmMet 394
      |||
Qy 454 -----GAATCCATGAAGATCTTTTCTTATTCAGAG 486
      |||
Db 395 GlyLyvAerProIleThrVal1leAerGlu1leAerAerLeuLy1leGlyLyvAer 414
      |||
Qy 487 AGGAGAGCTAATAGCTCTGCAGATCTTGCTGCAATTTGTTACTGTGTGT-----GTG 540
      |||
Db 415 ArgLyvAerProIleThrGluBnrlvLyvLeuAerValLyvAlPheVal1 433
      |||
Qy 541 AAAGATTTCAATAGACACAGCTGGCCCGGATGGCGAGACAGTAAGATCATGTGTTCCC 600
      |||
Db 435 AenGlnAlaen1leAenAlaLeuAlaSerLyvLyvAerAenGlnGln1lvAlPheLyv 455
      |||
Qy 601 TGAATATCAGCGCTTTTACGCTCTGCAGAGCATCATCATCATCAATTTGAAGAGTCTGC 660
      |||
Db 455 ValLyvAer---MetGluAenLeuGlnAerValPheLyvGlnMet1leAerGlnSer--- 472
      |||
Qy 661 ATCGAAATTTGACAGCTGAACCATCCATCATATGTGACAGAGATCATTTCAAGTTGTC 720
      |||
Db 473 -----GlnSerLeuSerLeuCy----- 478
      |||
Qy 721 GTGAGAGAAAGCGTTTCCGACATGCCGCCSAGAGTGAACGGGTCTCTGCAGCTTCAAG 780
      |||
Db 479 -----GlyMetVal1TPrGln1lvAerLyvGlyLThAerP----- 485
      |||
Qy 781 ATCAATGATCTCGGTACATCACTAGAGAAAGCCCTTTTGTGGAAGACATTAATTAAGT 840
      |||
Db 490 -----TyrNllyvGlnProIleThrGlnAlaLy1leSerVal----- 500
      |||
Qy 841 TGTCAGCGGCTATCTTAAAGAGAGTGGAGATGAAGAGTCACTGCAGTCAAGTGAAC 900
      |||
Db 502 -----IleAerProSerLyvGlnNllyvGlnSerCyMetGly----- 513
      |||
Qy 901 GATGCGCTCTCTTTATCTGCAGTTGTGTCATGATCATCAACACACACATCTGT 951
      |||
Db 514 -----AlaValAlaSerGlyTyrPheValleuThralAla1lvSerCy 527
      |||

RESULT 6
US-10-821-234-1034
; Sequence 1034, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Crafin, Birgit
; APPLICANT: Andarmann, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 66/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC SEQ_genes Version 1.0
; SEQ ID NO 1034
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1034

```

| Alignment Scores: | | | |
|---|--|----------------|-----|
| Pred. No.: | 0.00213 | Length: | 798 |
| Score: | 113.50 | Matches: | 66 |
| Percent Similarity: | 38.28% | Conservative: | 63 |
| Best Local Similarity: | 19.58% | Mismatches: | 109 |
| Query Match: | 5.67% | Indels: | 99 |
| DB: | 6 | Gaps: | 17 |
| US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-821-214-1034 (1-798) | | | |
| QY | 82 CAAGGGGACCGCAGGAGATGGG--- | GGTCCAGCC----- | 114 |
| DB | 277 GIUGLYValAaPAlAGLubapGlyhIeglyProGlyGluGlnGlnIuYsArglysIleVal | 296 | |
| QY | 115 -----TGCYACGGCGGATTTACCTGTACTTCATTTTGACAAACAGAGATGG--- | 155 | |
| DB | 297 LeuapProSerGlySerMetAsnIleTyLeuValLeuAspGlySerAspSerIleGly | 316 | |
| QY | 166 -----CTGCACCACTGGAATGAATCTATTACTTTGTGGAAACAGTTGGCTCAC | 213 | |
| DB | 317 AlaserAsenPheThcGlyAlalybysCysIeuValAsnIleuIleGluIuYsValAlaser | 336 | |
| QY | 214 AAATTCATCAGCCCACTGTAAGATGCTCTTATTGTTTCTCCACCCGAGAACACC | 273 | |
| DB | 337 TyrglyValIyLysPro-----ArgTyrglyLeuValThrTyxAlaThrTyxProIySile | 354 | |
| QY | 274 TTAATGAAGACACAGAA-----GACAGAGAAACAAATCCGTCAGGCTTAGAA | 321 | |
| DB | 355 TrpValIyValIserGlnAlaAspSerSerAsnAlaAsPTryValThrySgInIeuAsn | 374 | |
| QY | 322 GAATCC-----CAGAAAGTTCTGCCAGAGAGACACTTACATGCATGAAGA | 369 | |
| DB | 375 GluIleAsenTyGluAspHisIySleuYsSerGlyThrAsnThr----- | 389 | |
| QY | 370 TTGTAAAGGCCAGTGACGAGATTATTAATGAACAG----- | 408 | |
| DB | 390 ---LysIyValAlaLeuGlnAlaValTySerMetMetSerTrpProAspValProPro | 408 | |
| QY | 409 CAAGGGTAC---AGACAGCCAGCGCATTCATGCTTGACATGATGA----- | 453 | |
| DB | 409 GIUGlyTTPAsnArgThrArgHisValIleIleIeuMetThrAspIyLeuHisAsenMet | 428 | |
| QY | 454 -----GAATCCATGAAGATCTCTTTTCTATTACAG | 486 | |
| DB | 429 GIUGlyAspProIleThrValIleAspGluIleArgAspIeuMetTyxIleGlyLysAsp | 448 | |
| QY | 487 AGGAGGCTAATAGCTCTCGAAGTCTTGTCATTTGTTACTGTGTGT-----GTG | 540 | |
| DB | 449 ArgIyAsnProArgGluAspTyLeuAspValTyValPheGlyValGlyProIeuVal | 468 | |
| QY | 541 AAAGATTTCAATGAGACACAGCTGGCGGCGGATGGGACATGAAGATCTGTGTTCCC | 600 | |
| DB | 469 AsnGlnValAsnIleAsnAlaIeuAlaSerLysLysAspAsnGluGlnHisValPheLys | 488 | |
| QY | 601 GTGAATGACGGCTTTCCAGCTCTGCAAGGACATCATCATCTTATTTGAAGATCTGC | 660 | |
| DB | 489 ValIyAsp---MetGluAsnIeuGluAspValPheTyxIleMetIleAspGlnSer--- | 506 | |
| QY | 661 ATCGAAATTCAGACGCTGAACCATCATCATCTGTGCGAGAGAGTCATTCCAATTGTC | 722 | |
| DB | 507 -----GlnSerIeuSerIeuCys----- | 512 | |
| QY | 721 GTGAGAGAAACGGCTTCCGACATGCGCCCAACGTGACAGGGTCTCTTGACGTTCAAG | 788 | |
| DB | 513 -----GlyMetValTrpGluHisArgIySgIyThrAsp----- | 522 | |
| QY | 781 ATCAATGACTCGGTCACTCACTATGAGAAACCTTTTCTGTGGAAGACATTAATTAATG | 840 | |
| DB | 524 -----TyxHisIySgInProTrpGlnAlaIySileSerVal----- | 535 | |
| QY | 841 TGTCCAGCCCTATCTTAAAGAAAGTTGGCATGAAGGTGCATCCAGGTCAACATGAAC | 900 | |

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Db      536 -----IlaArgProSerLySgLyHISgluSerCywemcSly----- 545
Oy      901 GATGCGCTCTCTTTATTCGCCAGTTCTGCATCATCATCACCAACACACTGT 951
Db      548 -----AlaValValSerGluTyrPheValLeuThrAlaAlaHisCys 561

RESULT 7
US-10-131-826A-294
; Sequence 294, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Auecin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131, 826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 294
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-294

Alignment Scores:
Pred. No.: 0.00221 Length: 915
Score: 113.50 Matches: 55
Percent Similarity: 43.904 Conservative: 53
Best Local Similarity: 22.364 Mismatches: 103
Query Match: 5.67% Indels: 35
DB: 6 Gaps: 13

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-131-826A-294 (1-915)
OY      130 GACCTGTACTTATTTGGACAAATAGAGAGTGT---CTGACACCATGGAATGAAATC 186
|||||  |||||||:::||||| ||| ||||||| ||| |||

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Db      57 AepLeuValPheIleIleAspSerSerArgSerValaIaThThIaSerArgValaIuVal 76
Qy      187 TATTAACCTT---GTGGAAACAGTGTGGCTACAAATTCATTCAGCCCAACAGTGG---AGAAAG 240
Db      77 LysGIuPheIleValaAspIleLeuGIuPheLeuAspIleGlyProAspValaIaArgVal 96
Qy      241 TCCCTTATATGTTTCTCCACCCGAGGAACAACCTTA-----ATGAACAG 285
Db      97 GlyLeuLeuGIuTYR-----GlySerThrValIyVaGIuPheSerLeuTYR 113
Qy      286 ACAGAGAACAAGAAACAATCCCTGACAGCCCTAGAAAGATCTCAGAAACTTCTCCAGGA 345
Db      114 PheLysArgLysSerGIuValaGIuArgValaValIyVaGIuMetArgHileuSerThrgly 133
Qy      346 GGAACACCTTACATGCATGAAGAGATTGAAAGGCCAGTGCAGACAGATTATTAATGAAC 405
Db      134 ThrMetThrglyLeuAlaIleGIuTYR-----AlaLeuAsnIleIaPheSerGIu 150
Qy      406 AGACAAAGGGAACAGG-----ACAGCAGGCGTATCATCTTGTAGCTAGT 450
Db      151 AlaGIuGIuAlaArgProLeuArgGIuAsnValProArgValIleMetIleValaIaArg 170
Qy      451 GGAACATCCATGAAGATCTCTTTTCTATTTCAGAGAAGGAGCTTAATAGCTCCAGAT 510
Db      171 GlyArgProGIuAspSerVal-----AlaGIuValaIaAlaLysAlaArg 186
Qy      511 CTGGTGCATATGTTTACTGTGTGCTGTG-----AAAGATTCAATGACACAGCTG 564
Db      187 ThrglyIleLeuIlePheAlaIleGIuValaGIuValaAspPheAsnThrglySer 206
Qy      565 GCCCGAATGGGACAGTAAAGATATGATGTTCCTCCGTAATGACGGCTTTACAGCTCG 624
Db      207 IleGlySerGIuProHileGIuAspHileValPheLeuValaIaAsn---PheSerGlnIle 225
Qy      625 CAAGGACATCATCCATCAATTTTGAAGAAAGCTCTCATCGAATTTCTACAGCTGAACA 684
Db      226 GluThrglyLeuThrglySerValaPheGIuLysLysValaIaHileMetCysSerThrgly 245
Qy      685 TCACCATATGTGCAGAGAGACTATTTCAGATTGTGTCGAGAGAAACGGCTTCCGACAT 744
Db      246 GluHleAsnCysVala-----HilePheCysIleAsnIleProGIuSerValaCysArg 263
Qy      745 GCCCGC-----AACTGACAGAGGCTCTCTGAGCTCAAGATCAATGAC 789
Db      264 CysLysArgGIuTYRILEuAsnSerArgGIuThrglyCys-----ArgIleGIuAsp 281
Qy      790 TCGGTACACATCAATGAG 807
Db      282 LeuCysAlaMetGIuAsp 287

RESULT 8
US-11-113-424-39
/ Sequence 39, Application US/11113424
/ Publication No. US20050260713A1
/ GENERAL INFORMATION:
/   APPLICANT: Gamco11 et al.
/   TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
/   FILE REFERENCE: 21402-225
/   CURRENT APPLICATION NUMBER: US/11/113, 424
/   CURRENT FILING DATE: 2005-04-21
/   PRIOR APPLICATION NUMBER: 60/256,704
/   PRIOR FILING DATE: 2000-12-19
/   PRIOR APPLICATION NUMBER: 60/311,590
/   PRIOR FILING DATE: 2001-08-10
/   PRIOR APPLICATION NUMBER: 60/257,314
/   PRIOR FILING DATE: 2000-12-20
/   PRIOR APPLICATION NUMBER: 60/311,613
/   PRIOR FILING DATE: 2001-08-10
/   PRIOR APPLICATION NUMBER: 60/315,617
/   PRIOR FILING DATE: 2001-08-29
/   PRIOR APPLICATION NUMBER: 60/307,506
/   PRIOR FILING DATE: 2001-07-24
/   PRIOR APPLICATION NUMBER: 60/322,358

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Db      335 GluAlaLalaLeu-----LysAspAlaValaAspAlaLeuGlyAspArgIlePheSer 351
QY      622 CTCGACAGGC 630
        |||::|||
Db      352 LeuGluGly 354

RESULT 10
US-10-601-368-22
/ Sequence 22, Application US/10601368
/ Publication No. US20050260702A1
GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 073434-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 22
/ LENGTH: 1166
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-601-368-22

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| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 0.00412 | Length: | 1166 |
| Score: | 111.00 | Matches: | 49 |
| Percent Similarity: | 37.93% | Conservative: | 28 |
| Best local Similarity: | 24.14% | Mismatches: | 88 |
| Query Match: | 5.54% | Indels: | 38 |
| DB: | 6 | Gaps: | 9 |

US-09-970-076-1_COPY_104_1207 (1-1104) X US-10-601-368-22 (1-1166)

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Oy      115 TGCACGGCGGATTTGATACCGTCACTCATTTTGACCAATATCGAAAGTGTCTGCACAC 174
Db      137 CyAGlnhTrhYrmetcArlleVallelleAmlBrgYserAmsenlle--TyPPro 155
Oy      175 TGGATGATAATCTATTACTTGTGTGMAACGTTGGCTCAAAATTC--ATCAGCCCA-- 228
Db      156 TrpValGluValGlnHisPheLeuIleAmlIleuLysPheTyIleGlyProGly 175
Oy      229 CAGTTGAGAAATGTCCTTATTTGTTTCTCCACCCAGAACCAACTTATGAAATGACA 288
Db      176 GlnIleGlnValGlyIleValGlnTyGlyGluAraValHisGluPheIleu--- 194
Oy      289 GAAGACAGAGAACAAATCCGTCACAGGCTAGAAACATCCAGAAAGTTCTCCAGAGAGA 348
Db      195 AsnBeryrYrYserValIlyAserValIleGlnAlaIleAserHisIleGlnGlnArgGly 214
Oy      349 GACACTTACATGCATGAAGATTTGAA-----AGGCCAGTAGACAGATTATTTAT 399
Db      215 GlyThrGlnUhrArgThraIlePheGlyIleGluPheAlaArgSerGlnAlaIlePheGlnLys 234
Oy      400 GAAACACGACAGGGTACAGACAGCCAGCCGTCATCATTTCTGACTGATGGAGAAATC 458
Db      235 GlyIyYrArgIyGlnAlaLys-----LysValmetIleValIleThrAraBrgIyGlnSer 252
Oy      460 CATGAAAGAT----- 468
Db      253 HisAmsPsrProAbleuPleuGlnLysValIleArgGlnSerGlnLysAraPsnValThraArg 272
Oy      469 -----CTCTTTTCTTATTCAGAGAGGAGGATATATAGCTCTCGACATCTT 513
Db      273 TyrAlaValAlaIleuGlnTyTrpYrAraAraGArgGlyIleAmsProGlnThrPheLeu 292
Oy      514 GGTGCATTTGTTACTGTGTGTGGTGTGAAGAT-----TTCAATGACACACAG 561

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Db 293 AenGluIleIeTyTylleIeIaSeræProAspæPryæHisPhePheAsnValIthAsp 312

QY 562 CTGCGCCGAGATTCGGACAGTACAGATCATGTTCTCCCGGATGACCGGCTTCAAGCT 621

Db 313 GUAUAlaIleU-----LysAspIleValaIlePheAlaLeuGlyAspArgIlePheSer 329

QY 622 CTGCAAGGC 630

Db 330 LeuGluGly 332

```

RESULT 11
US-10-601-368-21
Sequence 21, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIORITY APPLICATION NUMBER: US/09/561,263A
PRIORITY FILING DATE: 2000-04-27
PRIORITY APPLICATION NUMBER: US 09/322,790
PRIORITY FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 1188
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-21

```

Alignment Scores

| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 0.00415 | Length: | 1188 |
| Score: | 111.00 | Matches: | 49 |
| Percent Similarity: | 37.93% | Conservative: | 28 |
| Best Local Similarity: | 24.14% | Mismatches: | 88 |
| Query Match: | 5.54% | Indels: | 38 |
| DB: | 6 | Gaps: | 9 |

US-09-970-076-1_COPY_104_1207 (1-1104) X US-10-601-368-21 (1-1188)

| | | | |
|----|-----|--|-----|
| Dy | 115 | TGCTACGGCGAGTTTGCACCTGTACTTCATTTTGCAACAATCAGGAAGTGTGTCACACC | 174 |
| | | ::: | ::: |
| Dd | 159 | CyggInThrTyrmEAsprIlleValIleValIleuAspArgLysAenSerIle---TyPro | 177 |
| | | ::: | ::: |
| OY | 175 | TGGAAATGAATCATTAATCTTTGTGGACAAGTTGGCTCCAAATTC---ATCAGGCCA--- | 228 |
| | | ::: | ::: |
| Dd | 178 | TrpValGlntValGlnHisPheLeuLlLeasnIleLeuLyAspVsrPetyLLeglyProGly | 197 |
| | | ::: | ::: |
| OY | 229 | CAGTTGAGAGTCTCTTATTGTTTTGTTTCCACCCGAGAACMACTTAATGAAACTGACA | 288 |
| | | ::: | ::: |
| Dd | 198 | GlnlleGlnValGlyLEvalGlnTryGlyGluAspAlaValHISgluPheHisLeu--- | 216 |
| | | ::: | ::: |
| OY | 289 | GAAGACAGAGAACCAATCCGTCAAGGCTTAGAGAATCCGAAAGTTCTCCSAGAGGA | 348 |
| | | ::: | ::: |
| Dd | 217 | AsnAspTryArgSerValLysAspValValGluAlaAlaSerHisVilegIuglnArgLy | 236 |
| | | ::: | ::: |
| OY | 349 | GACACTTACATGCATGAAGAGATTGAA-----ACGGCAGGTGAGCAGATTATATAT | 399 |
| | | ::: | ::: |
| Dd | 237 | GlyThrGluThrArgThrAlaPheGlyLleGluPheAlaArgSerGluAlaPheGlnLys | 256 |
| | | ::: | ::: |
| OY | 400 | GAATAACAGACAAGGTTCACAGCACACGCTCATCTTGTAGCTAGTGAAGAACTC | 459 |
| | | ::: | ::: |
| Dd | 257 | GlyGlyArgGlyGlyAlaLys-----LysValMetIleValIleTrnAspGlyGluSer | 274 |
| | | ::: | ::: |
| OY | 460 | CATGAAGAT----- | 466 |
| | | ::: | ::: |
| Dd | 275 | HIsAspSerProAspLeuGluLysValIleArgGlnSerGluLysAspAsnValThrArg | 294 |
| | | ::: | ::: |

```
Qy 469 -----CTCTTTTCTATTACAGAGGAGGCTAATAGCTCCAGACTT 513
Db 295 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 314
Qy 514 GGTCAATGTTTACTGTGTGGGTGAAGAT-----TTCATAGACACAG 561
Db 315 AsnGluIleLeuGlyTyrIleAlaSerAspProAspAspIleAspPheAsnValThrAsp 334
Qy 562 CTGGCCCGGATGCGGACAGTACATGATGTTCCCGTAATGACGGCTTCAGGCT 621
Db 335 GluAlaIleLeu-----LysAspIleValAlaAspAlaLeuGlyAspArgIlePheSer 351
Qy 622 CTGCAGGC 630
Db 352 LeuGluGly 354

RESULT 12
US-11-057-047-6
; Sequence 6, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Glikson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057, 047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-057-047-6

Alignment Scores:
Pred. No.: 0.00408 Length: 761
Score: 110.50 Matches: 71
Percent Similarity: 37.57% Conservative: 59
Best Local Similarity: 20.52% Mismatches: 99
Query Match: 5.52% Indels: 117
DB: 7 Gaps: 20

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-057-047-6 (1-761)
Qy 82 CAAGGGGAGCGAGGAGATGG----- 105
Db 240 GluGluIleAspAlaGluAspGlyHisSerProGluGluGlnGlnIleValArgLysIleVal 259
Qy 106 ---GCTCAGGCTGTCTACGGGGAATTGACCTGTAATTCATTGTTGGCAATTCAGAGT 162
Db 260 LeuAspProSer-----GlySerMetAsnIleTyrLeuValLeuAspGlySerAspSer 277
Qy 163 GTG-----CTGCACCACTGGAAATGAATCTAT 189
Db 278 IleGlySerSerAsnPheThrGlyAlaIleValArgCysLeuThrAsn----- 292
Qy 190 TACTTTGTGAACAGTTGGCTCACAAATTCACAGCCACAGTTGAGATGCTTTATT 249
Db 293 ---LeuIleGluIleValAlaSerTyrGlyValArgPro-----ArgTyrGlyLeuLeu 309
Qy 250 GTTTTCTCCACCGAGAAACCACTTAATGAACAGCAAGACAG----- 297
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Db 310 ThrTyrAlaThrValProLysValLeuValArgValSerAspGluArgSerSerAspAla 329
Qy 298 -----GACAAATCCCTCAAGGCTTGAAAGACTCCAGAAAGTTCTCCAGCA 345
Db 330 AspTyrValThrGluLysLeuAsnGlnIleSerTyrIleAspHisIleLeuLysSerGly 349
Qy 346 GAGACACTTACATGATGATGAAGATTGAAGGGCCAGTACAGATTAATTAAT----- 399
Db 350 ThrAsnThr-----LysArgAlaLeuGlnAlaValTyrSerMetMet 363
Qy 400 -----GAAAACAGAACGGGTAC---AGACACCCACCGCTATCTTGTCT 441
Db 364 SerTyrAlaGlyAspAlaProProGluGlyTyrAsnArgThrArgHisValIleIleIle 383
Qy 442 TTGACTGATGAGAACTCCAT-----GAAAGATCTC 471
Db 384 MetThrAspGly---LeuHisAsnMetGlyIleAsnProValThrValIleGlnAspIle 402
Qy 472 TTTTTCATTACAGAG-----AGGAGGCTAATAGTCTCGAGAT-----CTGTGCA 519
Db 403 ArgAlaLeuLeuAspIleGlyArgAspProLysAsnProArgGluAspTyrLeuAspVal 422
Qy 520 ATTGTTACTGTGTGTGT-----GTGAAAGATTTCATGACACACAGCTGGCCGAGTT 573
Db 423 TyrValPheGlyValGlyProLeuValAspSerValAsnIleAsnAlaLeuAlaSerLys 442
Qy 574 GCGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTACAGGCTTCGCAAGCATC 633
Db 443 LysAspAsnGlnHisIleValIlePheLysValLysAsp---MetGluAspLeuGluAsnVal 461
Qy 634 ATCAGCTCAATTTTGAAGAGTCCGTGATGAAATTTACAGCTGAACCATCCACATA 693
Db 462 PheTyrGlnMetIleAspGluThr-----LysSerLeuSerLeu 474
Qy 694 TGTGACAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCAGATGCCCGCAAC 753
Db 475 Cys-----GlyMetValTyrGlnIleLysLysGly 484
Qy 754 GTGACAGAGGCTCTCTGACAGCTTCAAGATCAATGACTCGGTCACTCAATAGAAACCC 813
Db 485 AsnAspTyrHisLysGlnProTyrGlnAlaLysIleSerValThr-----ArgPro 501
Qy 814 TTTTCTGTGAAGAAGACTTATTACTGTGTCCAGCGGCTTCTTAATAAAGAGTTGGCATG 873
Db 502 LeuLysGlyHisGluThr-----CysMetGlyAlaVal----- 512
Qy 874 AAAGCTCACTCCAGTCAAGATGAAAGATGAGCGCTCTTTTATCTCCAGTTCTGCATC 933
Db 513 -----ValSerGluTyrPheVal 518
Qy 934 ATCAGCAACACACACTGT 951
Db 519 LeuThrAlaAlaHisCys 524

RESULT 13
US-10-601-368-6
; Sequence 6, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Iora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
```

```
/ LENGTH: 1141
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-6

Alignment Scores:
Pred. No.: 0 00996 Length: 1141
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.34% Indels: 38
DB: Gaps: 9

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-601-368-6 (1-1141)
QY 115 TGTACGGCGGATTGACCTGTAATTTGGACAAATCAGGAAGTGTGTCACAC 174
Db 159 CysGlnThrTyrMetAspIleValIleValIleuAspGlySerAsnSerIle---TyrPro 177
QY 175 TGGAAATGAATCTATTACTTGTGGAAACAGTTGCTCACAATTC---ATCACCCCA--- 228
Db 178 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 197
QY 229 CAGTTGAGAAATGCTTTATGTTTCTCCACCCGAGAAACAACCTTAATGAACAGCA 288
Db 198 GlnIleGlnValGlyValGlnTyrGlyGluAspValValHisGluPheHisLeu--- 216
QY 289 GAAGACAGAGAACAAATCCGTCAGGCTTAGAAGAACTCCAGAAAGTTGTCAGAGAG 348
Db 217 AsnAspTyrArgSerValLysAspValValGluAlaIleSerHisIleGluGlnArgGly 236
QY 349 GACACTTACATCATGATGAAGATTGAA-----AGGCCAGTGACAGATTATTAT 399
Db 237 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 256
QY 400 GAAACAGACAAAGGTCACAGACAGCAGCATGCTTGAATGATGAGAACTC 459
Db 257 GlyGlyArgLysGlyAlaLys-----LysValMetIleValIleThrAspGlyGlnSer 274
QY 460 CATGAAGAT----- 468
Db 275 HisAspSerProAspLeuGluLysValIleGlnGlnSerGluArgAspAsnValThrArg 294
QY 469 -----CTCTTTTCTATTCAGAGAGGAGCTTAATAGTCTCGAGATCTT 513
Db 295 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyTyrIleAsnProGluThrPheLeu 314
QY 514 GGTGCAATTGTTACTGTGTGTGGTGAAGAT-----TTCAATGACACAG 561
Db 315 AsnGluIleLysTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 334
QY 562 CTGGCCCGGATTCGGACAGTAAGATCATGTCTTCCGTGAATGACGGCTTCAGGCT 621
Db 335 GluAlaAlaLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 351
QY 622 CTGCAAGGC 630
Db 352 LeuGluGly 354

RESULT 14
US-10-601-368-4
/ Sequence 4, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
```

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/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 1166
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-601-368-4

Alignment Scores:
Pred. No.: 0.01 Length: 1166
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.34% Indels: 38
DB: Gaps: 9

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-601-368-4 (1-1166)
QY 115 TGTACGGCGGATTGACCTGTAATTTGGACAAATCAGGAAGTGTGTCACAC 174
Db 137 CysGlnThrTyrMetAspIleValIleValIleuAspGlySerAsnSerIle---TyrPro 155
QY 175 TGGAAATGAATCTATTACTTGTGGAAACAGTTGCTCACAATTC---ATCACCCCA--- 228
Db 156 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 175
QY 229 CAGTTGAGAAATGCTTTATGTTTCTCCACCCGAGAAACAACCTTAATGAACAGCA 288
Db 176 GlnIleGlnValGlyValGlnTyrGlyGluAspValValHisGluPheHisLeu--- 194
QY 289 GAAGACAGAGAACAAATCCGTCAGGCTTAGAAGAACTCCAGAAAGTTGTCAGAGAG 348
Db 195 AsnAspTyrArgSerValLysAspValValGluAlaIleSerHisIleGluGlnArgGly 214
QY 349 GACACTTACATCATGATGAAGATTGAA-----AGGCCAGTGACAGATTATTAT 399
Db 215 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 234
QY 400 GAAACAGACAAAGGTCACAGACAGCAGCATGCTTGAATGATGAGAACTC 459
Db 235 GlyGlyArgLysGlyAlaLys-----LysValMetIleValIleThrAspGlyGlnSer 252
QY 460 CATGAAGAT----- 468
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QY 469 -----CTCTTTTCTATTCAGAGAGGAGCTTAATAGTCTCGAGATCTT 513
Db 273 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyTyrIleAsnProGluThrPheLeu 292
QY 514 GGTGCAATTGTTACTGTGTGTGGTGAAGAT-----TTCAATGACACAG 561
Db 293 AsnGluIleLysTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 312
QY 562 CTGGCCCGGATTCGGACAGTAAGATCATGTCTTCCGTGAATGACGGCTTCAGGCT 621
Db 313 GluAlaAlaLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 329
QY 622 CTGCAAGGC 630
Db 330 LeuGluGly 332

RESULT 15
US-10-601-368-3
/ Sequence 3, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
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? TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
? FILE REFERENCE: 07334-275001
? CURRENT APPLICATION NUMBER: US/10/601,368
? CURRENT FILING DATE: 2003-06-23
? PRIOR APPLICATION NUMBER: US/09/561,263A
? PRIOR FILING DATE: 2000-04-27
? PRIOR APPLICATION NUMBER: US 09/322,790
? PRIOR FILING DATE: 1999-05-28
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 3
? LENGTH: 1188
? TYPE: prt
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SIGNAL
? LOCATION: (1)...(22)
? -10-601-368-3

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| Score: | 107.00 |
| Percent Similarity: | 37.93% |
| Best Local Similarity: | 24.14% |
| Query Match: | 5.34% |
| DB: | 6 |
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| Length: | 1168 |
| Matches: | 49 |
| Conservative: | 28 |
| Mismatches: | 88 |
| Indels: | 38 |
| Gaps: | 9 |

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 Db 159 CysgIntHtYrIwteraspIleValIleValLeuaspGlySerasnSerIle---TyrPro 177
 QY 175 TGGATGAATCATTTACTTACTTGTGGAAACAGTTGGCTGCACAAATTC---ATCAGCCCA 228
 Db 178 TTPValGIValGIghntSpherleuIleasnIleleuLySerSpherYrIleGIYProGly 197
 QY 229 CAGTTGAGAATGCTCTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAACTGACA 288
 Db 198 GlnIleGIhValGIYValValGIhTyrGIYGIuaspValValhIseGIuPhehIleu--- 216
 QY 289 GAAAGCAGAGAACAAATCCGTCMAAGCCTTGAGGAACCTCCAGAAAGTTTCCGACAGAGA 348
 Db 217 AenAsePYrArgSerValIyAspValValGIuAlaIasehIstIleGIuInArgGly 236
 QY 349 GACACTTACATGCATGAAGATTTGA-----AGCGCACTGACAGATTTAT 399
 Db 237 GIYThrGIuThrArgThrAlaPheGlyIleGIuPheAlaArgSerGIuAlaPheGlnLyS 256
 QY 400 GAAACAGACMAAGGTACAGAGAACAGCCAGGTCTATCTTGCCTGACTGATGAGAACTC 455
 Db 257 GIYGIYArLyAspGIYAlaLyS-----LySValMetIleValIleThraSpGIYGIuSer 274
 QY 460 CATGAAGAT----- 468
 Db 275 hIAspSerProAspLeuGIuLySValIleGlnInSerGIuArgAspAsnValThrArg 299
 QY 469 -----CTCTTTTCTATTCAGAGAGAGAGCTTAATAGCTTCGAGATCTT 513
 Db 295 TyrAlaValAlaValIleuGIYTrYrYAsnArgArgGIYIleAsnProGIuThrPheLeu 314
 QY 514 GCGCAATGCTTACTGTGTGTGGTGCAGAAAGT-----TTCATAGAGACACAG 566
 Db 315 AenGIuIleLySTrIleAlaSerAspProAspSplyShIAspPheAsnValThrAsp 334
 QY 562 CTGGCCCGGATTCGCGACAGTAAGATCATGTGTTTCCGTAATGACGAGCTTCAGACT 621
 Db 335 GIuAlaIaleu-----LySAspIleValAspAlaLeuGIYAspArgIlePheSer 351
 QY 622 CTCGAAGGC 630
 Db 352 LeuGIuGly 354

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:02:37 ; Search time 33.1864 Seconds
(without alignments)
916.781 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 962.5 | 50.3 | 488 | US-10-104-047-2639 | Sequence 2639, Ap |
| 2 | 166 | 8.7 | 1155 | US-08-286-889-46 | Sequence 46, Appl |
| 3 | 166 | 8.7 | 1155 | US-08-485-618-46 | Sequence 46, Appl |
| 4 | 166 | 8.7 | 1155 | US-08-362-652-46 | Sequence 46, Appl |
| 5 | 166 | 8.7 | 1155 | US-08-605-672-46 | Sequence 46, Appl |
| 6 | 166 | 8.7 | 1155 | US-08-482-293A-46 | Sequence 46, Appl |
| 7 | 166 | 8.7 | 1155 | US-08-943-363-46 | Sequence 46, Appl |
| 8 | 166 | 8.7 | 1155 | US-09-193-043-46 | Sequence 46, Appl |
| 9 | 166 | 8.7 | 1155 | US-09-688-107A-46 | Sequence 46, Appl |
| 10 | 166 | 8.7 | 1155 | US-03-350-259-46 | Sequence 46, Appl |
| 11 | 166 | 8.7 | 1155 | US-08-485-618-53 | Sequence 53, Appl |
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| 14 | 166 | 8.7 | 1155 | US-08-482-293A-53 | Sequence 53, Appl |
| 15 | 166 | 8.7 | 1155 | US-08-943-363-53 | Sequence 53, Appl |
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| 17 | 166 | 8.7 | 1155 | US-09-688-107A-53 | Sequence 53, Appl |
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| 22 | 159.5 | 8.3 | 1151 | US-08-605-672-37 | Sequence 37, Appl |
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| 24 | 159.5 | 8.3 | 1151 | US-08-943-363-37 | Sequence 37, Appl |
| 25 | 159.5 | 8.3 | 1151 | US-09-193-043-37 | Sequence 37, Appl |
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| 28 | 159.5 | 8.3 | 1161 | US-08-173-497-2 | Sequence 2, Appl |
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| 31 | 159.5 | 8.3 | 1161 | US-08-485-618-55 | Sequence 55, Appl |
| 32 | 159.5 | 8.3 | 1161 | US-08-485-618-99 | Sequence 99, Appl |
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| 36 | 159.5 | 8.3 | 1161 | US-08-605-672-99 | Sequence 99, Appl |
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| 39 | 159.5 | 8.3 | 1161 | US-08-482-293A-99 | Sequence 99, Appl |
| 40 | 159.5 | 8.3 | 1161 | US-08-943-363-99 | Sequence 99, Appl |
| 41 | 159.5 | 8.3 | 1161 | US-08-943-363-55 | Sequence 55, Appl |
| 42 | 159.5 | 8.3 | 1161 | US-08-943-363-99 | Sequence 99, Appl |
| 43 | 159.5 | 8.3 | 1161 | US-09-193-043-2 | Sequence 2, Appl |
| 44 | 159.5 | 8.3 | 1161 | US-09-193-043-55 | Sequence 55, Appl |
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ALIGNMENTS

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| US-10-104-047-2639 | | | | |
| Sequence 2639, Application US/10104047 | | | | |
| Patent No. 6943241 | | | | |
| GENERAL INFORMATION: | | | | |
| APPLICANT: HELIX RESEARCH INSTITUTE | | | | |
| TITLE OF INVENTION: NO. 6943241el full length cDNA | | | | |
| FILE REFERENCE: H1-A0105 | | | | |
| CURRENT APPLICATION NUMBER: US/10/104,047 | | | | |
| CURRENT FILING DATE: 2002-03-25 | | | | |
| PRIOR APPLICATION NUMBER: | | | | |
| PRIOR FILING DATE: | | | | |
| NUMBER OF SEQ ID NOS: 4096 | | | | |
| SOFTWARE: PatentIn Ver. 2.1 | | | | |
| BEO ID NO 2639 | | | | |
| LENGTH: 488 | | | | |
| TYPE: PRT | | | | |
| ORGANISM: Homo sapiens | | | | |
| US-10-104-047-2639 | | | | |
| Query Match | | | | |
| Best Local Similarity 51.9%; Pred. No. 1.1e-97; | | | | |
| Matches 190; Conservative 63; Mismatches 106; Indels 7; Gaps 3; | | | | |
| QY | 4 | AERRALGIGFQWLSLATLVLCAGGG-RRRDEGPACYGGFDLYFLDKSGVYHHNNEI 62 | | |
| DB | 3 | AERSPARSPGSMFLPGMLLVLSGPGGLRAQGPSCRAFDLYFLDKSGSVANNWIEI 62 | | |
| QY | 63 | YVVEQLAKKEIPQRLMSFTVSTRTTLMKLTEDRBOJRGLELOKVLPGDITYME 122 | | |
| DB | 63 | YNEVQQLAERFVSPENRSLFVSSQATITLPLTGKRGKSKLEJEDLKRVSPVGETYIHE 122 | | |
| QY | 123 | GPERASQIYENKRGVTRTSVITALTDEGHLDLFPYSERBRANRSNDLAIYVCVCKD 182 | | |
| DB | 123 | GLKLANKQI--QKAGGKTSITLITLDGDLGVSPYAKKAKISRLASVYCVGLD 180 | | |
| QY | 183 | FNETOLARLIDSDHVPVNDGFQALQGIHSHILKSKCIEILAAEPSTICAGSPQVVR 242 | | |
| DB | 181 | FEDQQLERLIDSEQVFPVAGGFQALKGIINSLIAGSCIEILEQSPSVCVGEFQVLS 240 | | |
| QY | 243 | GNGPRHARNVDRVLCSEFKINDSVTLAEKPSVEDTYLCAPIIKXVGMKAAQVSMNDG 302 | | |
| DB | 241 | GRGFMGLSRNGSVLCYTVNREYTVTSVPVSVQVNSMLCPAPILNKAGETLIDVSVFNGG 300 | | |
| QY | 303 | LSPSSSVITTTTHGSDGSLATATLILFLLALALLMFWPCLCTVIKVEPPPPA--- 359 | | |
| DB | 301 | KSVISGSLVYATBCSNGIAITVILVLLGLGLMMWPLCCKVVIVDPPPPAPAP 360 | | |
| QY | 360 | -EESSE 364 | | |

DB 361 KEEBEE 366

RESULT 2

US-08-286-889-46
; Sequence 46, Application US/08286889
; Patent No. 5470953

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 547093el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLCULE TYPE: protein
US-08-286-889-46

Query Match

Best Local Similarity 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GPDLVFIIDKSGSV-LHNMNFIYFVEQLAHKFIISPOLMSPFVIFSTRTGLMK 94
DB 144 PCPCQEMDIAPFLIDSGSIDSDFTQMKDFVYALMGDLASTSTFSIMQYSLNLTHT 203
QY 95 LTEDR-----EOIRGLELQKVLPGDPTVMEHGFERASEQIYENRQGYRA-SVIAL 148
DB 204 FEFKSSLSPOSIVDAIYQLQ-----GLTYTASGIQVKVKELFHSGNGARKSAKILYI 258
QY 149 TDGELHEDLFPYSE--REANRSRDIGAIYVCVVD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQFRPDLERHVIPEAKA---GIRYALGVGDAPREPTALQELNLTIGSAPSQDHYF 315
QY 200 PVNDGFOALQGIHSLKSCIEIIAEPSTICAGSFQVWVGNGFRRARVD 253
DB 316 KVGN-FVALRSIORQIOEK-----IFAIGTSRSSSFQHEMSQGFSSALSM 364

RESULT 3

US-08-485-618-46
; Sequence 46, Application US/08485618
; Patent No. 5728533

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLCULE TYPE: protein
US-08-485-618-46

Query Match

Best Local Similarity 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GPDLVFIIDKSGSV-LHNMNFIYFVEQLAHKFIISPOLMSPFVIFSTRTGLMK 94
DB 144 PCPCQEMDIAPFLIDSGSIDSDFTQMKDFVYALMGDLASTSTFSIMQYSLNLTHT 203
QY 95 LTEDR-----EOIRGLELQKVLPGDPTVMEHGFERASEQIYENRQGYRA-SVIAL 148
DB 204 FEFKSSLSPOSIVDAIYQLQ-----GLTYTASGIQVKVKELFHSGNGARKSAKILYI 258
QY 149 TDGELHEDLFPYSE--REANRSRDIGAIYVCVVD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQFRPDLERHVIPEAKA---GIRYALGVGDAPREPTALQELNLTIGSAPSQDHYF 315
QY 200 PVNDGFOALQGIHSLKSCIEIIAEPSTICAGSFQVWVGNGFRRARVD 253
DB 316 KVGN-FVALRSIORQIOEK-----IFAIGTSRSSSFQHEMSQGFSSALSM 364

RESULT 4

US-08-362-652-46
; Sequence 46, Application US/08362652
; Patent No. 5766850

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-46

Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMK 94
DB 144 PECFGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQQLASTSTSFIMQYSNLTHTFT 203
QY 95 LTEDR-----EQIRGLIELOKVLPGGDTYMEGFERASQIYENRGYRTA-SVITIAL 148
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLFTYASGIQVVELFHSKNGARKSAKILLIIVI 258
QY 149 TDGELHEDLFYFSE--REANRSRDGAIVYCVGVKD-FNE-TQLARI-----ADSKDHF 199
DB 259 TDQCKRPDPLEYHVIVPEAKA---GIRVAIGVDAFREPTLQELNLTIGSAPSDQHF 315
QY 200 PVNDGFOALOGIHSILKKSCEILAAPEPTICAGSFQVAVVNGFRHARNVD 253
DB 316 KVGN-FVALRSIQROIQEK----IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 5
US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: 233 South Wacker Drive, 6300 Seear Tower

CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46

Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMK 94
DB 144 PECFGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQQLASTSTSFIMQYSNLTHTFT 203
QY 95 LTEDR-----EQIRGLIELOKVLPGGDTYMEGFERASQIYENRGYRTA-SVITIAL 148
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLFTYASGIQVVELFHSKNGARKSAKILLIIVI 258
QY 149 TDGELHEDLFYFSE--REANRSRDGAIVYCVGVKD-FNE-TQLARI-----ADSKDHF 199
DB 259 TDQCKRPDPLEYHVIVPEAKA---GIRVAIGVDAFREPTLQELNLTIGSAPSDQHF 315
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DB 316 KVGN-FVALRSIQROIQEK----IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 6
US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois

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/
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1155 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-482-293A-46
Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFLDKSGSV-LHHNMEIYFVEQLAHKFIQPLMSFVFSRGTTLMK 94
DB 144 PECPOGEMDIAPFLIDSSGSIIDSDFTQMDPVALMGQLASTSTPSLMQYNILKTHFT 203
QY 95 LTEDR-----EQIRGLEELQKVLPGDPTVMHEGFERASEQIYENRQGYTA-SVIAL 148
DB 204 FIEFKSLSPQSLVDALVOLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILYI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGYKD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQKFRDPLEYRHVIPAELKA---GIRYALGVDAFREPTALQELNTIGSAPSDHYF 315
QY 200 PVNDGFOALOGIHSILKSCIEILAAEPSTICAGSFQVVRGNGFRHARVD 253
DB 316 KYGN-FVALRSIORIOEK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364
RESULT 7
US-08-943-363-46
/ Sequence 46, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5837478 Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Seagr Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1155 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-943-363-46
Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFLDKSGSV-LHHNMEIYFVEQLAHKFIQPLMSFVFSRGTTLMK 94
DB 144 PECPOGEMDIAPFLIDSSGSIIDSDFTQMDPVALMGQLASTSTPSLMQYNILKTHFT 203
QY 95 LTEDR-----EQIRGLEELQKVLPGDPTVMHEGFERASEQIYENRQGYTA-SVIAL 148
DB 204 FIEFKSLSPQSLVDALVOLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILYI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGYKD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQKFRDPLEYRHVIPAELKA---GIRYALGVDAFREPTALQELNTIGSAPSDHYF 315
QY 200 PVNDGFOALOGIHSILKSCIEILAAEPSTICAGSFQVVRGNGFRHARVD 253
DB 316 KYGN-FVALRSIORIOEK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364
RESULT 8
US-09-193-043-46
/ Sequence 46, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ TITLE OF INVENTION: No. 6251395 Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ EARLIER FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
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EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1,1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMFSIVSTGTTLMK 94
DB 144 PECGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMYSNLIKTHFT 203
QY 95 LTEDR-----EQIROGLEELQKVLPGDVTYMHGFERASQIYYENRGYRTA-SVITIAL 148
DB 204 FTEFKSLSPOSLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGAKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDLAGIYVCVGYKD-FNE-TQLARI-----ADSKDHF 199
DB 259 TDGQKFRDPLEYRHVIVPEAKA---GIIRVAIGVGDAFREPTALQELINTIGSAPSDHVF 315
QY 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVNGNGFRHARNVD 253
DB 316 KVGK-FVALRSIQROIQEK----IFAIEGTERSSSSSFQHEMSQEGFSSALSMD 364

RESULT 9
US-09-688-307A-46
Sequence 46, Application US/09688307A
Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6432404e1 Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688.307A
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-688-307A-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1,1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMFSIVSTGTTLMK 94
DB 144 PECGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMYSNLIKTHFT 203
QY 95 LTEDR-----EQIROGLEELQKVLPGDVTYMHGFERASQIYYENRGYRTA-SVITIAL 148
DB 204 FTEFKSLSPOSLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGAKSAKKILIVI 258

QY 149 TDGELHEDLFFYSE--REANRSRDLAGIYVCVGYKD-FNE-TQLARI-----ADSKDHF 199
DB 259 TDGQKFRDPLEYRHVIVPEAKA---GIIRVAIGVGDAFREPTALQELINTIGSAPSDHVF 315
QY 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVNGNGFRHARNVD 253
DB 316 KVGK-FVALRSIQROIQEK----IFAIEGTERSSSSSFQHEMSQEGFSSALSMD 364

RESULT 10
US-09-350-259-46
Sequence 46, Application US/09350259
Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6620915e1 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-350-259-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1,1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMFSIVSTGTTLMK 94
DB 144 PECGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMYSNLIKTHFT 203
QY 95 LTEDR-----EQIROGLEELQKVLPGDVTYMHGFERASQIYYENRGYRTA-SVITIAL 148
DB 204 FTEFKSLSPOSLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGAKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDLAGIYVCVGYKD-FNE-TQLARI-----ADSKDHF 199
DB 259 TDGQKFRDPLEYRHVIVPEAKA---GIIRVAIGVGDAFREPTALQELINTIGSAPSDHVF 315
QY 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVNGNGFRHARNVD 253
DB 316 KVGK-FVALRSIQROIQEK----IFAIEGTERSSSSSFQHEMSQEGFSSALSMD 364

RESULT 11
US-08-485-618-53
Sequence 53, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seair Tower
CITY: Chicago
STATE: Illinois

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/
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,618
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32797
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-485-618-53

Query Match
Best Local Similarity 28.2%; Score 166; DB 1; Length 1161;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GPDLVITLKSQSV-LHNMETIYFVEQLAHKFIQPLKMSPIVSTRTGLTK 94
DB 144 PCPCQEMDIAPLIDSGSIDSDFTQKDFVQALMGQLASTSTFSLMQYNIILKTHPT 203
QY 95 LTEDR-----EQIRQGLEIQLKVLPGDPTVMHEGFERASBOIYYENRGYRTA-SVIAL 148
DB 204 FTEFKSSLPQSLVDAIVQLQ-----GLTYTASGIQKVKELPHSKNGARKSAKILLIYI 258
QY 149 TDGELHEDLFFYSE--REANRSRLGAIYVCVQKD-FNE-TQLARI-----ADSKDHVF 199
DB 259 TDGQKFRDPLEYRHVIPLEAKA---GIIRYAGVGDAPREPTALQELNTIGSAPSQDHVF 315
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGSFQVYVRGNGFRARAVD 253
DB 316 KVGNG-FVALRSIORQIOEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 12
US-08-362-652-53
/ Sequence 53, Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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US-08-362-652-53

Query Match
Best Local Similarity 28.2%; Score 166; DB 1; Length 1161;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GPDLVITLKSQSV-LHNMETIYFVEQLAHKFIQPLKMSPIVSTRTGLTK 94
DB 144 PCPCQEMDIAPLIDSGSIDSDFTQKDFVQALMGQLASTSTFSLMQYNIILKTHPT 203
QY 95 LTEDR-----EQIRQGLEIQLKVLPGDPTVMHEGFERASBOIYYENRGYRTA-SVIAL 148
DB 204 FTEFKSSLPQSLVDAIVQLQ-----GLTYTASGIQKVKELPHSKNGARKSAKILLIYI 258
QY 149 TDGELHEDLFFYSE--REANRSRLGAIYVCVQKD-FNE-TQLARI-----ADSKDHVF 199
DB 259 TDGQKFRDPLEYRHVIPLEAKA---GIIRYAGVGDAPREPTALQELNTIGSAPSQDHVF 315
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGSFQVYVRGNGFRARAVD 253
DB 316 KVGNG-FVALRSIORQIOEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 13
US-08-605-672-53
/ Sequence 53, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Query Match 8.7%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

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| Qy | 37 | PACYG-GPDLVFLDKSGSV-LHHNWEIYFEVQLAHKFI | SPQLRMSFIVFSTRGTTLMK | 94 |
| Db | 144 | PECPGQEMDIAFLIDSGSIDQSDFTQMKDFVXALMGOLASTSTSF | LMQYSNLTHTPT | 203 |
| Qy | 95 | LTEDR-----EQROGLEELQKVLPGDPTMHGFEERASQIYENRQGVRTA-SVIT | AL | 148 |
| Db | 204 | FTEFKSLSLPQSLVDAIVQLQ-----GLTYTASGIQVVKELPHSRNARKSKAKTLIV | I | 258 |
| Qy | 149 | TDEGLHEDLFFYSE--REANRSRLGAIYVCVGKD-FNE-TQLARI-----ADSKDHVF | | 199 |
| Db | 259 | TGQKRDLELHYHVAPEAKA---GIRVAIGVGDAPREPTALQELANTIGSAPSGDHVF | | 315 |
| Qy | 200 | PVNDGFQALQGIHSILKKSCHITLAEPTTCAGESFOVVVRGNGFRHARNVD | | 253 |
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Search completed: December 14, 2005, 11:21:04
Job time : 34.1864 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 14, 2005, 11:18:07 ; Search time 110.867 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914

Sequence: 1 MATERRALGIGFOWLSLAT.....VILKEVPPPAESENKIK 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417629326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1914 | 100.0 | 368 | 6 US-11-047-278-2 | Sequence 2, Appl1 |
| 2 | 1894 | 99.0 | 564 | 3 US-09-918-715-187 | Sequence 187, App |
| 3 | 1894 | 99.0 | 564 | 3 US-09-918-715-232 | Sequence 232, App |
| 4 | 1894 | 99.0 | 564 | 4 US-10-301-822-199 | Sequence 199, App |
| 5 | 1894 | 99.0 | 564 | 4 US-10-408-765A-1823 | Sequence 1823, App |
| 6 | 1894 | 99.0 | 564 | 4 US-10-474-794-187 | Sequence 187, App |
| 7 | 1894 | 99.0 | 564 | 4 US-10-474-794-232 | Sequence 232, App |
| 8 | 1894 | 99.0 | 564 | 5 US-10-979-159-187 | Sequence 187, App |
| 9 | 1894 | 99.0 | 564 | 5 US-10-979-159-232 | Sequence 232, App |
| 10 | 1894 | 99.0 | 564 | 6 US-11-047-278-6 | Sequence 6, Appl1 |
| 11 | 1889 | 98.7 | 403 | 3 US-09-833-245-621 | Sequence 621, App |
| 12 | 1870 | 97.7 | 403 | 3 US-09-833-245-620 | Sequence 620, App |
| 13 | 1793 | 93.7 | 562 | 3 US-09-918-715-194 | Sequence 194, App |
| 14 | 1793 | 93.7 | 562 | 3 US-09-918-715-301 | Sequence 301, App |
| 15 | 1793 | 93.7 | 562 | 4 US-10-474-794-194 | Sequence 194, App |
| 16 | 1793 | 93.7 | 562 | 4 US-10-474-794-301 | Sequence 301, App |
| 17 | 1793 | 93.7 | 562 | 5 US-10-979-159-194 | Sequence 194, App |
| 18 | 1793 | 93.7 | 562 | 5 US-10-979-159-301 | Sequence 301, App |
| 19 | 1661 | 86.8 | 551 | 4 US-10-038-307-18 | Sequence 18, Appl1 |
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| 21 | 1649 | 86.2 | 333 | 4 US-09-796-753-12 | Sequence 12, Appl1 |
| 22 | 1649 | 86.2 | 333 | 4 US-10-038-307-2 | Sequence 2, Appl1 |
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| 32 | 1634.5 | 85.4 | 342 | 4 US-10-201-292-22 | Sequence 22, Appl1 |
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| 38 | 1619 | 84.6 | 543 | 4 US-10-201-292-10 | Sequence 10, Appl1 |
| 39 | 1548 | 80.9 | 529 | 4 US-10-201-292-36 | Sequence 36, Appl1 |
| 40 | 1488 | 77.7 | 534 | 4 US-10-038-307-12 | Sequence 12, Appl1 |
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| 43 | 1307 | 68.3 | 479 | 4 US-10-201-292-32 | Sequence 32, Appl1 |
| 44 | 1193 | 62.3 | 460 | 4 US-10-201-292-28 | Sequence 28, Appl1 |
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ALIGNMENTS

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RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Query Match      100.0%  Score 1914; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 4.4e-184;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATERRALGIGFOWLSLATLVLI CAGGGRREDGGPACYGFDLYI LDKSGSVLHNN 60
      1 MATERRALGIGFOWLSLATLVLI CAGGGRREDGGPACYGFDLYI LDKSGSVLHNN 60
Db      1 MATERRALGIGFOWLSLATLVLI CAGGGRREDGGPACYGFDLYI LDKSGSVLHNN 60
QY      61 EIIYFPEQIAHKFISQGLMSFIVSRTGTTLMKLTEDBQIRQGLEIYOKVLPBGDTY 120
      61 EIIYFPEQIAHKFISQGLMSFIVSRTGTTLMKLTEDBQIRQGLEIYOKVLPBGDTY 120
Db      61 EIIYFPEQIAHKFISQGLMSFIVSRTGTTLMKLTEDBQIRQGLEIYOKVLPBGDTY 120
QY      121 HSGFERASQIYENKQGYRTASVITALTDELHEHDLFPYSREARSRDLGIYVCVGV 180
      121 HSGFERASQIYENKQGYRTASVITALTDELHEHDLFPYSREARSRDLGIYVCVGV 180
Db      121 HSGFERASQIYENKQGYRTASVITALTDELHEHDLFPYSREARSRDLGIYVCVGV 180
QY      181 KQFNETQLARLADSKDHPVNDGFOALQGIHLSILKSCIBILAEPSTICAGSEFOVY 240
      181 KQFNETQLARLADSKDHPVNDGFOALQGIHLSILKSCIBILAEPSTICAGSEFOVY 240
Db      181 KQFNETQLARLADSKDHPVNDGFOALQGIHLSILKSCIBILAEPSTICAGSEFOVY 240
QY      241 VRGNGRHRARNDVLCRKINDSVTLNKPVSVEVTYLLCPAPILKEVGMKRALLOVSN 300
      241 VRGNGRHRARNDVLCRKINDSVTLNKPVSVEVTYLLCPAPILKEVGMKRALLOVSN 300
Db      241 VRGNGRHRARNDVLCRKINDSVTLNKPVSVEVTYLLCPAPILKEVGMKRALLOVSN 300
QY      301 DGLSFISSSVITTTTCSDGSLALALILFLFLALALALMFWPLCCTVYI KEVPPPAE 360
      301 DGLSFISSSVITTTTCSDGSLALALILFLFLALALALMFWPLCCTVYI KEVPPPAE 360
```

```
Db      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Qy      361 ESEENKIK 368
Db      361 ESEENKIK 368
```

RESULT 2

```
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187
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Query Match 99.0%; Score 1894; DB 3; Length 564;

Best Local Similarity 100.0%; Pred. No. 8.7e-182; Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MATARRALGIGFQWLSLTLVLICAGGGRREDGSPACYGFDLYFLIDKSGSVLHMN 60
Db      1 MATARRALGIGFQWLSLTLVLICAGGGRREDGSPACYGFDLYFLIDKSGSVLHMN 60
Qy      61 EIIYFVEQLAHKFIQPLMSFIVSTGTITMKLTEDREQIRQGLEELQKVLPGDITM 120
Db      61 EIIYFVEQLAHKFIQPLMSFIVSTGTITMKLTEDREQIRQGLEELQKVLPGDITM 120
Qy      121 HEGFERASEQIYYENRQGRITASVITALTDEGLHEDLPFYSEREANRSHDLGAIYCVG 180
Db      121 HEGFERASEQIYYENRQGRITASVITALTDEGLHEDLPFYSEREANRSHDLGAIYCVG 180
Qy      181 KQFNETQLARIADSKDHVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Db      181 KQFNETQLARIADSKDHVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Qy      241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
Db      241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
Qy      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Db      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Qy      361 ESEE 364
Db      361 ESEE 364
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RESULT 3

```
US-09-918-715-232
; Sequence 232, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
```

```
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-232
```

Query Match 99.0%; Score 1894; DB 3; Length 564;

Best Local Similarity 100.0%; Pred. No. 8.7e-182; Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MATARRALGIGFQWLSLTLVLICAGGGRREDGSPACYGFDLYFLIDKSGSVLHMN 60
Db      1 MATARRALGIGFQWLSLTLVLICAGGGRREDGSPACYGFDLYFLIDKSGSVLHMN 60
Qy      61 EIIYFVEQLAHKFIQPLMSFIVSTGTITMKLTEDREQIRQGLEELQKVLPGDITM 120
Db      61 EIIYFVEQLAHKFIQPLMSFIVSTGTITMKLTEDREQIRQGLEELQKVLPGDITM 120
Qy      121 HEGFERASEQIYYENRQGRITASVITALTDEGLHEDLPFYSEREANRSHDLGAIYCVG 180
Db      121 HEGFERASEQIYYENRQGRITASVITALTDEGLHEDLPFYSEREANRSHDLGAIYCVG 180
Qy      181 KQFNETQLARIADSKDHVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Db      181 KQFNETQLARIADSKDHVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Qy      241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
Db      241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
Qy      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Db      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Qy      361 ESEE 364
Db      361 ESEE 364
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RESULT 4

```
US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgate, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP001-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
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/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361, 978
/ PRIOR FILING DATE: 2002-03-05 60/381, 988
/ PRIOR APPLICATION NUMBER: US 60/381, 988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 199
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-301-822-199

Query Match          99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSLATLVLCAGQGRREDGPGACGFDLYFILDKSGSVLHHN 60
DB 1 MATERRALGIGFOWLSLATLVLCAGQGRREDGPGACGFDLYFILDKSGSVLHHN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
QY 121 HEGPERASEQIYYENRGYRTASVIALTDGELHEDLFYSEERANRSRDGAIVYCVGV 180
DB 121 HEGPERASEQIYYENRGYRTASVIALTDGELHEDLFYSEERANRSRDGAIVYCVGV 180
QY 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSLKSCIEILAAEPSTICAGESFOV 240
DB 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSLKSCIEILAAEPSTICAGESFOV 240
QY 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVEDTYLLCPAPILKEVGMKALQVSMN 300
DB 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVEDTYLLCPAPILKEVGMKALQVSMN 300
QY 301 DGLSFSSSVITTTTSCDSGSIILAILLIFLLALALLMFWPMLCCTVLIKEVPPPAE 360
DB 301 DGLSFSSSVITTTTSCDSGSIILAILLIFLLALALLMFWPMLCCTVLIKEVPPPAE 360
QY 361 ESEE 364
DB 361 ESEE 364

RESULT 5
US-10-408-765A-1823
/ Sequence 1823, Application US/10408765A
/ Publication NO. US20040101874A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Fahy, Eoin D.
/ APPLICANT: Zhang, Bing
/ APPLICANT: Gibson, Bradford W.
/ APPLICANT: Taylor, Steven W.
/ APPLICANT: Glenn, Gary M.
/ APPLICANT: Warnock, Dale E.
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
/ FILE REFERENCE: 660088.465
/ CURRENT APPLICATION NUMBER: US/10/408, 765A
/ NUMBER OF SEQ ID NOS: 3077
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1823
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-408-765A-1823

Query Match          99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSLATLVLCAGQGRREDGPGACGFDLYFILDKSGSVLHHN 60
DB 1 MATERRALGIGFOWLSLATLVLCAGQGRREDGPGACGFDLYFILDKSGSVLHHN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
QY 121 HEGPERASEQIYYENRGYRTASVIALTDGELHEDLFYSEERANRSRDGAIVYCVGV 180
DB 121 HEGPERASEQIYYENRGYRTASVIALTDGELHEDLFYSEERANRSRDGAIVYCVGV 180
QY 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSLKSCIEILAAEPSTICAGESFOV 240
DB 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSLKSCIEILAAEPSTICAGESFOV 240
QY 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVEDTYLLCPAPILKEVGMKALQVSMN 300
DB 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVEDTYLLCPAPILKEVGMKALQVSMN 300
QY 301 DGLSFSSSVITTTTSCDSGSIILAILLIFLLALALLMFWPMLCCTVLIKEVPPPAE 360
DB 301 DGLSFSSSVITTTTSCDSGSIILAILLIFLLALALLMFWPMLCCTVLIKEVPPPAE 360
QY 361 ESEE 364
DB 361 ESEE 364

RESULT 6
US-10-474-794-187
/ Sequence 187, Application US/10474794
/ Publication NO. US20040213793A1
/ GENERAL INFORMATION:
/ APPLICANT: Carson-Walter, Eleanor
/ APPLICANT: St. Croix, Brad
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Kinzler, Kenneth
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107,00179
/ CURRENT APPLICATION NUMBER: US/10/474, 794
/ PRIOR FILING DATE: 2003-10-14
/ PRIOR APPLICATION NUMBER: 60/282, 850
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 60/308, 829
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 359
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 187
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-474-794-187

Query Match          99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Db      181 KPFNETQLARIADSKDHVPVNDGFOALQGIHHSILKSCIEILAEPSITCAGESFOYV 240
        |||
Qy      241 VRNGFRHARNVDRVLCSPFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        |||
Db      241 VRNGFRHARNVDRVLCSPFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        |||
Qy      301 DGLSFSSSVIITTHCSGDSIIAIALILFLLLALALLMFWPMLCCTVIKEVPPPPAB 360
        |||
Db      301 DGLSFSSSVIITTHCSGDSIIAIALILFLLLALALLMFWPMLCCTVIKEVPPPPAB 360
        |||
Qy      361 ESEE 364
        |||
Db      361 ESEE 364
```

```
RESULT 7
US-10-474-794-232
; Sequence 232, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-232
```

```
Query Match      99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MATERRALGIGFOMLSLTLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
        |||
Db      1 MATERRALGIGFOMLSLTLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
        |||
Qy      61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
        |||
Db      61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
        |||
Qy      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Db      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Qy      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Db      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Qy      181 KPFNETQLARIADSKDHVPVNDGFOALQGIHHSILKSCIEILAEPSITCAGESFOYV 240
        |||
Db      181 KPFNETQLARIADSKDHVPVNDGFOALQGIHHSILKSCIEILAEPSITCAGESFOYV 240
        |||
Qy      241 VRNGFRHARNVDRVLCSPFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        |||
Db      241 VRNGFRHARNVDRVLCSPFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        |||
Qy      301 DGLSFSSSVIITTHCSGDSIIAIALILFLLLALALLMFWPMLCCTVIKEVPPPPAB 360
        |||
Db      301 DGLSFSSSVIITTHCSGDSIIAIALILFLLLALALLMFWPMLCCTVIKEVPPPPAB 360
        |||
Qy      361 ESEE 364
        |||
Db      361 ESEE 364
```

```
RESULT 8
US-10-979-159-187
; Sequence 187, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-187
```

```
Query Match      99.0%; Score 1894; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MATERRALGIGFOMLSLTLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
        |||
Db      1 MATERRALGIGFOMLSLTLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
        |||
Qy      61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
        |||
Db      61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
        |||
Qy      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Db      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Qy      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Db      121 HGFEPASQIYYENRQGYRTASVIALTDGELHEDLFYSSREARNSDLAGIYVCVY 180
        |||
Qy      181 KPFNETQLARIADSKDHVPVNDGFOALQGIHHSILKSCIEILAEPSITCAGESFOYV 240
        |||
Db      181 KPFNETQLARIADSKDHVPVNDGFOALQGIHHSILKSCIEILAEPSITCAGESFOYV 240
        |||
Qy      241 VRNGFRHARNVDRVLCSPFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        |||
Db      241 VRNGFRHARNVDRVLCSPFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        |||
Qy      301 DGLSFSSSVIITTHCSGDSIIAIALILFLLLALALLMFWPMLCCTVIKEVPPPPAB 360
        |||
Db      301 DGLSFSSSVIITTHCSGDSIIAIALILFLLLALALLMFWPMLCCTVIKEVPPPPAB 360
        |||
Qy      361 ESEE 364
        |||
Db      361 ESEE 364

RESULT 9
US-10-979-159-232
; Sequence 232, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
```

```

RESULT 10
US-11-047-278-6
; Sequence 6, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: COLLIER, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960286.97745
; CURRENT APPLICATION NUMBER: US/11/047, 278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970, 076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: patentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens

```

| | | | | |
|-----------------------|----------------|---|----------|------------|
| Query Match | 98.7% | Score 1889 | DB 3 | Length 403 |
| Best Local Similarity | 100.0% | Pred. No. 1.7e-181 | | |
| Matches 363 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | MATAERRALGIGFOWMLSLATLVLCAGQGGRRRGGPACGYGFDLYLIDKSGSVLHHN | 60 | |
| Db | 1 | MATAERRALGIGFOWMLSLATLVLCAGQGGRRRGGPACGYGFDLYLIDKSGSVLHHN | 60 | |
| QY | 61 | EIYYPVQOLAHKRIISPOLRMSFIVFSRGTGLTKLTEDRQIRQGLKEILQKVLPGGDTM | 120 | |
| Db | 61 | EIYYPVQOLAHKRIISPOLRMSFIVFSRGTGLTKLTEDRQIRQGLKEILQKVLPGGDTM | 120 | |
| QY | 121 | HEGFERASEQIYYENRQGYRTASVILALTDGELHEDLFYSEEDANRSRDGLAIYVCGV | 180 | |

Db 121 HEGFERASEQIYYENKQYRTASVIALITDGLHEDLFFYSERBANRSDLAIVYCVG 180
QY 181 KDFNETOLARIADSKDHVPVNDGFOALOGIIHSILKSCIEILAAPESTICAGESFOVV 240
Db 181 KDFNETOLARIADSKDHVPVNDGFOALOGIIHSILKSCIEILAAPESTICAGESFOVV 240
QY 241 VANGFRHARANDRVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSNV 300
Db 241 VANGFRHARANDRVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSNV 300
QY 301 DGLSFSSSVIITTHCSGDSIIALAILFLALLALMLMFWPLCCTVYIKEVPPPAE 360
Db 301 DGLSFSSSVIITTHCSGDSIIALAILFLALLALMLMFWPLCCTVYIKEVPPPAE 360
QY 361 ESE 363
Db 361 ESE 363

RESULT 12

US-09-833-245-620
; Sequence 620, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 620
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (331)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (368)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Query Match 97.7%; Score 1870; DB 3; Length 403;
Best Local Similarity 99.2%; Pred. No. 1.4e-179;

Matches 360; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSTLVLCAGGGRREDGPGACYGFDLYIILDKSGSVLHHNN 60
Db 1 MATERRALGIGFOWLSTLVLCAGGGRREDGPGACYGFDLYIILDKSGSVLHHNN 60
QY 61 EIIYFVEQLAHKISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLELOKVLPGDPTM 120
Db 61 EIIYFVEQLAHKISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLELOKVLPGDPTM 120
QY 121 HEGFERASEQIYYENKQYRTASVIALITDGLHEDLFFYSERBANRSDLAIVYCVG 180
Db 121 HEGFERASEQIYYENKQYRTASVIALITDGLHEDLFFYSERBANRSDLAIVYCVG 180
QY 181 KDFNETOLARIADSKDHVPVNDGFOALOGIIHSILKSCIEILAAPESTICAGESFOVV 240

Db 181 KDFNETOLARIADSKDHVPVNDGFOALOGIIHSILKSCIEILAAPESTICAGESFOVV 240
QY 241 VANGFRHARANDRVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSNV 300
Db 241 VANGFRHARANDRVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSNV 300
QY 301 DGLSFSSSVIITTHCSGDSIIALAILFLALLALMLMFWPLCCTVYIKEVPPPAE 360
Db 301 DGLSFSSSVIITTHCSGDSIIALAILFLALLALMLMFWPLCCTVYIKEVPPPAE 360
QY 361 ESE 363
Db 361 ESE 363

RESULT 13

US-09-918-715-194
; Sequence 194, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FaestSO for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-194

Query Match 93.7%; Score 1793; DB 3; Length 562;
Best Local Similarity 96.1%; Pred. No. 1.4e-171;
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 9 LGIGFOWLSTLVLCAGGGRREDGPGACYGFDLYIILDKSGSVLHHNNIYFVRO 68
Db 7 LGAGLRGLCVAAVLVYCAHGGRREDGPGACYGFDLYIILDKSGSVLHHNNIYFVRO 66
QY 69 LAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLELOKVLPGDPTMHGFERAS 128
Db 67 LAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLELOKVLPGDPTMHGFERAS 126
QY 129 EOIYYENKQYRTASVIALITDGLHEDLFFYSERBANRSDLAIVYCVGVDFNETOL 188
Db 127 EOIYYENKQYRTASVIALITDGLHEDLFFYSERBANRSDLAIVYCVGVDFNETOL 186
QY 189 ARIADSKDHVPVNDGFOALOGIIHSILKSCIEILAAPESTICAGESFOVVVANGFRH 248
Db 187 ARIADSKDHVPVNDGFOALOGIIHSILKSCIEILAAPESTICAGESFOVVVANGFRH 246
QY 249 ARNVDRVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSNV DGLSFSS 308
Db 247 ARNVDRVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSNV DGLSFSS 306
QY 309 SVIITTHCSGDSIIALAILFLALLALMLMFWPLCCTVYIKEVPPPAESSE 364
Db 307 SVIITTHCSGDSIIALAILFLALLALMLMFWPLCCTVYIKEVPPPAESSE 362

RESULT 14

US-09-918-715-301

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; Sequence 301, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-301
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```
Query Match          93.7%; Score 1793; DB 3; Length 562;
Best Local Similarity 96.1%; Pred. No. 1,4e-171;
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 9 LGIGFQWLSATVTLVLCAGGCGRRDGGPACYGFDLYFLIDKSGSVLHHMNEIYYFVEQ 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 LGAGLGLCVAAALVLCAGHGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYYFVEQ 66
QY 69 LAHKFISPOLRMSFIVFSTRTGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRAS 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 LAHRFISPOLRMSFIVFSTRTGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRAS 126
QY 129 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 188
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 EQIYENSQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 186
QY 189 ARIADSKDHYFPVNDGFQALOGIHSILKKSCEIILAEPSITCAGESFOVVRGNGFRH 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 ARIADSKDHYFPVNDGFQALOGIHSILKKSCEIILAEPSITCAGESFOVVRGNGFRH 246
QY 249 ARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFIS 308
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 ARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFIS 306
QY 309 SVIITTHCSGDSILAIALLILFLALALALLMWFPLCCTVIIKEVPPPAESEE 364
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 SVIITTHCSGDSILAIALLILFLALALALLMWFPLCCTVIIKEVPPPAESEE 362
```

```
RESULT 15
US-10-474-794-194
; Sequence 194, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
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; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-474-794-194
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```
Query Match          93.7%; Score 1793; DB 4; Length 562;
Best Local Similarity 96.1%; Pred. No. 1,4e-171;
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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```
QY 9 LGIGFQWLSATVTLVLCAGGCGRRDGGPACYGFDLYFLIDKSGSVLHHMNEIYYFVEQ 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 LGAGLGLCVAAALVLCAGHGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYYFVEQ 66
QY 69 LAHKFISPOLRMSFIVFSTRTGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRAS 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 LAHRFISPOLRMSFIVFSTRTGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRAS 126
QY 129 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 188
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 EQIYENSQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 186
QY 189 ARIADSKDHYFPVNDGFQALOGIHSILKKSCEIILAEPSITCAGESFOVVRGNGFRH 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 ARIADSKDHYFPVNDGFQALOGIHSILKKSCEIILAEPSITCAGESFOVVRGNGFRH 246
QY 249 ARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFIS 308
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 ARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFIS 306
QY 309 SVIITTHCSGDSILAIALLILFLALALALLMWFPLCCTVIIKEVPPPAESEE 364
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 SVIITTHCSGDSILAIALLILFLALALALLMWFPLCCTVIIKEVPPPAESEE 362
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Search completed: December 14, 2005, 11:58:58
Job time : 112.034 secs
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Db      121 HEGFERASQIYENKQRTASVIALDDELHEDLFFYSEREARSRDLGAIYCVGV 180
Qy      181 KQNFETQLARIKSDKHVPVNDGFOALGGIHSILKSCIEIILAEPTICAGSEFOVV 240
Db      181 KQNFETQLARIKSDKHVPVNDGFOALGGIHSILKSCIEIILAEPTICAGSEFOVV 240
Qy      241 VAGNGFRHARNDVRLCSFKINDSVTLNKEPFSVEDTYLLCPAPILKEYGMKALQVSNM 300
Db      241 VAGNGFRHARNDVRLCSFKINDSVTLNKEPFSVEDTYLLCPAPILKEYGMKALQVSNM 300
Qy      301 DGLSFISSSVIITTTGCSGSIILALLILFLILALALIMWEPILCCTVIYIKVPPPPAE 360
Db      301 DGLSFISSSVIITTTGCSGSIILALLILFLILALALIMWEPILCCTVIYIKVPPPPAE 360
Qy      361 ESEE 364
Db      361 ESEE 364

```

```

RESULT 2
US-11-080-026-4
; Sequence 4, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimooka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CFBF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; PRIOR FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-026-4

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```

Query Match      7.6%; Score 145.5; DB 7; Length 1152;
Best Local Similarity 26.2%; Pred. No. 1.4e-05;
Matches 60; Conservative 45; Mismatches 81; Indels 43; Gaps 12;

Qy      44 DLYFIIDKSGSVL-HHMEIYYFVEQLAHKFIPOLRMSFIVSTRTTLMKLTED---- 98
Db      150 DIAFLIDGSGSIIPHPFRMKKEVST-----VMEQLKSKSTLFS-----LMQVSEFRH 199
Qy      99 -----RQIIRQGLEELQKVLPGDVTWHEGFERASEQIYENKQRTA-SVIALT 149
Db      200 FTFKEFQNNPNRSLVKVPIQLL--GRTHATGIRKVRBELFITGARKNAFKIIVIT 257
Qy      150 DGLHHDLPFYSE--REARSRDLGAIYCVGVKDNENQOLAR-----IADS--KDHVP 200
Db      258 DGEKFDPLGYEIVPEADRE--GVIRYIVGVGDVFRSEKSRQELINTJASKPRDHVQ 314
Qy      201 VNDGFOALGGIHSILKSCIEIILAEPTICAGSEFOVVVNDGFRHA 249
Db      315 VNN-FEALKTIOQLREK----IFAIEGTOTGSSSFHEHMSQEGSAA 358

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RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison

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; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE REFERENCE: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

```

```

Query Match      6.8%; Score 131; DB 7; Length 3063;
Best Local Similarity 29.8%; Pred. No. 0.0014;
Matches 59; Conservative 38; Mismatches 75; Indels 26; Gaps 13;

Qy      44 DLYFIIDKSGSV-LHHMEIYYFVEQLAHKFI-ISP-QLRMSFIVST--RGTLMKLT 97
Db      440 DIVFLVDGSYSGIANFVYRAFLVLYKSFISPRRQVLSLVQVMSRDHTEFTLKPK 499
Qy      98 DREQIRQGLEELQKVLPGDVTWHEGFERASEQIYENKQRTA-SVIALTDEL 153
Db      500 VEDII-----EAINTFPYKSGSTNKGKMTYVREKIFVPSK-GSRSNVPEKWMILLTDGK 552
Qy      154 HEDLPFYSEREARSRDLGAIYCVGVKDNENQOLARID--SKDHVPVNDGFOALGGI 211
Db      553 SSDAF---RDPALKLRNSDVEIFAVGVKDVAVRSELEALASPAETHVTEVD-FDAFQRI 608
Qy      212 IHSILKSCIEI---LAA 226
Db      609 SEFLQSTICLRIEQLAA 626

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RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: Methods Related Thereof
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2

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/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 6
/ LENGTH: 761
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-11-057-047-6

Query Match 5.8%; Score 110.5; DB 7; Length 761;
Best Local Similarity 20.5%; Pred. No. 0.015;
Matches 71; Conservative 59; Mismatches 99; Indels 117; Gaps 20;

QY 28 OGGRREDG-----GPACYGFDLYFLDKSGSV-----LHWNREY 63
DB 240 EGADADGHSPEGQQRKTVLDPS--GSNATYVLVDSBSIGSNTGAKRCLTN----- 292
QY 64 YFVEQLAHKRFISPOLMSFVFSRGTITMKTLED-----EQIROGLEBELQVLP 115
DB 293 -LIEKVASYGVR--RYGLLTATVPKVLVRVSDERSADADWTERKLNQISYEDHKLKSG 349
QY 116 GDTYHMEGRASEQIYY-----ENRQCY-RTASVITALTDEGLH-----EDL 157
DB 350 TMT-----KRALQAVYSMMWSMAGDAPREGMNRTRHVIIMTDG-LHNGGNPVTVIODI 402
QY 158 FPFYSE--REANRSRD--LGAIVYCVG--VKDFNETQLARIADSKDHVPVNDGFOALQGI 211
DB 403 RALDDGRDPKPREYLDVYVGVGPLVDSVINNALASKKDEHNVFVKD-MEDLENV 461
QY 212 IHSILKSCIEILAEPTICAGESFOVYVNGNPFHARNVRLCSFKINDSVTLNEKP 271
DB 462 FYQMIDET-----KSLSLC-----GWVWEHKKGNDYHKQPMQAKISVT---RP 501
QY 272 FSVEDTYLLCPAPILKEVCKKALQVSMNDGLSFISSVIITTHC 317
DB 502 LKQHER---CMGAV-----VSEYFLTAHNC 524

RESULT 13
US-10-601-368-6
/ Sequence 6, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 1141
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-6

Query Match 5.6%; Score 107; DB 6; Length 1141;

Best Local Similarity 24.1%; Pred. No. 0.058;

Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 39 CYGFPDLYFLDKSGSVLHHMNEIYFVEQLAHKF-ISP-QLRMSFVFSRGTITMKT 96
DB 159 CQTYMDIYVLDDGNSI-YPWVEVQHFLINILKKFYIGQIQGVGVGVEDVYHEFHL- 216

QY 97 EDREIQROGLEBELQVLPFGDTYHMEGR--RASEQIYYENRQGYRTASVITLTDEGL 153
DB 217 NDYRSVKDVEAASHIEQRGTETRTAFGIEPARSEAFQKGRKAK--KVMIVITDGS 274
QY 154 HED-----LFFYSEBEANRSRDLGAIYCVGVKD-----FNETQ 187
DB 275 HDSPLLEKVIQSERDNTRYAVAVLGYNRRGINPETFLNEIKYIASDPDDKHFPNVTD 334
QY 188 LARIADSKDHVPVNDGFOALQG 210
DB 335 EAAL---KDIYDALGDRIFSLG 354

RESULT 14
US-10-601-368-4
/ Sequence 4, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 1166
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-601-368-4

Query Match 5.6%; Score 107; DB 6; Length 1166;
Best Local Similarity 24.1%; Pred. No. 0.06;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 39 CYGFPDLYFLDKSGSVLHHMNEIYFVEQLAHKF-ISP-QLRMSFVFSRGTITMKT 96
DB 137 CQTYMDIYVLDDGNSI-YPWVEVQHFLINILKKFYIGQIQGVGVGVEDVYHEFHL- 194
QY 97 EDREIQROGLEBELQVLPFGDTYHMEGR--RASEQIYYENRQGYRTASVITLTDEGL 153
DB 195 NDYRSVKDVEAASHIEQRGTETRTAFGIEPARSEAFQKGRKAK--KVMIVITDGS 252
QY 154 HED-----LFFYSEBEANRSRDLGAIYCVGVKD-----FNETQ 187
DB 253 HDSPLLEKVIQSERDNTRYAVAVLGYNRRGINPETFLNEIKYIASDPDDKHFPNVTD 312
QY 188 LARIADSKDHVPVNDGFOALQG 210
DB 313 EAAL---KDIYDALGDRIFSLG 332

RESULT 15
US-10-601-368-3
/ Sequence 3, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28

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/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 1188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-3
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Query Match      5.6%; Score 107; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.061;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;
```

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QY 39 CYGQFDLYFLDKSGSVLHHNEIYVFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLT 96
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Db 159 CQTYMDIVIVLDGSNSI-YPMVEVQHFLINILKKFYIGPGQIQGVVQYGEDVVEHFL- 216
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QY 97 EDREQIRQGLEELQKVLPGDLYMHGFE--RASEQIYYENRQGYRTASVITATDDEL 153
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Db 217 NDYRSVADVEAASHLEQRGSTETRTAFGIEPARSEAFQKGRKGA--KVMIVITDGS 274
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QY 154 HED-----LFFYSEREARNSRDLGAIYVCVVKD-----FNETQ 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 275 HDSPDLEKVIQSERDVTTRYAVAVLGYNNRGINPETFLNEIKYIASDPDDKHFRVTD 334
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QY 188 LARIADSKDHFVPVNDGFOALQG 210
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Db 335 EAAL---KDIYDALGDRIFSLEG 354
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Search completed: December 14, 2005, 11:59:26
Job time : 6.40815 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37, Search time 258.362 Seconds

(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914
Sequence: 1 MATERRALDGTGOWLSLAT.....VITKEVPPAPSESENKIK 358

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| Ygapop 10.0, Ygapext 0.5 | |
| Fgapop 6.0, Fgapext 7.0 | |
| Delop 6.0, Delext 7.0 | |

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DB=Isued_Patents_NA -OPMT=fastcap -SUFFIX=rm1 -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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Database:

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8: /cgn2_6/ptodates/1/lna/RE.COMB.seq:*
9: /cgn2_6/ptodates/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1392 | 72.7 | 1609 | 3 | US-09-620-312D-8 |
| 2 | 962.5 | 50.3 | 2234 | 3 | US-10-104-047-669 |
| 3 | 891 | 46.6 | 3981 | 3 | US-09-799-451-250 |
| 4 | 859 | 44.9 | 1492 | 3 | US-09-774-528-297 |
| 5 | 859 | 44.9 | 1492 | 3 | US-10-120-988-297 |
| 6 | 240 | 12.5 | 450 | 3 | US-10-131-827-8330 |
| 7 | 166 | 8.7 | 3519 | 2 | US-08-286-889-45 |
| 8 | 166 | 8.7 | 3519 | 2 | US-08-485-618-45 |
| 9 | 166 | 8.7 | 3519 | 2 | US-08-362-652-45 |

| | | | | | | |
|----|-------|-----|------|---|-------------------|-------------------|
| 10 | 166 | 8.7 | 3519 | 2 | US-08-605-672-45 | Sequence 45, Appl |
| 11 | 166 | 8.7 | 3519 | 2 | US-08-482-293A-45 | Sequence 45, Appl |
| 12 | 166 | 8.7 | 3519 | 2 | US-08-943-363-45 | Sequence 45, Appl |
| 13 | 166 | 8.7 | 3519 | 3 | US-09-193-043-45 | Sequence 45, Appl |
| 14 | 166 | 8.7 | 3519 | 3 | US-09-688-307A-45 | Sequence 45, Appl |
| 15 | 166 | 8.7 | 3519 | 3 | US-09-350-259-45 | Sequence 45, Appl |
| 16 | 166 | 8.7 | 3803 | 2 | US-08-485-618-52 | Sequence 52, Appl |
| 17 | 166 | 8.7 | 3803 | 2 | US-08-362-652-52 | Sequence 52, Appl |
| 18 | 166 | 8.7 | 3803 | 2 | US-08-605-672-52 | Sequence 52, Appl |
| 19 | 166 | 8.7 | 3803 | 2 | US-08-482-293A-52 | Sequence 52, Appl |
| 20 | 166 | 8.7 | 3803 | 2 | US-08-943-363-52 | Sequence 52, Appl |
| 21 | 166 | 8.7 | 3803 | 3 | US-09-193-043-52 | Sequence 52, Appl |
| 22 | 166 | 8.7 | 3803 | 3 | US-09-688-307A-52 | Sequence 52, Appl |
| 23 | 166 | 8.7 | 3803 | 3 | US-09-350-259-52 | Sequence 52, Appl |
| 24 | 159.5 | 8.3 | 2499 | 2 | US-08-485-618-96 | Sequence 96, Appl |
| 25 | 159.5 | 8.3 | 2499 | 2 | US-08-605-672-96 | Sequence 96, Appl |
| 26 | 159.5 | 8.3 | 2499 | 2 | US-08-482-293A-96 | Sequence 96, Appl |
| 27 | 159.5 | 8.3 | 2499 | 2 | US-08-943-363-96 | Sequence 96, Appl |
| 28 | 159.5 | 8.3 | 2499 | 3 | US-09-193-043-96 | Sequence 96, Appl |
| 29 | 159.5 | 8.3 | 2499 | 3 | US-09-688-307A-96 | Sequence 96, Appl |
| 30 | 159.5 | 8.3 | 2499 | 3 | US-09-350-259-96 | Sequence 96, Appl |
| 31 | 159.5 | 8.3 | 3528 | 2 | US-08-286-889-36 | Sequence 36, Appl |
| 32 | 159.5 | 8.3 | 3528 | 2 | US-08-485-618-36 | Sequence 36, Appl |
| 33 | 159.5 | 8.3 | 3528 | 2 | US-08-362-652-36 | Sequence 36, Appl |
| 34 | 159.5 | 8.3 | 3528 | 2 | US-08-605-672-36 | Sequence 36, Appl |
| 35 | 159.5 | 8.3 | 3528 | 2 | US-08-482-293A-36 | Sequence 36, Appl |
| 36 | 159.5 | 8.3 | 3528 | 2 | US-08-943-363-36 | Sequence 36, Appl |
| 37 | 159.5 | 8.3 | 3528 | 3 | US-09-193-043-36 | Sequence 36, Appl |
| 38 | 159.5 | 8.3 | 3528 | 3 | US-09-688-307A-36 | Sequence 36, Appl |
| 39 | 159.5 | 8.3 | 3528 | 3 | US-09-350-259-36 | Sequence 36, Appl |
| 40 | 159.5 | 8.3 | 3597 | 2 | US-08-485-618-54 | Sequence 54, Appl |
| 41 | 159.5 | 8.3 | 3597 | 2 | US-08-362-652-54 | Sequence 54, Appl |
| 42 | 159.5 | 8.3 | 3597 | 2 | US-08-605-672-54 | Sequence 54, Appl |
| 43 | 159.5 | 8.3 | 3597 | 2 | US-08-482-293A-54 | Sequence 54, Appl |
| 44 | 159.5 | 8.3 | 3597 | 2 | US-08-943-363-54 | Sequence 54, Appl |
| 45 | 159.5 | 8.3 | 3597 | 3 | US-09-193-043-54 | Sequence 54, Appl |

ALIGNMENTS

RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Uian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillingshaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

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Score: 1392.00 Matches: 267
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.26% Mismatches: 0
Query Match: 72.73% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2 (1-368) x US-09-620-312D-8 (1-1609)

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Db ATGGCACACGGCGAGAGGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 368

QY 21 LeuValIleuIleCysAlaGlyGlnGlyGlyArgArgGluAspGlyGlyProAlaCysTyr 40
Db CTGGTCTCATCTGCCCGCGGCAAGGGGGACGACGAGGAGATGGGGGTCCAGCCTGTAC 428

QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db GGGGGATTGACCTGACTTCACTTATTTGGACAAATCAGAAAGTGTGTGACCACTGGAAAT 488

QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db GAAATATAATTACTTTGTGGAAAGTGGCTCAAAATTCATCAGCCCAAGTTGAAAG 548

QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db TCTTTATTTGTTTTCACACCCGAGAAACAACTTAATGAAATGACAGAAACAGAGAA 608

QY 101 GlnIleArgGlnGlyLeuGlnGluIleValIleuProGlyGlyAspThrTyrMet 120
Db CAATCGCTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACAG 668

QY 121 HisGluGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGlnuAsnArgGlnGlyTyrArg 140
Db CATGAAGATTTCAAAAGCGCCAGTACAGAGATTATTAAGAAACAGACAGGCTACAG 728

QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db ACAGCCAGCGCTCATCTTTGCTTGAATGAGAACTCCATGAAATCTCTTTTCTAT 788

QY 161 SerGluuArgGluuAsnArgSerArgAspLeuGluAlaIleValTyrCysValGlyVal 180
Db TCAGAGAGGAGGCTAATAGCTTCAGAGATCTTGGTGTGCAATTTTACTGTGTGTGTG 848

QY 181 LysAspPheAsnGlnuArgIleuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db AAAGATTTCATAGACACACAGCTGGCCGATGGCCGACAGTAAAGATCATGTGTTCC 968

QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
Db GTGAAATGACGGCTTTCAGGCTTCGCAAGGCATCATCTCAATTTTGAAGAAGTCTGC 968

QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db ATCGAAATTTCTACACACTGAACCATCCACATATGTGCAAGAGAGATTCATTCAAGTTGTC 1028

QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPheLys 260
Db GTGAGAGAAACGGCTTCCGACATGCCCGCAACGTGACAGGGTCTCTGCACTTCAAG 1088

QY 261 IleAsnAspSerValThrLeuAsnGlu 269
Db |||||||
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Db 1089 ATCAATGACTCGGTCACTCAGTAAG 1115

RESULT 2
US-10-104-047-669
/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. 6943241el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 1,88e-107 Length: 2234
Score: 962.50 Matches: 190
Percent Similarity: 69.13% Conservative: 63
Best Local Similarity: 51.91% Mismatches: 106
Query Match: 50.29% Indels: 7
DB: 3 Gaps: 3

US-09-970-076-2 (1-368) x US-10-104-047-669 (1-2234)

QY 4 AlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValLeu 23
Db GCGAGCGGCTCCCGCGCGCGAGCCCGGAGACTGGCTTCCCGCGGCTGGCGCTGG 594

QY 24 IleCysAlaGlyGlnGlyGly--ArgArgGluAspGlyGlyProAlaCysTyrGlyGly 42
Db GGTCTACGCGGCTCCCGGGGGGCTGCTGCCGCCAGACAGACCCCTGCGCAAGAGGCC 654

QY 43 PheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIleTrpAsnGluIle 62
Db |||||||

QY 655 TTTGATCTTACTTGTCTGAGCAAGTCTGGAGTGTGGCAAAATACAGATTGAAAT 714

QY 63 TyrTyrPheValGlnGlnLeuAlaHisIlePheIleSerProGlnLeuArgMetSerPhe 82
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QY 715 TATATTTCTGACAGCACTTCCGAGAGATTGTGAGCCCTGAATATGATATCTTTC 774

QY 83 IleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIle 102
Db |||||||

QY 775 ATTGTGTTTTCTTCAAGCACTATTATTATTGCACTTAATCTGAGACAGAGCAAAATC 834

QY 103 ArgGlnGlyLeuGlnGluLeuGlnIleuValIleuProGlyGlyAspThrTyrMetHisGlu 122
Db |||||||

QY 835 AGTAAAGCTTGAGAGATTAAACGTGTACTCCAGTAGAGAGACATATATCCATGAA 894

QY 123 GlyPheGluArgAlaSerGlnGlnIleTyrTyrGlnuAsnArgGlnGlyTyrArgThrAla 142
Db |||||||

QY 895 GGACTTAAAGCTAGCAATTAACAAT-----CAGAAAGCAGAGGCTTGAAGAACTCC 948

QY 143 SerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu 162
Db |||||||

QY 949 AGTATCATATTTGCTCTGACAGATGGCAAGTTGACCGCTGTCCATCATATGACAGAG 1008

QY 163 ArgGluuAlaAsnArgSerArgAspLeuGluAlaIleValTyrCysValGlyValLysAsp 182
Db |||||||

QY 1009 AAAAGGCAAGATATACAGTCACTTGGGCTAGTGTATGTGTGTGTGCTTGTAT 1068

QY 183 PheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsn 202
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QY 1069 TTTGAACAAACACAGCTTAAAGAAATGCTGATTTCCAAAGAGACAGATTTTCCCTGTCAA 1128

QY 203 AspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIleGlu 222
Db |||||||
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QY 360 ---GLUGIUSERGLUGIU 364
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RESULT 3
US-09-799-451-250
; Sequence 250, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Keena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 250
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297) .. (1118)
; US-09-799-451-250
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Alignment Scores:
Pred. No.: 2,87e-98 Length: 3981
Score: 891.00 Matches: 172
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.55% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2 (1-368) x US-09-799-451-250 (1-3981)
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DB 3 GACAGTAGAGATCATGTGTTTCCCGTAAGAGAGCGCTTACAGGCTCGCAAGCATATC 62
QY 213 HISERILEUUYLYSERYGIIIEGIIIELEUUALAGIUPROSETHRIEY 232
DB 63 CACTCAATTTTGAAGAAGCTCCTCATCGAAATCTGACAGCTGAACCATCCACCATATGT 122
QY 233 ALAGIUGIUSERPHEGINVALVALARGIYASNGIYPHEARGHISALARGASNVALL 252
DB 123 GCAGGAGAGTCATTTCAAGTTGTGAGAGAGAAAGCGCTTCGACATGCGCCGACATGTG 182
QY 253 ASPARGVALLEUCYSSERPHELYSILEASNAASERVALTHREUANGIULYSPROPH 272
DB 183 GACAGGCTCTCTGCAGCTTCAAGATCAATGACTCGGTCACTCATATGAGAACCTTT 242
QY 273 SERVALGULASPTHRYTHREUUCYSPROALAPROIIEUUYSGIUALGYMETLYS 292
DB 243 TCTGTGGAAGATCTTAATTAATGCTGTCCAGCCGCTTAATAAGAAAGTTGGCATGAAA 302
QY 293 ALALAEUGIINALSERMETASNAASPGIYUSERPHEIIESESERSEVALIIEIIE 312
DB 303 GCTGCACTCCAGGTGAGCATGAAGAGGCTCTCTTTATCTTCAGTTGTGCATATC 362
QY 313 THRTHRTHRIEYSSERASPGIYSERILEUUALIEALAEULEUILEUPHELEU 332
DB 363 ACCACCAACACACGTTCTGACGTTCCATCTGCGCATGCGCTCGTGACCTGTTCTG 422
QY 333 LEUUAIALAEUUALAEULEUTRTPPHEITRTPPOLEUCYCYSTRHVALIIEIIEYS 352
DB 423 CTCCTGACCTCGGCTCTCCTCTGTGTGTTCTGCGCTCGTCACTGATTAATCAAG 482
QY 353 GIVUALPROPROPOALAAGIUGIUSERGLUGIU 364
DB 483 GAGTCCCTCCACCCCTCGAGAGAGTGAAGAA 518

RESULT 4
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
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| TYPE: | DNA | | |
| ORGANISM: | Homo sapiens | | |
| FEATURE: | | | |
| NAME/KEY: | CDS | | |
| LOCATION: | (179) .. (1434) | | |
| US-09-774-528-297 | | | |
| Alignment Scores: | | | |
| Pred. No.: | 4,97e-95 | Length: | 1492 |
| Score: | 859.00 | Matches: | 165 |
| Percent Similarity: | 71.47% | Conservative: | 58 |
| Best Local Similarity: | 52.88% | Mismatches: | 83 |
| Query Match: | 44.88% | Indels: | 6 |
| DB: | 3 | Gaps: | 2 |
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| Db | 16 | AATACTGGATTGAATTATATATATTCGTAACGAACTTGGCGGAATTTGGACCCCT | 75 |
| QY | 77 | GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrMetLeuThr | 96 |
| Db | 76 | GAAATGAGATTATCTTTCAATGTGTCTTCTTCAAGCACTTATTTTGGCATTAACT | 135 |
| QY | 97 | GluAspArgGluGlnIleArgGlnGlyLeuGluGluLeuGlnIleValLeuProGlyGly | 116 |
| Db | 136 | GGAGACAGAGCGCAAAATCAGTAAAGGCTTGGAGGATTTAAAGCTGTATGTCAGTAGGA | 195 |
| QY | 117 | AspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArg | 136 |
| Db | 196 | GAGACATATATCATCATGACGACTAAAGCTAAAGCAAGCAAACTT-----CAGAAAGCA | 249 |
| QY | 137 | GlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp | 156 |
| Db | 250 | GGAGGCTTGAAAACCTCCACGATCATTAATTTGCTCTGACAGATGGCAAGTTGACGGCTCG | 309 |
| QY | 157 | LeuphePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr | 176 |
| Db | 310 | GTGCCATCATATGSCAGAGAAAGCGAAAGATATCCAGGCTTGGGGCTAGTGTATTAT | 369 |
| QY | 177 | CysValGlyValIleYpAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIleYpAsp | 196 |
| Db | 370 | TGTGTGGGGGCTCTTGATTTTGAACAAGCAGCAGCTTGAAGAAATTAATTTCTATATCA | 429 |
| QY | 197 | HisValPheProValAsnArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu | 216 |
| Db | 430 | CAAGTTTCCCTGTCAAGAGGTGATTCAGGCTCTTAAAGAAATTAATTTCTATATCA | 489 |
| QY | 217 | IleYpSerCysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSer | 236 |
| Db | 490 | GCTCACTCATGTAAGTAAATCCTAAGATTGSCAACCTCAAGTGTCTGTGTGGGGAGGAA | 549 |
| QY | 237 | PheGlnValValValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeu | 256 |
| Db | 550 | TTTTCAGATTGTCTTAAGTGAAGAAGGATTCATCTGGGACGTGCGAATGGCAGATGTTCTC | 609 |
| QY | 257 | CysSerPheValIleAsnArgSerValThrLeuAsnGlyIleYpProPheSerValGluAsp | 276 |
| Db | 610 | TGCACCTTAACTGTAAATGAACATATTAACAAGAGGTAAACAGTAAGTATGACGTTT | 669 |
| QY | 277 | ThrTyrLeuLeuCysProAlaProIleLeuGlyGlnValGlyMetLeuValAlaIleLeu | 296 |
| Db | 670 | AATTCATATGCTTGTCTGCACTTATCTGATATTAAGCTGGAGAACTCTTATGTTTCA | 729 |
| QY | 297 | ValSerMetAsnArgGlyLeuSerPheIleSerSerSerValIleIleThrThrHis | 316 |
| Db | 730 | GTGAGCTTTAATGAGAGAAATCTGTCATTTCAAGATCATTAATTTTTCACAGCACAGAA | 789 |
| QY | 317 | CysSerAspGlySerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeu | 336 |

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| Db | 790 | TCGTTCAACGGGATGCGACGCACCATATTGTTATTTGGTGTACTGTACTCCCGGGGATC | 849 |
| Qy | 337 | AlaLeuLeuTTPTrpPheTrpProLeuCyCySerThrValIleIleYsgluValProPro | 356 |
| Db | 850 | GGTTTGATGTGGTGGTTTGGCCCTTGGCTGCAAGTGGTATTAAAGATCCTCCACCA | 909 |
| Qy | 357 | Pro-----ProAlaGluGluSerGluGlu | 364 |
| Db | 910 | CCACCCCCCTTCGACCAAAAGAGAGAGAGAGA | 945 |
| RESULT 5 | | | |
| US-10-120-988-297 | | | |
| Sequence 297, Application US/10120988 | | | |
| Patent No. 6919193 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Tang, Y. Tom | | | |
| APPLICANT: Goodrich, Ryle | | | |
| APPLICANT: Liu, Chenghua | | | |
| APPLICANT: Ren, Peiyun | | | |
| APPLICANT: Wang, Dunrui | | | |
| APPLICANT: Drmanac, Radoje T. | | | |
| TITLE OF INVENTION: No. 6919193el Nucleic Acids and | | | |
| TITLE OF INVENTION: Polypeptides | | | |
| FILE REFERENCE: 802CON | | | |
| CURRENT APPLICATION NUMBER: US/10/120, 988 | | | |
| PRIOR APPLICATION NUMBER: 09/774,528 | | | |
| PRIOR FILING DATE: 2001-01-30 | | | |
| NUMBER OF SEQ ID NOS: 441 | | | |
| SOFTWARE: pc_FL_genes Version 2.0 | | | |
| SEQ ID NO 297 | | | |
| LENGTH: 1492 | | | |
| TYPE: DNA | | | |
| ORGANISM: Homo sapiens | | | |
| FEATURE: | | | |
| NAME/KEY: CDS | | | |
| LOCATION: (79) ..(1434) | | | |
| US-10-120-988-297 | | | |
| Alignment Scores: | | | |
| Prid. No.: 4,976-95 Length: 1492 | | | |
| Score: 859.00 Matches: 165 | | | |
| Percent Similarity: 71.47% Conservative: 58 | | | |
| Best Local Similarity: 52.88% Mismatches: 83 | | | |
| Query Match: 44.88% Indels: 6 | | | |
| DB: 3 Gaps: 2 | | | |
| US-09-970-076-2 (1-368) x US-10-120-988-297 (1-1492) | | | |
| Qy | 57 | HisHisTPAangGluIleTyrTyrPheValGluGluLeuAlaHisLysPheIleSerPro | 76 |
| Db | 16 | AATAACTGGATTGAAATTTATATATTTTCGACACCAACTTGGCGAGAGATTTGAGGCCCT | 75 |
| Qy | 77 | GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr | 96 |
| Db | 76 | GAAATGAGATTATCTTCACTTCACTTGTTCTTCTTCAAGCAACTATATTTTGGCATTAACT | 139 |
| Qy | 97 | GluAspArgGluGlnIleLeuArgGlnGlyLeuGluGlnLysValLeuProGlyGly | 116 |
| Db | 136 | GGAGACAGGCAAAATCAGTAAAGGCTTGGAGGATTTAAACGTGTAGTCCAGTACGGA | 199 |
| Qy | 117 | AspThrTyrMetHisGluGluIlePheGluArgAlaSerGluGlnIleTyrTyrGluAsnArg | 136 |
| Db | 196 | GAGACATATATTCATGAGAGACTAAAGCTACGCAATGAAACAATTT-----CAGAAAGCA | 249 |
| Qy | 137 | GlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp | 156 |
| Db | 250 | GGAGGCTTGAACACCTCCAGTATCATAAATTGGCTCTACAGATGGCAAGTTGGGACGCTCG | 306 |
| Qy | 157 | LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspSerGluValAlaIleValTyr | 176 |
| Db | 310 | GGGCCCATCATATGACAGAGAAAGGCGAAAGATATCCAGGTCACCTTGGGGCTAGCTTTAT | 366 |

[illegible][illegible]

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|------------------------|--------|---------------|----|
| Score: | 166.00 | Matches: | 66 |
| Percent Similarity: | 46.15% | Conservative: | 42 |
| Best Local Similarity: | 28.21% | Mismatches: | 96 |
| Query Match: | 8.67% | Indels: | 30 |
| DB: | 2 | Gaps: | 12 |

US-09-970-076-2 (1-368) X US-08-286-889-45 (1-3519)

[illegible]

US-08-485-618-45

Sequence ID: Application US/0005030
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA: 09/10/88 09.00

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FILING DATE: 4/25/2011

PRIOR APPLICATION DATA:

FILING DATE: 23-DEC-1993

APPLICATION NUMBER: US 08/286,889

PRIOR APPLICATION DATA: WFO 00/0000 0000
 ; APPLICATION NUMBER: WFO 00/0000 0000

FILING DATE: 21-DEC-1994

NAME: Williams Jr., Joseph A.

REFERENCE/DOCKET NUMBER: 27866/322

TELEPHONE: 312-474-6300

TELEX: 25-3856

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

TOPOLOGY: linear

FEATURE: [www.ymv.com](#)

LOCATION: 52..3519

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| Pred. No.: | 2.42e-09 | Le |
| | 165.00 | M |

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|---------------------|--------|----|
| Percent Similarity: | 46.15% | Cc |
| Percent Identity: | 38.31% | Mj |

Query Match: 8.67%
IP: 2
C3

NYC 00-070-076-2 (1-368) ~ NYC-08-485-618-A

37 **Bucuraj** **de** **la** **stare** **si** **de** **la** **moarte**

401

As a result of the above, the following is the proposed solution:

541 :::: :::::

75 SerProC]nIaVrcMotSerPhat]e

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Oy      37  ProLaaCyGyrgly----GlyPheAsrLeuTyrrPheIleLeuAspLysSerGlySerVal  55
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Db      481  CGAGAGTGTCCAGACGACAAAGATGGACATGCTTTCCTGATTTGATGGCTCCGGCAGCATT  540

Oy      56  --LeuHisHsIeTPrAsnGluIleTyrrPheValGluGlnLeuHisIleValPheIle  74
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Db      541  GATCAAAATGACTTTAACCCAGATGTAAAGAACTTCGTCMAAGCTTTGATGGCCAGTTGGCC  600

Oy      75  SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys  94
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      601  AGCAGCACACACCTGCTTCTCCTGATGTGAATACTCAAAATCCTGTAAGATCTATTTTACC  660

Oy      95  LeuThrGlnAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu  109
        |||  |||  |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
Db      661  TTCAACGGAATTCAAAGACAGCCTGAGCCTCAGAGCCTGTGGATGCATGTCGACAGCTC  720

Oy      110  GlnLysValLeuProGlnGlyAspThrTyrrMetHisGlnGlyPheGlnArgLysSerGln  129
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      721  CAA-----GGCCTGACGTAAACAGCCTCGGGCATCCAGAAAGGTGTGAA  765

Oy      130  GlnIleTyrrGlnAsnArgGlnLeuTyrrArgThrAla---SerValIleIleAlaLeu  148
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Db      766  GAGCATATTTCATGCGACAGATGGGCGCCGAAAGAAGTGCACAGAAAGATCTAAATTGTCATC  825

Oy      149  ThrArgGlyGlnLeuHisGlnLysArgLeuPhePheTyrrSerGln-----ArgGlnIleAsn  166
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FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-482-293A-45

Alignment Scores:
Pred. No.: 2,42e-09 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
Gaps: 12

US-09-970-076-2 (1-368) x US-08-482-293A-45 (1-3519)

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Qy 37 ProAlaCySTyrgly---GlyPheAapLeuTyrrPheileuAapLysserGlySerVal 55
Db 481 CCAAGAGTGTCCAGACAGAGATGACATTCCTTCCTGATTGATGCTCCGGCAGCAT 540
Qy 56 ---LeuHishTTPraAngluileTyrrTyrrPheValGluGluInleuAlahislyPheile 74
Db 541 GATCAAGTACCTTACCCAGATGAAGACATTCCTCAAGCTTGATGGCCAGTTGGCG 600
Qy 75 SerProGluLeuAargMetSerPheileValPheSerThrArgGlyThrThrLeuMetly 94
Db 601 AGCACAGCAGCACTGCTTCCTCCGATGACATCAACAATCCCGAAGACTCATTTTACC 660
Qy 95 LeuThrGluAapArg-----GluGluInleAargGluInleuGluGlu 109
Db 661 TTCACGGAAATTCAGAGCAGCCTGAGCCCTCAGAGCTGGTGATGTCATCTGCAGCTC 720
Qy 110 GlnlyValleuPProGlyAapThrTyrrMechisgluGlyPheGluAargAlaserGlu 129
Db 721 CAA-----GGCTGACGTAACACAGCTTCGGCATCCAGAAAGTGTGAAA 765
Qy 130 GlnileTyrrGluAanaArgGlnGlyTyrrArgThrAla---SerValileleAlaLeu 148
Db 766 GAGCTATTTCATGCAAGAAATGGGGCCGCAAAAAGTCCCAAGAAATCTATTCATC 825
Qy 149 ThrAapGlyLeuHishgluAapLeuPhePheTyrrSerGlu-----ArgGluAlaAan 166
Db 826 ACAGATGGGCAAAATTCAGAGACCCCTCGAGATATGACATGTCATCCCTGAAGCAGAG 885
Qy 167 ArgSerThrAapLeuGlyAlaileValTyrrCyrrValGlyVallyAap---PheAnglu 185
Db 886 AAAGCT-----GGATCATTCGCTATGCTATAGGGGGGAGATGCTTCGGGAAA 936
Qy 186 ---ThrGlnleuAlaArglyle-----AlaAapSerlyAapPheileValPhe 199
Db 937 CCCACTGCCCTACAGAGCTGAACACATTCGCTCACTCCCTCGCAGACACAGCTTTC 996
Qy 200 ProValAanaAapGlyPheGluAlaLeuGlnGlyleileHishSerileLeuAllySer 219
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGCGAGCATCCAGCGGCAAAATTCAGAGAAA--- 1050
Qy 220 CyrlleGluileuAlaAagluPProSerThrileCyrrAlaGlyGluSerPheGluVal 239
Db 1051 -----ATCTTGGCATTTGAAGAAACCAATCAAGTCAAGTACTCTTCCTTCAGCAC 1101
Qy 240 ValValAargGlyAangGlyPheAargHishAlaAargAanValAap 253
Db 1102 GAATGTCAAGAAAGTTTCACTCACTCACTCTCAATGAT 1143

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ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45
Alignment Scores:
Pred. No.: 2,42e-09 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
Gaps: 12
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Qy 56 ---LeuHishTTPraAngluileTyrrTyrrPheValGluGluInleuAlahislyPheile 74
Db 541 GATCAAGTACCTTACCCAGATGAAGACATTCCTCAAGCTTGATGGCCAGTTGGCG 600
Qy 75 SerProGluLeuAargMetSerPheileValPheSerThrArgGlyThrThrLeuMetly 94
Db 601 AGCACAGCAGCACTGCTTCCTCCGATGACATCAACAATCCCGAAGACTCATTTTACC 660
Qy 95 LeuThrGluAapArg-----GluGluInleAargGluInleuGluGlu 109
Db 661 TTCACGGAAATTCAGAGCAGCCTGAGCCCTCAGAGCTGGTGATGTCATCTGCAGCTC 720
Qy 110 GlnlyValleuPProGlyAapThrTyrrMechisgluGlyPheGluAargAlaserGlu 129
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; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

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Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2 (1-368) x US-09-688-307A-45 (1-3519)
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Qy 56 ---LeuH1st1rPaNgLuIeTyTy-rPheValGluInleuA1st1sYsPheIle 74
Db 541 GATCAAGTACCTTACCCAGATGAGACTTCGTCAAAGCTTGATGGCGCAGTTGGCG 600
Qy 75 SerProGluInleuAryMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db 601 AGCACCGACACCTGTTCTCTCCGTGATGCAATCTCAACATCTGAAAGCTCATTTTACC 660
Qy 95 LeuThGluAparG-----GluGlnIleArgGlnGlyLeuGluInleu 109
Db 661 TTCACGGAATTCAGAGACAGCCTGAGCCCTCAGAGCCTGGATGCCATCTCCACTC 720
Qy 110 GlnIleValLeuProGlyGlyAerThrTyMetH1st1sGluGlyPheGluAryA1sSerGlu 129
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Qy 130 GlnIleTyTyGluAparGlnGlyTyArgThrAla---SerValIleIleAlaLeu 148
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Qy 149 ThrAparGlyGluLeuH1st1sGluAparLeuPhePheTySerGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGCAGAAATTCAGAGACCCCTGAGATGACATGTCATCTCCGAAAGCAG 885
Qy 167 ArgSerArgAparLeuGlyAlaIleValTyTyCyValGlyValIlyApar---PheAparGlu 185
Db 886 AAAGCT-----GGATCATTCGCTATGCTATAGGGGGTGGAGATGCCCTCCGGGA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAparSerLysAparH1sValPhe 199
Db 937 CCCACTGCCCTACAGAGCTGAACACCATTTGGCTCCTCCCTGCGAGCAACAGTCTTC 996
Qy 200 ProValAparGlyPheGlnAlaLeuGlnGlyTyIleH1sSerIleLeuLysSer 219
Db 997 AAGTGGGCAAT---TTTGAACACTTCGCGACATCCAGCGCAATTCAGAGAA--- 1050
Qy 220 CyelIleGluIleLeuAlaIleValTyTyPheSerThrIleCyValAglIyAparPheGlnVal 239
Db 1051 -----ATCTTGCCATTGAGAAAGCAATCAAGCTCAAGTCAAGTCTTCCTTCAAGC 1101
Qy 240 ValValAparGlyAparGlyPheAparGlyAlaAparAparValApar 253
Db 1102 GAGATGTCACAGAAAGTTTCAAGCTCAGCTCTCTCAATGAT 1143

RESULT 15
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; Sequence 45: Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
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; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; EARLIER FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-45

Alignment Scores:
Pred. No.: 2,42e-09 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2 (1-368) x US-09-350-259-45 (1-3519)
Qy 37 ProLaCyEYrGly---GlyPheApLeuTy-rPheIleuAplySerGlySerVal 55
Db 481 CCAGAGTGTCCAGACAGAGATGACATTCCTTCTCGATGATGCTCCGCGACAT 540
Qy 56 ---LeuH1st1rPaNgLuIeTyTy-rPheValGluInleuA1st1sYsPheIle 74
Db 541 GATCAAGTACCTTACCCAGATGAGACTTCGTCAAAGCTTGATGGCGCAGTTGGCG 600
Qy 75 SerProGluInleuAryMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
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Db 721 CAA-----GGCCTGACGTACACAGCCTCGGACACAGAAAGTGCTGAA 765
Qy 130 GlnIleTyTyGluAparGlnGlyTyArgThrAla---SerValIleIleAlaLeu 148
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Qy 167 ArgSerArgAparLeuGlyAlaIleValTyTyCyValGlyValIlyApar---PheAparGlu 185
Db 886 AAAGCT-----GGATCATTCGCTATGCTATAGGGGGTGGAGATGCCCTCCGGGA 936
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Db 937 CCCACTGCCCTACAGAGCTGAACACCATTTGGCTCCTCCCTGCGAGCAACAGTCTTC 996
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Run on: December 18, 2005, 07:35:12 ; Search time 1178.98 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2

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Fgapop 6.0 , Fgapext 7.0
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1914 | 100.0 | 1454 | US-10-133-937-58 | Sequence 58, Appl1 |
| 3 | 1914 | 100.0 | 1454 | US-10-159-563-58 | Sequence 59, Appl1 |
| 4 | 1894 | 99.0 | 5540 | US-09-918-715-176 | Sequence 176, Appl1 |
| 5 | 1894 | 99.0 | 5540 | US-09-918-715-231 | Sequence 231, Appl1 |
| 6 | 1894 | 99.0 | 5540 | US-10-301-822-198 | Sequence 198, Appl1 |
| 7 | 1894 | 99.0 | 5540 | US-10-474-794-176 | Sequence 176, Appl1 |
| 8 | 1894 | 99.0 | 5540 | US-10-474-794-231 | Sequence 231, Appl1 |

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| 9 | 1894 | 99.0 | 5540 | US-10-979-159-176 | Sequence 176, App |
| 10 | 1894 | 99.0 | 5540 | US-10-979-159-231 | Sequence 231, App |
| 11 | 1894 | 99.0 | 5540 | US-11-047-278-5 | Sequence 5, Appl1 |
| 12 | 1793 | 93.7 | 5220 | US-09-918-715-186 | Sequence 186, App |
| 13 | 1793 | 93.7 | 5220 | US-09-918-715-300 | Sequence 300, App |
| 14 | 1793 | 93.7 | 5220 | US-10-474-794-186 | Sequence 186, App |
| 15 | 1793 | 93.7 | 5220 | US-10-474-794-300 | Sequence 300, App |
| 16 | 1793 | 93.7 | 5220 | US-10-979-159-186 | Sequence 186, App |
| 17 | 1793 | 93.7 | 5220 | US-10-979-159-300 | Sequence 300, App |
| 18 | 1661 | 86.8 | 1674 | US-10-038-307-17 | Sequence 17, Appl1 |
| 19 | 1661 | 86.8 | 1674 | US-10-201-292-17 | Sequence 17, Appl1 |
| 20 | 1650 | 86.2 | 1650 | US-10-038-307-13 | Sequence 13, Appl1 |
| 21 | 1650 | 86.2 | 1650 | US-10-038-307-15 | Sequence 15, Appl1 |
| 22 | 1650 | 86.2 | 1650 | US-10-201-292-13 | Sequence 13, Appl1 |
| 23 | 1650 | 86.2 | 1650 | US-10-201-292-15 | Sequence 15, Appl1 |
| 24 | 1649 | 86.2 | 1056 | US-10-038-307-23 | Sequence 23, Appl1 |
| 25 | 1649 | 86.2 | 1056 | US-10-201-292-23 | Sequence 23, Appl1 |
| 26 | 1649 | 86.2 | 1713 | US-10-038-307-19 | Sequence 19, Appl1 |
| 27 | 1649 | 86.2 | 1713 | US-10-201-292-19 | Sequence 19, Appl1 |
| 28 | 1649 | 86.2 | 2112 | US-11-047-278-7 | Sequence 7, Appl1 |
| 29 | 1649 | 86.2 | 2272 | US-09-796-753-11 | Sequence 11, Appl1 |
| 30 | 1649 | 86.2 | 2272 | US-10-038-307-1 | Sequence 1, Appl1 |
| 31 | 1649 | 86.2 | 2272 | US-10-201-292-1 | Sequence 1, Appl1 |
| 32 | 1649 | 86.2 | 2353 | US-10-198-846-9957 | Sequence 9957, App |
| 33 | 1640 | 85.7 | 1650 | US-10-038-307-9 | Sequence 9, Appl1 |
| 34 | 1640 | 85.7 | 1650 | US-10-201-292-9 | Sequence 9, Appl1 |
| 35 | 1636 | 85.5 | 1008 | US-10-038-307-25 | Sequence 25, Appl1 |
| 36 | 1636 | 85.5 | 1008 | US-10-201-292-25 | Sequence 25, Appl1 |
| 37 | 1634.5 | 85.4 | 1047 | US-10-038-307-21 | Sequence 21, Appl1 |
| 38 | 1634.5 | 85.4 | 1047 | US-10-201-292-21 | Sequence 21, Appl1 |
| 39 | 1548 | 80.9 | 1608 | US-10-062-674-1757 | Sequence 1757, App |
| 40 | 1520 | 79.4 | 2397 | US-10-038-307-11 | Sequence 11, Appl1 |
| 41 | 1509 | 78.8 | 1623 | US-10-201-292-11 | Sequence 11, Appl1 |
| 42 | 1509 | 78.8 | 1623 | US-10-038-307-11 | Sequence 11, Appl1 |
| 43 | 1423 | 74.3 | 1534 | US-10-201-292-33 | Sequence 33, Appl1 |
| 44 | 1392 | 72.7 | 1609 | US-10-037-270-8 | Sequence 8, Appl1 |
| 45 | 1392 | 72.7 | 1609 | US-10-117-722-8 | Sequence 8, Appl1 |

ALIGNMENTS

RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Antitoxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Alignment Scores:
Pred. No.: 4.87e-229
Score: 1914.00
Percent Similarity: 100.00%
Length: 1414
Matches: 368
Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-2 (1-368) x US-11-047-278-1 (1-1414)

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DB 104 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGAGGCTCTTTGGCCACT 163
QY 21 LeuValLeuIleCyValaGluGlnGlyValArgGluAspGlyGlyProAlaCysTrp 40
DB 164 CTGGGCTCATCTGCCCGGCAAGGGAGCGAGGAGAGGGGGTCCAGCTCTAC 223
QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisTrpAsn 60
DB 224 GGGGATTGACCTGACTTCACTTTGGACAAATCAGAAAGTGTCTGCACCACTGGAA 283
QY 61 GluIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 284 GAAATCTATTACTTTGTGGAAAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAA 343
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
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QY 101 GlnIleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
DB 404 CAATCCGTCAGGCGCTTAGAAGAACTCCAGAAAGTTCTCCGAGAGAGACACTTAC 463
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140
DB 464 CATGAAGATTGTAAGGGCCAGTAGAGACAGATTATTATGAAACAGACAAAGGTACAG 523
QY 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTrp 160
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DB 884 ATCAATGACTCGGTGCACATCAATGAAAGCCCTTTCTGTGGAAGCACTTTTAACTG 943
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QY 321 SerIleLeuAlaIleIleAlaLeuLeuIleLeuPheLeuLeuLeuAlaLeuLeuTrp 340
DB 1064 TCCATCTGTGCAATCGCCCTGATGATCTGTCTGTCTGAGCCCTGCTCTCTCTG 1123

QY 341 TrpPheTrpProLeuCysCysThrValIleIleLysGluValaProProProAlaGlu 360
DB 1124 TGCTTGGCCCCCTCGCTGACATGTGATTATCAAGAGAGTCCCTCCACCCCTGCCAG 1183
QY 361 GluSerGluGluAsnLysIleLys 368
DB 1184 GAGAGTAGAGAAATTAATAA 1207

RESULT 2

US-10-133-937-58
/ Sequence 58, Application US/10133937
/ Publication No. US20030207278A1
/ GENERAL INFORMATION:
/ APPLICANT: Khan, Javed
/ APPLICANT: Ringner, Markus
/ APPLICANT: Peterson, Carsten
/ APPLICANT: Metzger, Paul
/ TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
/ TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
/ FILE REFERENCE: 11613.56US01
/ CURRENT APPLICATION NUMBER: US/10/133, 937
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 58
/ LENGTH: 1454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:

Pred. No.: 5,1e-229 Length: 1454
Score: 1914.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2 (1-368) x US-10-133-937-58 (1-1454)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGAGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCysValaGluGlnGlyValArgGluAspGlyGlyProAlaCysTrp 40
DB 204 CTGGGCTCATCTGCCCGGCAAGGGAGCGAGGAGAGGGGGTCCAGCTCTAC 263
QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisTrpAsn 60
DB 264 GGGGATTGACCTGACTTCACTTTGGACAAATCAGAAAGTGTCTGCACCACTGGAA 323
QY 61 GluIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 324 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAA 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCTTTATTGTTTCTCCACCCGAGGAAACCTTAATGAATGACAGAAACAGAGAA 443
QY 101 GlnIleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
DB 444 CAATCCGTCAGGCGCTTAGAAGAACTCCAGAAAGTTCTCCGAGAGAGACACTTAC 503
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140
DB 504 CATGAAGATTGTAAGGGCCAGTAGAGACAGATTATTATGAAACAGACAAAGGTACAG 563
QY 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTrp 160
DB 564 ACAGCCAGCGTCATCTGCTTGCATGATGAGAACTCCATGAAGATCTTTTCTAT 623

QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyValAlaIleValTyrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTTAATAGATCTCGAGATCTTGTCATATGTTTACTGTGTGGTGTG 663
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgAlaAspSerLysAspHisValPhePro 200
DB 684 AAGATTTCATATAGACACAGCTGGCCGGATTGGGACAGTAAGATCATATGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValLysSerCys 220
DB 744 GTCAATGACCGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAGTCTGCG 803
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
DB 804 ATCGAATTCATAGAGCTGAAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTGTG 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCGACATCGCCGCAAGCTGACAGGCTCTCTGACGTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACCTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAAGACACTTATTTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCACGCGCTTATTAAGAAGATGGTCATGAAGACTGCTCCAGGTCACATGAAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTTTATCTCAGATTCTGTATCATCCACACACACTTTCTGACGCT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTyr 340
DB 1104 TCCATCTGGCCATCGCCCTGCTGATCTCTGCTCTGCTCTGCTCTGCTCTGCTG 1163
QY 341 ThrPheThrProLeuCysCysThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCTGATTAATCAAGAGGATCCCTCCACCCCTGCGGAG 1223
QY 361 GluSerGluGluAsnLysIleLys 368
DB 1224 GAGAGTGAGGAAATTAATTAATA 1247

RESULT 3
US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US2004009154A1
GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
FILE REFERENCE: 11613.56US11
CURRENT APPLICATION NUMBER: US/10/159,563
PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:
Pred. No.: 5,1e-229 Length: 1454
Score: 1914.00 Matches: 368
Percent Similarity: 100.004 Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-970-076-2 (1-368) x US-10-159-563-58 (1-1454)
QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnThrPheLeuSerLeuAlaThr 20
DB 144 ATGGCCACGGCGGAGGAGGAGGAGCCCTCGGATGCGCTTCCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCysAlaGlyGlnGlyIleArgArgGluAspGlyGlyProAlaCysTyr 40
DB 204 CTGGTCTCATCTGCGCCCGGCAAGGGGAGCGCAGGAGGAGTGGGGTCCAGCTGCTAC 263
QY 41 GlyGlyPheAspLeuThrPheIleLeuAspLysSerGlySerAlaLeuHisIleSTPAsn 60
DB 264 GGGGATTGACCTGTAATTCATTGACAAATTCAGGAAGTGTGCTGACCCACTGAAT 323
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 324 GAAATCTATTACTTTGTGAAACGTTGCTCACAATTCATCAGCCCAAGTTGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCTTATTATTGTTTCTCCACCGAGGAAACAACCTTAATGAACTGACAGAAACAGAGAA 443
QY 101 GlnIleArgGlnGlyLeuGluGlnLysValLeuProGlyGlyAspThrTyrMet 120
DB 444 CAATCCGTCACAGCCCTAGAAACATCCAGAAAGTCTGCGAGAGAGACACTTACATG 503
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
DB 504 CATGAAGATTGAAGAGGCGCATGAGCAGATTTATTAAGAAACAGACAGGATACAGG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr 160
DB 564 ACAGCCAGGCTCATCATTTGCTTGAATGAGAACTCATGAAAGATCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyValAlaIleValTyrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGGGCAATGTTTAACTGTGTGTGGTGTG 663
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAGATTTCATATAGACACAGCTGGCCGGATTGGGACAGTAAGATCATATGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
DB 744 GTCAATGACCGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAGTCTGCG 803
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
DB 804 ATCGAATTCATAGAGCTGAAACCATCCACATATGTGACAGAGTCAATTTCAAGTGTG 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCGACATCGCCGCAAGCTGACAGGCTCTCTGACGTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACCTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAAGACACTTATTTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCACGCGCTTATTAAGAAGATGGTCATGAAGACTGCTCCAGGTCACATGAAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTTTATCTCAGATTCTGTATCATCCACACACACTTTTCTGACGCT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTyr 340
DB 1104 TCCATCTGGCCATCGCCCTGCTGATCTCTGCTCTGCTCTGCTCTGCTCTGCTGCTG 1163

QY 341 TrpPheTrpProLeuCySerThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTCACAGAGAGTCCCTCCACCCCTGCGAG 1223
QY 361 GluSerGluGluAsnIleIleIle 368
DB 1224 GAGAGTGAGGAAATGAAATGAAA 1247
RESULT 4
US-09-918-715-176
; Sequence 176, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-176
Alignment Scores:
Pred. No.: 1,486-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-2 (1-368) x US-09-918-715-176 (1-5540)
QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCACGGCGGAGGAGAGGCCCTCGCATCGCTTCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValIleuIleCyAlaGlnGlnGlyArgArgGluAspGlyGlyProAlaCybTyx 40
DB 204 CTGGTCTCATCTGCGCCCGGCAAGGGGAGCGCAGGAGGATGGGGGTCCAGCTCTGAC 263
QY 41 GlyIlePheAspLeuTyrrPheIleLeuAspLeuSerGlySerValLeuHisIleTPAa 60
DB 264 GGGGGAATTTGACCTGATCTCATTTTGGCAAAATCGAAGTGTGCTGCACCACTGGAA 323
QY 61 GlnIleTyrrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
DB 324 GAATCTATTAATCTTTGGAAACAGTTGGCTCACAAATTCACAGCCCACTTGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLeuSerGluAspArgGlu 100
DB 384 TCTTTATTTGTTTCTCCACCGAGAAACAACCTTAATGAAATGACAGAAAGACAGAA 443
QY 101 GlnIleArgGlnIleLeuGlnGlnLeuGlnLeuValLeuProGlyGlyAspThrTyxMet 120
DB 444 CAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATG 503
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrrTyrrGluAsnArgGlnGlyTyxArg 140
DB 504 CATGAAGGATTTGAAAGGCGCAGATGAGCAGATTTATATGAAACAGACAAAGGCTACGG 563

QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyx 160
DB 564 ACAGCCAGGCGTCATGATGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGluAlaIleValTyrrCybValGlyVal 180
DB 624 TCAGAGAGGAGGCTTAATGATGCTTCGAGATCTTGCAATGTTTACTGTGTGGTGG 683
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAGATTTCAATGAGACACAGCTGGCCCGGATTTGGGACAGTAAAGATCATGTGTTTCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleLysSerCy 220
DB 744 GTGAATGACGCGCTTCAGGCTCTGCAGAGCATCATCTCAATTTTGAAGAGTCTTCG 803
QY 221 IleGluIleLeuAlaGluProSerThrIleCybAlaGlyGluSerPheGlnVal 240
DB 804 ATCGAAATTTGACAGCTGACCATTCACCATATGTGCAGAGAGTCATTTCAAGTTGTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGGAAACGCTTCGACATGCCCGCAACGTGACAGGGTCTCTGCAGCTTCAAG 923
QY 261 IleAsnAspSerValThrIleuAsnGluLysProPheSerValGluAspThrTyrrLeu 280
DB 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGATCTTATTTACTG 983
QY 281 CybProAlaProIleLeuLysGluValGlyMetLysAlaIleLeuGlnValSerMetAsn 300
DB 984 TGTCCAGCGCTATCTTAAAGAGTGGCATGAAAGCTGCACCTCCAGGTCCAGCATGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
DB 1044 GATGGCTCTCTTTATCTCCAGTTCTGTCATCATCACCAACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleuPheLeuLeuAlaLeuAlaLeuTrp 340
DB 1104 TCCATCTGTCGATGCGCCCTGCTGATCCGTTCCTGCTCTGCTGCTCTCTCTG 1163
QY 341 TrpPheTrpProLeuCySerThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTCACAGAGAGTCCCTCCACCCCTGCGAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235
RESULT 5
US-09-918-715-231
; Sequence 231, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-231

Alignment Scores:

Pred. No.: 1,48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2 (1-368) x US-09-918-715-231 (1-5540)

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QY 1 MetAlaThraGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
DB 144 ATGGCCACGGCGGAGGAGGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 203

QY 21 LeuValLeuIleCybaIaGlyIngIyGlyArgGluAspGlyGlyProAlaCyArg 40
DB 204 CTGGTCTCATCTGCGCGGCGGAGGAGGAGCGCAGGAGGATGGGGGTCCAGCTCTAC 263

QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLeuSerGlySerValLeuHisIleTrpAsn 60
DB 264 GGGGATTGACCTGATCTTCACTTTGGACAAATCAGAAATGCTGTGCACACCTGAAAT 323

QY 61 GluIleTyTrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
DB 324 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAAT 383

QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIleLeuThrGluAspArgGlu 100
DB 384 TCTTATTATTGTTTCTCCACCGAGGAAACCTTAAATGAACTGACAGAAAGACAGAA 443

QY 101 GlnIleArgGlnIleLeuGluLeuGlnIleValLeuProGlyGlyAspTrpMet 120
DB 444 CAATCGCTCAGAGCCCTAGAAAGACTCCAGAAAGTCTCGCAGAGAGACACTTACAT 503

QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyTrGluAsnArgGlnIyTyArg 140
DB 504 CATGAAAGATTGAAAGGCGGCAAGTGAATTTATTTAATAAAGACAGAGGTTACAG 563

QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTrp 160
DB 564 ACAGCCAGCGCTCATCTGCTTGAAGTGAAGAACTCATGAAGATCTCTTTCTAT 623

QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyArgValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATTTTAACTGTGTGTGAGTG 683

QY 181 LysAspPheAsnGluTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAGGATTTCAATAGACACAGCTGGCCGGAATGGGACAGTAAAGATCATGTGTTCCC 743

QY 201 ValAsnAspGlyPheGlnAlaLeuGlnIyIleIleHisSerIleLeuIyLysSerCy 220
DB 744 GTGAAATGACGGCTTTGAGGCTTCGCAAGGATCATTCACATTTTGAAGAGTCCG 803

QY 221 IleGluIleLeuAlaIleGluProSerThrIleCybaIaGlyGluSerPheGlnVal 240
DB 804 ATGAAATCTTACAGCTGAAACATCCATATGTGACAGAGATCATTTCAAGTTGTC 863

QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCCGACATGCCGCAAGCTGACAGGCTCTCTGACCTTCAAG 923

QY 261 IleAsnAspSerValThrLeuAsnGluLysAspPheSerValGluAspTrpTyLeuLeu 280
DB 924 ATCAATGACTCGGTGCACACTCAATGAGAACCCCTTTCTGTGGAAGTACTTTATTA 983

QY 281 CysProAlaProIleLeuLysGluValGlyMetIleAlaIleGlnIleValSerMetAsn 300
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCTCCAGGTCACATGAA 1043

QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
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DB 1044 GATGCGCTCTTTTATCTCCAGTTCTGATCATCATCACACACACTGTTTCAGCGT 1103

QY 321 SerIleLeuAlaIleAlaIleLeuIleLeuPheLeuLeuAlaIleLeuTrp 340
DB 1104 TCCATCTCGGCATGCGCCCTGCTGATCCCTGCTCTGCTGCTGCTGCTCTGCTG 1163

QY 341 TrpPheTrpProLeuCybaSerThrValIleIleGlyGluValProProProAlaGlu 360
DB 1164 TGGTTTGACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223

QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAAGAA 1235
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RESULT 6

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US-10-301-822-198
; Sequence 198, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-0292PRM
; CURRENT APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144) ... (1838)
US-10-301-822-198
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Alignment Scores:

Pred. No.: 1,48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2 (1-368) x US-10-301-822-198 (1-5540)

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QY 1 MetAlaThraGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
DB 144 ATGGCCACGGCGGAGGAGGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 203

QY 21 LeuValLeuIleCybaIaGlyIngIyGlyArgGluAspGlyGlyProAlaCyArg 40
DB 204 CTGGTCTCATCTGCGCGGCGGAGGAGGAGCGCAGGAGGATGGGGGTCCAGCTCTAC 263

QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLeuSerGlySerValLeuHisIleTrpAsn 60
DB 264 GGGGATTGACCTGATCTTCACTTTGGACAAATCAGAAATGCTGTGCACACCTGAAAT 323

QY 61 GluIleTyTrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
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DB 324 GAAATCTATTACTTTGTGGAACAGTGGCTCAAAATTCATCAGCCACAGTTGAGAAAG 383
QY SerPheIleValPheSerThrArgGlyThrThrLeuMetLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTGTTTCTCCACCCGAGGAAACACTTAATGAAATGACAGAGACAGAGAA 443
QY GlnIleArgGlnGlyLeuGlnGluLeuGlnLeuValLeuProGlyGlyAspThrTyrmec 120
DB 444 CAATTCGTCAGAGCCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACAG 503
QY 121 HsGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrrTyrrGluAsnArgGlnGlyTyraG 140
DB 504 CATGAAGGATTGAAAGGCGCAGTGCAGATTTATTATGAAACAGACAGAGGTCACAG 563
QY 141 ThrAlaSerValIleIleIleAlaLeuThrPheArgGlyLeuLeuHsGlnuAspLeuPhePheTy 160
DB 564 ACAGCCAGGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGCGCAATGTTTACTGTGTGTGTGTC 683
QY 181 LysAspPheAsnGlnuThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAAGATTTCAATGAGACACAGCTGGCCGGATGGCGAGACGTAAAGATCATGTGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsSerIleLeuLysLysSerCys 220
DB 744 GTGAATGACGGCTTTCAGGCTCTGCAGAGCATCATCTCAATTTTGAAGAGTCTGCG 803
QY 221 IleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGlnuSerPheGlnVal 240
DB 804 ATCGAATTTCTACACCTGAAACCATCCATCATGTGTCAGAGAGATTCATTCAAGTTGTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTGAGAGGAAACCGCTTCCACATGCGCCGCAACGTGCAGAGGCTCTGCACTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGlnuLysProPheSerValGluAspThrTyrrLeuLeu 280
DB 924 ATCAATGACTCGGCTCACTCAATGAGAAACCTTTTCTGTGGAAGATCTTATTACAG 983
QY 281 CysProAlaProIleLeuLysGlnuValGlyMetLysAlaIleGlnuValSerMetAsn 300
DB 984 TGTCACGCGCTTCTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGGTCACAGAGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCCTCTCTTTTATCTCCAGTTCGTATCATCATCACACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleIleAlaLeuLeuIleLeuPheLeuLeuLeuAlaLeuLeuTyr 340
DB 1104 TCCATCTGCGCATCGCGCTGCTGATCTGTCTCTCTGCTTACCTGAGCTTCTCTGCG 1163
QY 341 TrpPheTrpProLeuCysCysThrValIleIleIleLysGlnuValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCACTGTGATTAATCAAGAGGTCCCTCCACCCCTGCGAG 1223
QY 361 GluSerGlnuGlu 364
DB 1224 GAGAGTGAGGAA 1235
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RESULT 7
US-10-474-794-176
; Sequence 176, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
```

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; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-176
```

```
Alignment Scores:
Pred. No.: 1,48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 8 Gaps: 0
```

US-09-970-076-2 (1-368) x US-10-474-794-176 (1-5540)

```
QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCAGCGCGGAGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCysAlaGlyGlnGlyValArgGlnuAspGlyGlyProAlaCysTyrr 40
DB 204 CTGGGCTCATGTGGCGCGGCAAGGGGACGACAGGAGAGATGGGGGTCACGCTGCTAC 263
QY 41 GlyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
DB 264 GCGGATTTGACCTGACTTCTTCAATTTTGACAAATCAGAAAGTGTGTCACCACTGGAAT 323
QY 61 GlnIleTyrrPheValGlnuLeuAlaHisLysPheIleSerProGlnuLeuArgMet 80
DB 324 GAAATCTATTACTTTGTGGAACAGTTGCTCAAAATTCATCAGCCACAGTTGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTGTTTCTCCACCCGAGGAAACCTTAATGAAACAGACAGAGGTCACAG 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLeuValLeuProGlyGlyAspThrTyrmec 120
DB 444 CAATTCGTCAGAGCCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACAG 503
QY 121 HsGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrrTyrrGluAsnArgGlnGlyTyraG 140
DB 504 CATGAAGGATTGAAAGGCGCAGTGCAGATTTATTATGAAACAGACAGAGGTCACAG 563
QY 141 ThrAlaSerValIleIleIleAlaLeuThrPheArgGlyLeuLeuHsGlnuAspLeuPhePheTy 160
DB 564 ACAGCCAGGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGCGCAATGTTTACTGTGTGTGTGTC 683
QY 181 LysAspPheAsnGlnuThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAAGATTTCAATGAGACACAGCTGGCCGGATGGCGAGACGTAAAGATCATGTGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsSerIleLeuLysLysSerCys 220
DB 744 GTGAATGACGGCTTTCAGGCTCTGCAGAGCATCATCTCAATTTTGAAGAGTCTGCG 803
QY 221 IleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGlnuSerPheGlnVal 240
DB 804 ATCGAATTTCTACACCTGAAACCATCCATCATGTGTCAGAGAGATTCATTCAAGTTGTC 863
```


QY 241 ValArgGlyAenGlyPheArgHLeAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGAAACGGCTTCCGACATGCCGCACTGACAGGCTCTGCACTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAenGlyLysProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCACTCAATGAGAGCCCTTTCTGTGGAAGATCTATTACTG 983
QY 281 CyProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCCACGGCTTACTTAAAGAGTTGGATGAAAGCTGACCTCCAGGTGAGTGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
DB 1044 GATGGCTCTCTTTTACTTCAAGTTCTGTATCTATCCACACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLys 340
DB 1104 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTGCTGAGCCCTGCTCTG 1163
QY 341 TrpPheTrpProLeuCySerThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235

RESULT 8

US-10-474-794-231
; Sequence 231, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carlson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107,00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-474-794-231

Alignment Scores:

Prod. No.: 1,48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 8 Gaps: 0

US-09-970-076-2 (1-368) x US-10-474-794-231 (1-5540)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCACGGCGGAGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 203
QY 21 LeuValLeuIleCysValIleGlyGlnGlyValArgArgGluAspGlyGlyProAlaCysTyr 40
DB 204 CTGGTGTCTCATCTGCGCGGCGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 263
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60

DB 264 GCGGATTTGACCTGACTTTCATTTTGGACAAATTCAGAAAGTGTGTCACCACTGGAAAT 323
QY 61 GlnIleTyrThrPheValGluGlnLeuAlaHisIleLysPheIleSerProGlnLeuArgMet 80
DB 324 GAATCTATTACTTGTGTGGAACGTTGCTCAAAATTCATCTGACCCAGGTGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTGTTTCTTCCACCCGAGAACACTTAAATGAACTGACAGAAAGCAGAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
DB 444 CAATCCGTCAAGGCTTAAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
QY 121 HisGlnGlyPheGlnArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
DB 504 CATGAAGGATTTAAAGGGCCAGTGAAGCATTTATTATTAAGAAACAGAAAGGTTACAG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGluAspLeuPhePheTyr 160
DB 564 ACAGCCAGGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAGATCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGTGCAATGTTACTGTGTGTGTG 683
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValIlePro 200
DB 684 AAAGATTTCAATGACACAGCTGCGCCGAGATGCGAGACGTGAAGATCATGTGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
DB 744 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATATCATCTCAATTTTGAAGAGTCTGC 803
QY 221 IleGlnIleLeuAlaIleAlaProSerThrIleCysAlaGlyGluSerPheGlnVal 240
DB 804 ATCGAATCTTACACACTGAAACCATCCACATATGTGCGAGAGATCATTTCAAGTTGTC 863
QY 241 ValArgGlyAenGlyPheArgHLeAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGAAACGGCTTCCGACATGCCGCACTGACAGGCTCTGCACTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAenGlyLysProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCACTCAATGAGAGCCCTTTCTGTGGAAGATCTATTACTG 983
QY 281 CyProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCCACGGCTTACTTAAAGAGTTGGATGAAAGCTGACCTCCAGGTGAGTGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
DB 1044 GATGGCTCTCTTTTACTTCAAGTTCTGTATCTATCCACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLys 340
DB 1104 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTGCTGAGCCCTGCTCTG 1163
QY 341 TrpPheTrpProLeuCySerThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235

RESULT 9

US-10-979-159-176
; Sequence 176, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein

APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-979-159-176

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1,48e-225 | Length: | 5540 |
| Score: | 1894.00 | Matches: | 364 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 98.96% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-970-076-2 (1-368) x US-10-979-159-176 (1-5540)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGCCACGGCGGAGGCGGAGGCGCTCGGCATCGGCTCCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCySaIaGlyGlnGlyArgArgGluAspGlyGlyProAlaCyArg 40
DB 204 CTGGCTCATCTGCGCGCGGCAAGGGGAGCGAGGAGGATGGGGTCCAGCCTCTAC 263
QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLeuSerGlySerValLeuHisIleTrpPan 60
DB 264 GGGGAGATTGACCTGATCTTCACTTTGGACAAATCAGAAAGTGTGCTGCACCACTGAAAT 323
QY 61 GluIleTyTrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuAspGly 80
DB 324 GAATCTATTAATCTTGTGGAAAGCTTGGCTCACAATTCATCAGCCCAAGTTGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIleLeuThrGluAspArgGlu 100
DB 384 TCCTTAATGTTTCTCCACCGAGGAACTTAATGAACCTGAACCTGACAGAAACAGAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnValLeuProGlyGlyAspTrpMet 120
DB 444 CAATCCGCTCAAGCCCTGAGAAAGCTCCAGAAAGTCTGCGAGAGAGACACTTCATG 503
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyTrGluLeuArgGlnGlyArg 140
DB 504 CATGAAGATTTGAAAGGCGCAGTGAAGATTTATTAATAAACAAGACAGGCTACAG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 160
DB 564 ACAGCCAGCGCTCATCATCTTGTGATGATGAGAACTCATGAAGATCTCTTTCTAT 623
QY 161 SerGluArgGluAlaAspArgSerArgAspLeuGlyValAlaIleValTyCySaValGlyVal 180
DB 624 TCAGAGAGGAGGCTTAATAGCTCTCGAATCTTGCAATTTTAACTGTGTGGGTG 663
QY 181 LysAspPheAsnGluTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAAGATTTCAATGAGACACAGCTGGCCCGATTCGGACAGTAAGATCATGTGTTCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCy 220

DB 744 GTGAATGACGGCTTTCAGGCTCTGCAGGACATCATCAATTTTGAAGAAGTCTGCC 803
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCySaIaGlyGluSerPheGlnValVal 240
DB 804 ATCGAATTTCTGACGCTGAAACCATCCACATATGTGACGAGAGATTTCAAGTGTG 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGGAAAGCGCTTCGACATGCCGCAACGTGACAGGGTCTCTGACGTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyTrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCATATAGAAAGCCCTTTCTGTGAAAGATTAATTAATG 983
QY 281 CyProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCCAGCGCTTATCTTAATAAAGATTGGCATGAAGCTGCATCCAGGTCAAGATGAA 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
DB 1044 GATGGCTCTCTTTATCTCCAGTTCTGTCATCATCACACACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
DB 1104 TCCATCTGGCCATGCGCTCGTGAATCCGTGTCTGCTCTGAGCCCTGCTCTCTG 1163
QY 341 TrpPheTrpProLeuCySerThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTAACAAGAGTCCCTCCACCCCTGCCGAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235

RESULT 10

US-10-979-159-231

Sequence 231, Application US/10979159

Publication No. US20050142138A1

GENERAL INFORMATION:

APPLICANT: Brad St. Croix

APPLICANT: Bert Vogelstein

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: US/10/979,159

CURRENT FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US/09/918,715

PRIOR FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/222,599

PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR FILING DATE: 2000-04-11

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 231

LENGTH: 5540

TYPE: DNA

ORGANISM: Homo sapiens

US-10-979-159-231

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1,48e-225 | Length: | 5540 |
| Score: | 1894.00 | Matches: | 364 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 98.96% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-970-076-2 (1-368) x US-10-979-159-231 (1-5540)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20


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|||||
Db      624 TCAGAGAGGAGGCTAATAGAGTCTCGAGATCTGGGCAATGTTACTGTGTGTG 683
      181 LVAAAPPhaenGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPhePro 200
      684 AAAGATTTCAATGACACACAGCTGGCCGGATTGGGACAGTAAGATCATGTGTTCC 743
      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleuSerCys 220
      744 GTGAAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCATTTTGAAGAAGTCTTC 803
      221 IleguIleleuAlaIleagluProSerThrIleCysAlaGlyIleuSerPheGlnVal 240
      804 ATGGAATTTCTAGCAGCTGAAACCATCCATCATGTGCAAGAGATCATTTCAAGTTGTC 863
      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPhe 260
      864 GTGAGAGGAAACGGCTTCCACATGCCCGCACGTGACAGGGTCTCTGCAGCTTCAG 923
      261 ILeaAsnAspSerValThrLeuAsnGluIleuProPheSerValGluAspThrTyrlLeu 280
      924 ATCAATGATCTGGTTCACATCATGAGAACCTTTTCTGTGAAAGTACTTATTTACTG 983
      281 CysProAlaProIleuIleuIleuGlyValGlyMetIleValAlaLeuGlnValSerMet 300
      984 TGTCAGCGCTTATCTTAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 1043
      301 AsnGlyIleuSerPheIleSerSerSerValIleIleIleThrThrHisCysSerAsp 320
      1044 GATGGGCTCTCTTTATCTTCACAGTTCTGTCATCATCACCCACACAGCTGTTCAGCG 1103
      321 SerIleleuAlaIleAlaLeuIleuIleuPheLeuLeuAlaLeuAlaLeuTrp 340
      1104 TCATCTGGCCATTCGCCCTCGCTGATCTCTGCTCTGCTTACCTGCTCTCTCTG 1163
      341 TrpPheTrpProLeuCysCysThrValIleIleIleGlyValProProProAlaGlu 360
      Db      1164 TGGTTCTGGCCCTCTGCTGCTGCACTGATATATCAAGAGGTCCTCCACCCCTGCCG 1223
      361 GluSerGluGlu 364
      1224 GAGAGTGAGGAA 1235
      Db

RESULT 12
US-09-918-715-186
; Sequence 186, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Bred St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 186
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-918-715-186

Alignment Scores:
Pred. No.: 6,5e-213 Length: 5220
Score: 1793.00 Matches: 342
Percent Similarity: 97.75% Conservative: 6

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Best Local Similarity: 96.07% Mismatches: 8
Query Match: 93.68% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2 (1-368) x US-09-918-715-186 (1-5220)

      9 IleguIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValIleCysAlaGlyGln 28
      292 CTGGGTGGGGGCTCGGGGACTGTGCGGTGCACTGCTGCTGCTGCGCCCGGACAC 351
      29 GlyIleArgArgGluAspGlyGlyProAlaCysTyrlGlyGlyPheAspLeuTyrlPhe 48
      352 GGGGGCCGGGAGAGATGGGGACAGCTTCTACGGAGATTCAGCTTCACTTCATC 411
      49 LeuAspIleSerGlySerValLeuHisIleSerPheAsnGluIleTyrlTyrlPheVal 68
      412 CTGGACAACTCAGAAAGTGTCTGCACCACTGGAATGAATTACTTCTTCTGAGCAG 471
      69 ILeuAlaIleValPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 88
      472 TTGGCTCATAGATTTCATCAGCCACAGCTAAGATGTCCTTCAATGTCCTTCTACTCGA 531
      89 GlyThrThrLeuMetIleLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGluGlu 108
      532 GGGACAACTTATATGAATTAATTAATGAGACAGGAAACAATCCGACAAAGCTTGAAGAG 591
      109 LeuGlnIleValIleuProGlyIleAspThrTyrlMetHisGlyGlyPheGluArgAlaSer 128
      592 CTCGAAAGATTCCTGCCAGAGAGACACTTTCATGACAGAAAGATTCAGAGGGCCAGT 651
      129 GluGlnIleTyrlTyrlGluAsnArgGlnGlyTyrlArgThrAlaSerValIleIleAlaLeu 148
      652 GAGCAGATTTATTAATGAGAAACAGTCAAGGATCAGGACGGGCAAGCTCATCCGCTGG 711
      149 ThrAspGlyGluLeuHisGluIleuAspLeuPhePheTyrlSerGluArgGluAlaAsnArg 168
      712 ACGGATGGGAGACTGACAGAGACCTCTTCTTACTACAGAGGGAGGCTTAACCAATCC 771
      169 ArgAspLeuGlyAlaIleValTyrlCysValGlyValIleAspPheAsnGluThrGlnLeu 188
      772 CGAGACCTTGGTGGCATTTGTTTACCTGCTGGCGTGAAGATTTCAATGAATCACTGATT 831
      189 AlaArgIleAlaAspSerIleAspHisValPheProValAsnAspGlyPheGlnAlaLeu 208
      832 GCTCGGATTCAGACAGTAAGACCAAGTGTTCCTGTAACAGACGGCTTCCAGGCTCTC 891
      209 GlnGlyIleIleHisSerIleLeuIleuIleuSerCysIleGluIleleuAlaIleuPro 228
      892 CAAGCATTTATCCACTCAATTTTAAAGAAATCTGCATGAATTTGCGGCTGAACCA 951
      229 SerThrIleCysAlaGlyIleuSerPheGlnValIleValArgGlyAsnGlyPheArgHis 248
      952 TCACCATTTGGCGGGAGAGTCTTTCAAGTGTGCTGAAGAGAAATGGCTTCCAGACAT 1011
      249 AlaArgAsnValAspArgValIleuCysSerPheIleAsnAspSerValThrLeuAsn 268
      1012 GCCCGAATGTGACAGGGTCTCTGCACTTCAAAATCAATGATCACTGACGCTCAAT 1071
      269 GluIleProPheSerValGluAspThrTyrlLeuLeuCysProAlaProIleLeuIleu 288
      1072 GAGAAACCTTGTCTGTGAAGACATTTATTTGCTGTGCCAGACCAATCTTGAAGAA 1131
      289 ValGlyMetIleValAlaLeuGlnValIleSerMetAsnAspGlyIleuSerPheIleSer 308
      1132 GTTGGCATTAAGCTGCACTGCAAGTCAAGTCAAGAGAGGCTGCTCTTCACTCCAGT 1191
      309 SerValIleIleThrThrHisCysSerAspGlySerIleleuAlaIleAlaLeu 328
      1192 TGTGTCATCATCACCAACACACATGTCAGAGGCTCATCTGCGATGCTGCTGCTG 1251
      329 IleuPheLeuLeuLeuAlaLeuAlaLeuLeuTrpThrPheTrpProLeuCysCysThr 348
      1252 GTCTCTTCTGCTGCTGCGCCCTGGGCTGCTGTGTGTCTGCGCCCTCTGCTGACA 1311
      Db

```


US-09-970-076-2 (1-368) x US-10-474-794-186 (1-5220)

```
QY      9 LeuGLIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValIleuIleCysAlaGlyGln 28
Db      292 CTGGGTCGGGGCTTGGGGGACTCTGCGTGGCTGCATCTGCTGCTGCTGCGCGGACAC 351
QY      29 GtYgLYARgARgGLuARgLYgLYProAlaCYeTYrGLyGLyPheARpLeuTYrPheIle 48
Db      352 GGGGGCGCGCGAGAGATGGGGGACCGAGCTTGTACGAGAGATTGACCTTACTTCATC 411
QY      49 LeuARpLYSeSeGLySeValIleuH1sH1sTPAsngLUleTYrTYrPheValIGluGln 68
Db      412 CTGGACAAGTCAGAGAAGTGTGCTGCACCTAGAAAGAAATCTACTACTTCGAGGACG 471
QY      69 LeuAlaH1sLYsPheIleSeSeProGlnLeuARgMeSeSePheIleValPheSeThrArg 88
Db      472 TTGGCTCATAGATTCTACGCCACAGCTTAGAGATGCTCTTCTTCTTCTTCTTCTTCA 531
QY      89 GtYrThrThLeuMeLysLeuThrgLUAsPARgGLuGlnIleARgGlnLYLeuGlnGln 108
Db      532 GGGACAACCTTATTAAGAACTTAAGAGACAGGAAAGATCCGACAGGCGCTTAAGAG 591
QY      109 LeuGlnLYsValLeuProGLyGLyARpThrTYrMeTh1sGLyGLyPheGluATgAlaSer 128
Db      592 CTCACAAAGATTCTGCAGAGAGAGACCTTACTCATGACAAAGATTCGAGGCGCAGT 651
QY      129 GlnGlnIleTYrTYrGLuARgARgGLyTYrARgThrAlaSerValIleIleAlaLeu 148
Db      652 GACCAAGATTACTATAGAACAGTCAAGATACAGAGCGGCGCTCATCTCGCGTTG 711
QY      149 ThrARpGLyGLuLeuH1sGLyARpLeuPhePheTYrSeSeGLyARgLUAlaAsnARgSer 168
Db      712 ACGGATGGGGAGCTGCACGAGGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCA 771
QY      169 ARgARpLeuGLyAlaIleValTYrCYeValGLyValIleARpPheAsngLUTrgInLeu 188
Db      772 CGAGACCTTGTGTCGATGTGTTTACTGCTGCGTGAAGATTTCAATGAACTTCAAGTTG 831
QY      189 AlaARgIleAlaARpSerLYsARpH1sValPheProValAsnARpGLyPheGlnAlaLeu 208
Db      832 GCTCGGATTTGCAACAGTAAAGACAGGTTTCTGTAAGACAGGCTTCCAGGCTCTC 891
QY      209 GlnGLyIleIleH1sSerIleLeuLYsLYsSeSeCYeIleGlnIleLeuAlaAlaGluPro 228
Db      892 CAAGCATTAATCACTCAATTTAAAGAAATCTGCATGAAATTCGGCGGCTGAACCA 951
QY      229 SeSeThrIleCYeValaGLyGluSeSePheGlnValValValARgLYsngLYPheARgH1s 248
Db      952 TTCACCATCTGCGCGGAGAGTCTTTCAGTGTGCTAAAGAAATGGCTTCCACAT 1011
QY      249 AlaARgAsnValaARpARgValLeuCYsSeSePheLYsIleAsnARpSeSeValThrLeuAsn 268
Db      1012 GCCCGCAATGTGAACAGGCTCTCTGCACTTCAAAATCATATCATCAGTCAAGCTCAAT 1071
QY      269 GlnLYsProPheSeSeValaGLuARpThrTYrLeuLeuCYeProAlaProIleLeuLYsGln 288
Db      1072 GAGAAAGCCCTTGTCTGTGGAAGACATTATTTGCTGTGCCACCAACAATCTTGAAGA 1131
QY      289 ValGLyMeLysValaAlaLeuGlnValSeSeMeThAsnARpGLyLeuSeSePheIleSeSe 308
Db      1132 GTTGGCATGAAGCTGACAGTCAAGTCAAGTCAAGACAGCGCTGTCTTCACTCTCAG 1191
QY      309 SeSeValIleIleThrThrH1sCYsSeSeARpGLySeSeIleLeuAlaIleAlaLeu 328
Db      1192 TCTGTATCATCAACCAACACACTGTTCAGACGCTCCATCTGGGAGATTGCTGTGCG 1251
QY      329 IleLeuPheLeuLeuAlaLeuAlaLeuLeuTrIPheThrProLeuCYsCYsThr 348
Db      1252 GTCTCTTCTCTGCTGCGCGCTGCGGCTGCTGTGAGTTCGGCGCTCTGCTGACAC 1311
QY      349 ValIleIleLYsGLyValaProProProProAlaGlnGluSeSeGln 364
Db      1312 GTGATCATCAAGAGGTCCTTCAACCCCTGTGAGAGAGTGAAGAA 1359
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RESULT 15

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US-10-474-794-300
; Sequence 300, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Mouse
; US-10-474-794-300
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Alignment Scores:

| Pred. No.: | 6.5e-213 | Length: | 5220 |
|------------------------|----------|---------------|------|
| Score: | 1793.00 | Matches: | 342 |
| Percent Similarity: | 97.75% | Conservative: | 6 |
| Best Local Similarity: | 96.07% | Mismatches: | 8 |
| Query Match: | 93.68% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-09-970-076-2 (1-368) x US-10-474-794-300 (1-5220)

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QY      9 LeuGLyIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValIleuIleCysAlaGlyGln 28
Db      292 CTGGGTCGGGGCTTGGGGGACTCTGCGTGGCTGCATCTGCTGCTGCTGCGCGGACAC 351
QY      29 GtYgLYARgARgGLuARgLYgLYProAlaCYeTYrGLyGLyPheARpLeuTYrPheIle 48
Db      352 GGGGGCGCGCGAGAGATGGGGGACCGAGCTTGTACGAGAGATTGACCTTACTTCATC 411
QY      49 LeuARpLYSeSeGLySeValIleuH1sH1sTPAsngLUleTYrTYrPheValIGluGln 68
Db      412 CTGGACAAGTCAGAGAAGTGTGCTGCACCTAGAAAGAAATCTACTACTTCGAGGACG 471
QY      69 LeuAlaH1sLYsPheIleSeSeProGlnLeuARgMeSeSePheIleValPheSeThrArg 88
Db      472 TTGGCTCATAGATTCTACGCCACAGCTTAGAGATGCTCTTCAATGCTTCTTCTTCTCA 531
QY      89 GtYrThrThLeuMeLysLeuThrgLUAsPARgGLuGlnIleARgGlnLYLeuGlnGln 108
Db      532 GGGACAACCTTATTAAGAACTTAAGAGACAGGAAAGATCCGACAGGCGCTTAAGAG 591
QY      109 LeuGlnLYsValLeuProGLyGLyARpThrTYrMeTh1sGLyGLyPheGluATgAlaSer 128
Db      592 CTCACAAAGATTCTGCAGAGAGAGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCA 651
QY      129 GlnGlnIleTYrTYrGLuARgARgGLyTYrARgThrAlaSerValIleIleAlaLeu 148
Db      652 GACCAAGATTACTATAGAACAGTCAAGATACAGAGCGGCGCTCATCTCGCGTTG 711
QY      149 ThrARpGLyGLuLeuH1sGLyARpLeuPhePheTYrSeSeGLyARgLUAlaAsnARgSer 168
Db      712 ACGGATGGGAGACTGCACAGGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCA 771
QY      169 ARgARpLeuGLyAlaIleValTYrCYeValGLyValIleARpPheAsngLUTrgInLeu 188
Db      772 CGAGACCTTGTGTCGATGTGTTTACTGCTGCGTGAAGATTTCAATGAACTTCAAGTTG 831
QY      189 AlaARgIleAlaARpSerLYsARpH1sValPheProValAsnARpGLyPheGlnAlaLeu 208
```

| | | | |
|----|------|--|------|
| Db | 832 | GCTGGGATTCGAGACAGTAAAGCACCGTGTTCCTGTGAAACGACGGCTTCAGGCTTC | 891 |
| Qy | 209 | GLNGLYILEIIEHLSERIIEULYBIYSECYIIIEGIUIELEUALAAGIURO | 228 |
| Db | 892 | CAGGCAATTATTCACATCAATTTTAAGAAATCTGCATCGAAATTCCTGGCGGTGAACCA | 951 |
| Qy | 229 | SERTHRIIECYBALIGLYIUSERPHGINVAIIVALAARGLYAANGLYPHEARGHS | 248 |
| Db | 952 | TCCACCAATCTGGCGGGAGAGTCCITTTCAAGTGCGTAAAGGAAAGGGCTTCGCAAT | 1011 |
| Qy | 249 | ALAARGANVALAARGVAIRGVALLEUCYSSERPHELYSIIAENASPSERVALTHIREUBN | 268 |
| Db | 1012 | GCCGCAATGTGACACGGGTCTCTGCGACGCTTCAAAATCMATGACTCAGTCAAGTCAAT | 1071 |
| Qy | 269 | GLIUSPROPHESERVALGIUAPRTHRTYRIEULEUCYSPROIAPIELEULYSGIU | 288 |
| Db | 1072 | GAGAAAGCCCTTGTGCTGGAAAGACCTTATTGTGCTGCCAGCACCAATCTTGAAAGAA | 1131 |
| Qy | 289 | VALIGMEULYBALAIALEUGINVAISERMETANASPGIYLEUSERPHEISESER | 308 |
| Db | 1132 | GTTGGCAATGAAGCGACACTGAGAGGTACGACGAAGACAGCGGTCTTCATCTCCAGT | 1191 |
| Qy | 309 | SERVALIIEIETHRTHRTIIECYSSERAPGIYSERILELEUALIIEALAEULEU | 328 |
| Db | 1192 | TCTGTCATCATACCAACACACACTGTTCAGACGGCTCATCTGGCAATTCCTGCTG | 1251 |
| Qy | 339 | ILELEUPHEULEULEULAEUALAEULEUNTPTIPRPHETIPROLEUCYSEYTHR | 348 |
| Db | 1252 | GNCTCTTCCTGCTGCTGGCCCTGGCGGCTGCTGTGTGCTTCGGCCCTCTGCTGCACA | 1311 |
| Qy | 349 | VALIIEIIEIYEGUIVALIPROPROPROAAGIUGIUSERGUGIU | 364 |
| Db | 1312 | GGATCATCATAGAGAGTCCCTTCACCCCTGTGTGAGAGAGTGAAGAA | 1359 |

Search completed: December 19, 2005, 02:09:34
Job time : 1230.98 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 296.957 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914

Sequence: 1 MATERRAALIGFQWLSLAT.....VILKEYPPPEASEENKIK 368

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cg2_1/USPTO.spool/US09970076/runac_14122005_11853_21065/app_query.fasta_1.2410
-DB=Published Applications NA New -QMT=fastcap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 @CGN_1_1_675 @runac_14122005_11853_21065
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.*

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2: /cg2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cg2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cg2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cg2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /cg2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cg2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cg2_6/prodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cg2_6/prodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cg2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1894 | 99.0 | 5540 | 7 | US-11-186-284-198 |
| 2 | 145.5 | 7.6 | 4740 | 7 | US-11-080-026-3 |
| 3 | 131 | 6.8 | 11447 | 7 | US-11-186-284-25 |
| 4 | 122 | 6.4 | 2834 | 6 | US-10-750-185-39040 |
| 5 | 113.5 | 5.9 | 1325 | 6 | US-10-750-185-56394 |
| 6 | 113.5 | 5.9 | 2501 | 6 | US-10-821-234-182 |
| 7 | 113.5 | 5.9 | 3449 | 6 | US-10-131-826A-293 |
| 8 | 111 | 5.8 | 3564 | 6 | US-10-601-368-20 |

| | | | | | | |
|----|-------|-----|--------|---|---------------------|-------------------|
| 9 | 111 | 5.8 | 4858 | 6 | US-10-601-368-19 | Sequence 19, Appl |
| 10 | 107.5 | 5.6 | 3175 | 6 | US-10-995-561-464 | Sequence 464, App |
| 11 | 107.5 | 5.6 | 3464 | 6 | US-10-995-561-465 | Sequence 465, App |
| 12 | 107.5 | 5.6 | 3468 | 6 | US-10-995-561-466 | Sequence 466, App |
| 13 | 107 | 5.6 | 3564 | 6 | US-10-601-368-2 | Sequence 2, Appl |
| 14 | 107 | 5.6 | 3967 | 7 | US-11-000-463-574 | Sequence 574, App |
| 15 | 107 | 5.6 | 3969 | 7 | US-11-000-463-102 | Sequence 102, App |
| 16 | 107 | 5.6 | 5042 | 6 | US-10-601-368-1 | Sequence 1, Appl |
| 17 | 105.5 | 5.5 | 3868 | 6 | US-10-995-561-404 | Sequence 404, App |
| 18 | 103.5 | 5.4 | 2765 | 6 | US-10-750-185-25275 | Sequence 1356, A |
| 19 | 101.5 | 5.3 | 47572 | 6 | US-10-995-561-13356 | Sequence 2356, A |
| 20 | 100 | 5.2 | 2773 | 7 | US-11-102-240-33 | Sequence 33, Appl |
| 21 | 96 | 5.0 | 3884 | 6 | US-10-601-368-17 | Sequence 17, Appl |
| 22 | 94 | 4.9 | 1062 | 7 | US-11-137-465-11 | Sequence 11, Appl |
| 23 | 94 | 4.9 | 1347 | 7 | US-11-137-465-12 | Sequence 12, Appl |
| 24 | 91.5 | 4.8 | 1881 | 6 | US-10-467-657-5431 | Sequence 5431, Ap |
| 25 | 90.5 | 4.7 | 3144 | 6 | US-10-392-234A-17 | Sequence 17, Appl |
| 26 | 88 | 4.6 | 3189 | 7 | US-11-137-465-10 | Sequence 10, Appl |
| 27 | 87 | 4.5 | 2715 | 6 | US-10-507-475-4 | Sequence 4, Appl |
| 28 | 86 | 4.5 | 1705 | 6 | US-10-750-185-50386 | Sequence 50386, A |
| 29 | 85.5 | 4.5 | 1278 | 6 | US-10-467-657-2551 | Sequence 2551, Ap |
| 30 | 85.5 | 4.5 | 2538 | 7 | US-11-147-047-20 | Sequence 20, Appl |
| 31 | 82 | 4.3 | 3989 | 6 | US-10-750-185-47454 | Sequence 47454, A |
| 32 | 81.5 | 4.3 | 1688 | 6 | US-10-510-386-157 | Sequence 157, App |
| 33 | 81 | 4.2 | 11135 | 6 | US-10-513-786-6 | Sequence 6, Appl |
| 34 | 81 | 4.2 | 1115 | 7 | US-10-513-786-8 | Sequence 8, Appl |
| 35 | 80.5 | 4.2 | 3586 | 7 | US-11-080-991-51 | Sequence 51, Appl |
| 36 | 80 | 4.2 | 1413 | 7 | US-11-055-822-411 | Sequence 411, App |
| 37 | 79.5 | 4.2 | 2317 | 6 | US-10-793-626-4357 | Sequence 4357, Ap |
| 38 | 79.5 | 4.2 | 2987 | 6 | US-10-793-626-3398 | Sequence 3398, Ap |
| 39 | 79.5 | 4.2 | 3366 | 6 | US-10-467-657-6111 | Sequence 6111, Ap |
| 40 | 79.5 | 4.2 | 5576 | 6 | US-10-995-561-517 | Sequence 517, App |
| 41 | 79.5 | 4.2 | 5808 | 6 | US-10-995-561-517 | Sequence 517, App |
| 42 | 78.5 | 4.1 | 1895 | 6 | US-10-750-185-42451 | Sequence 42451, A |
| 43 | 78.5 | 4.1 | 118996 | 7 | US-11-121-086-84 | Sequence 84, Appl |
| 44 | 78 | 4.1 | 1339 | 6 | US-10-467-657-3293 | Sequence 3293, Ap |
| 45 | 78 | 4.1 | 1443 | 6 | US-10-467-657-3291 | Sequence 3291, Ap |

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILR REFERENCE: MEMO1-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA

ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)...(1838)
US-11-186-284-198

Alignment Scores:

| Pred. No.: | 3, 276-218 | Length: | 5540 |
|------------------------|------------|---------------|------|
| Score: | 1894.00 | Matches: | 364 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 98.96% | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |

US-09-970-076-2 (1-368) x US-11-186-284-198 (1-5540)

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTGGCCACT 203
QY 21 LeuValLeuIleCyAlaGluGlnGlyArgArgGluAspGlyGlyProAlaCyArgTy 40
DB 204 CTGGCTCTCATCTGCGCGGCAAGGGGCGAGGAGGATGGGGTCCAGGCTCTC 263
QY 41 GlyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisIstPasn 60
DB 264 GGGGAGTTTGACCTGTATCTTCAATTTGGACAATTCAGGAAGTGTGCTGCACCACTGGAA 323
QY 61 GluIleTyrrTyrrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 324 GAAATCTATTAATCTTTGGGAAAGTTGGCTCACAAATTCATCGCCACAGTGGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTTGTTTCTCCACCCAGAGAACCTTAAATGAACTGACAGAGCAAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrmec 120
DB 444 CAATTCGTCAAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGCACTTACATG 503
QY 121 HisGlnGlyPheGluArgAlaSerGluGlnIleTyrrTyrrGluAsnArgGlnGlyTyrrArg 140
DB 504 CATGAAGATTTGAAAAGGGCGACGTGAGCAGATTATTTATGAAAACAGACAGGGTCAAG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrArgGlyGluLeuHisGluAspLeuPhePheTy 160
DB 564 ACAGCCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrrCyValGlyVal 180
DB 624 TCAGAGAGGGAGGCTAATAGTCTCGAGATCTTGTCGCAATTTGTTAATGTGTGGTGTG 683
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAAGATTTTCATATGACACACAGCTGCGCCGATGGCGACAGTAAGATCATGTGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCy 220
DB 744 GTAAATGACGGCTTTCAGGCTCTGCAAGGCACTCATCTCAATTTTGAAGAGTCTCTGC 803
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCyAlaGluGlnLeuSerPheGlnVal 240
DB 804 ATGAATTTCTAGACGTGAACCATCCACATATGTCCAGAGAGTCAATTTCAAGTTGTC 863
QY 241 ValArgGlyValGlnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTAGAGGAAACGGCTTCCACATGCCCCGCAACGTGACAGGGGCTCTTCACACTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrrLeuLeu 280
DB 924 ATCAATGACTCGGTGCACACTCAATGAGAGCCCTTTTCTGTGGAAGTACTTATTTATCTG 983
QY 281 CyseProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300

DB 984 TGTCCAGCCCTATCTTAAAGAGTTGGCATGAAGCTGCATCCAGCTCAGCATGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThiGlyCySerAspGly 320
DB 1044 GATGGCTCTCTTATCTTCAATCTGATCTGATCATCATCACACACACACTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
DB 1104 TCCATCTCGGCATGGCCCTGCTGATCTGATCTGCTCTGCTCTGAGCCCTGCTCTG 1163
QY 341 TrpPheTrpProLeuCyseThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TGGTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAAGAA 1235

RESULT 2

US-11-080-026-3
Sequence 3, Application US/11080026
Publication No. US20050260192A1
GENERAL INFORMATION:
APPLICANT: Springer, Timothy A.
APPLICANT: Shimooka, Motomu
APPLICANT: Lu, Chafan
TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
FILE REFERENCE: CFBF-P02-021
CURRENT APPLICATION NUMBER: US/11/080,026
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 09/945,265
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,700
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 4740
TYPE: DNA
ORGANISM: Homo sapiens
US-11-080-026-3

Alignment Scores:

| Pred. No.: | 5, 69e-06 | Length: | 4740 |
|------------------------|---|---------------|------|
| Score: | 145.50 <td>Matches:</td> <td>60</td> | Matches: | 60 |
| Percent Similarity: | 45.85% <td>Conservative:</td> <td>45</td> | Conservative: | 45 |
| Best Local Similarity: | 26.20% <td>Mismatches:</td> <td>81</td> | Mismatches: | 81 |
| Query Match: | 7.60% <td>Indels:</td> <td>43</td> | Indels: | 43 |
| DB: | 7 | Gaps: | 12 |

US-09-970-076-2 (1-368) x US-11-080-026-3 (1-4740)

QY 44 AspLeuTyrrPheIleLeuAspLysSerGlySerValLeu--HisIstPheAsnGluIle 62
DB 520 GACATGCGCTCTTGAATGATGAGCTGTGATGATCATCCATGACTTCCGCGGAGT 579
QY 63 TyrrTyrrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPhe 82
DB 580 AAGAGCTGTGTCAACT-----GTATGAGAGCAATTTAAAGATCCAA 624
QY 83 IleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAsp----- 98
DB 625 ACCTTGTCTCT-----TTGATGCACTACTCTGAAAGATTTCCGATTCAC 669
QY 99 -----ArgGluGlnIleArgGlnGlyLeuGlnGluGln 110
DB 670 TTTACTTCAAGAGTTTCAGAAACACCTTAACCAAGATCACTGTGAAGCCAATPACG 729
QY 111 LysValLeuProGlyLysAspThrTyrrMetHisGluGlyPheGluArgAlaSerGluGln 130
DB 730 CAGCTGCTT-----GGGGGACACACACGGCCACGGGATTCGCAAAAGTGTACGAGAG 783

QY 131 IletYrTgRlUaSnArgSnglYrYrArgThraA---SerVallelleAlaLeuThr 149
Db 784 CTGTTTAACATCCACCAAGAGCCCGAAGAAATGCTTTAAGATCTAGTGTTCATCAG 843
QY 150 AspGlyLeuUhiSglUaPhePhePheTySergUu-----ArgGluAlaAsnArg 167
Db 844 GATGGAGAAAAGTTGGCGATCCCTTGGATATGAGATGATCCCTGAGGCGACAGA 903
QY 168 SerArgAspLeuGlyAlaIleValTYrCYeValGlyValUySaPheAsnGluThrGln 187
Db 904 GAG-----GGAGTCATTCCGCTACGTCATGCGGAGATGCGCTCCGCGATGAG 954
QY 188 LeuAlaArg-----lleAlaAspSer-----LysAspHisValPhePro 200
Db 955 AAATCCGCGCAAGAGCTTAATACCATGTCATCCAGCCGCTCGTATCAGTGTTCAG 1014
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIlelleHisSerlleLeuUySergCys 220
Db 1015 GTGAATTAAC---TTTGAGGCTCTGAGACATTCAGAAACGCTTCGGGAGAG--- 1065
QY 221 lIeGluIleuAlaIleGluProSerThrIleCYeValaGlyUserPheGlnVal 240
Db 1066 -----ATCTTGGCATCGAGGGTACTCAGACAGAGAGTAGACGCTCTTGACATGAG 1119
QY 241 ValArgGlyAsnGlyPheArgHisAla 249
Db 1120 ATGCTCAGAGAGGCTTCAGCGCTGCC 1146

RESULT 3
US-11-186-284-25
Sequence 25. Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Ribodreau, Stephen N.
APPLICANT: Burgate, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MEMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
PRIOR FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 11447
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (9192)
US-11-186-284-25

Alignment Scores:
Pred. No.: 0.00135 Length: 11447
Score: 131.00 Matches: 72
Percent Similarity: 43.11% Conservative: 72
Best Local Similarity: 21.56% Mismatches: 118
Query Match: 6.84% Indels: 72

DB: 7 Gaps: 17
US-09-970-076-2 (1-368) x US-11-186-284-25 (1-11447)
QY 44 AspLeuTyRPhelIleuAspLysSergLysSerVal---LeuHisThrPaangluIle 62
Db 418 GATTTGGTTTCTCTCGATGAGCTCTTGAGAGTGGAGAAATATTTCAATGTCATT 477
QY 63 TyRTrPheValGluGlnLeuAlaHisLysPheIle-----SerProGlnLeuArgMet 80
Db 478 TTAGACTTCAATTCCTGCTCTTGTGTCTCTTGTGACATGGGAGAGAGACAGAGTT 537
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysSerThrglu-----Asp 98
Db 538 GAGTTGTTTAATACAGCTCTGACACAGAGATGAAATTTAATCTTAATCAGTACCA 597
QY 99 ArgGluGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyLysPThr 118
Db 598 AGGATGAATCTTCTGTCGATTAATAAAATTCGA-----TATAAAGTGGCAACACA 651
QY 119 TyRMeHisGluGlyPheGluArgAlaSerGluGlnIleTyRTrGluAsn----- 135
Db 652 ATGACAGGGGATGCCATTGATTATTATTAAATAATCTTTCAGGAATCTGCGGCA 711
QY 136 ArgGlnGlyTyRArgThrAlaSerValIlelleAlaLeuThrAspGlyGluLeuHisGlu 155
Db 712 AGAGTTGGCTTCTCTTAAGTGGCAATTTATT---ACGATGAAATATCCAGAT 765
QY 156 AspLeuPhePheTySergLysArgGluAlaAsnArgSerArgAspLeuGlyAlaIleVal 175
Db 766 GAAGTG-----GAAATTCAGCAAGAGAGCTTGATGTGAGTTGAAGTT 813
QY 176 TyRCyeValGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp----- 193
Db 814 TTCTCTTGGCAATTAAAGCTGCAAGTCAAAAGAACTCAAAAGATTTGCTTCACACT 873
QY 194 SerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIlelleHis 213
Db 874 TCACGTGAACCATGTTTCAATGAGGCCAAC---TTTGATGCAATGTGGATATTCAGAT 930
QY 214 SerlleLeuLysSergCysIle-----GluIleuAlaAla 226
Db 931 GAATCATCTCCAGAGTGTCTCAGAGTGTGATGAGAGCTTGTAATGTAGTGA 990
QY 227 Glu-----ProSerThrIleCYeValaGlyUserPheGlnValVal 241
Db 991 GAAAGAGTTGTGAGCTCTCTCAAAATTGATTCATGAGTGAAGTCTTCAAAATATGTT 1050
QY 242 ArgGlyAsn-----GlyPheArg----- 247
Db 1051 AAGCTTAATTTGAATCATCTCTAGTCCAGTACGATGAGCTTCAAAAGTCACTCACCA 1110
QY 248 -----HisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db 1111 ATGACTGCAGAGAGCGAGACAGACGCTCAGTGGCG----- 1149
QY 261 lIeAsnAspSerValThrIleuAsnGluLysPhePheSerValGluAspThrTYrLeuLeu 280
Db 1150 ---CCTCAGACAAACGCTCAGTGTTCGAGCTCTCAGACACAGCGAGTAC----- 1200
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 1201 -----CAGATCAGTGTTCGCGCATGAAAGGAATGATCCTCAGT 1239
QY 301 AspGlyLeuSerPheIle---SerSerSerValIlelleThrThrHisCysSerAsp 319
Db 1240 GAACCATTTCAATATGAGAGAGACTCAGCAGCATGAAAGTCAAGTGAATGTTCACGT 1299
QY 320 GlySerlleLeuAlaIleAlaLeuLysIleLeuPheLeuLeu 333
Db 1300 GGT-----GTGATATATAAAGCCGATATTGTGTTTGGTT 1335

RESULT 4

| | | | |
|--|------|--|------|
| Qy | 200 | ProvaIaenABPGLyPheGlnAlaLeuGlnGlyIleIleHISerIleLeuYLySer | 219 |
| Db | 966 | CTGTGTGCCAAC---TTCAGCCAGATGAGACCGCTGACCTCAGTGTTCAGAAAGAGTTG | 1022 |
| Qy | 220 | Cys-----IleGlnIleLeuAlaIaIa-----Glu | 227 |
| Db | 1023 | TGCATGAATGCTCTGCTCTGCTCTGTGTGTGCTCTTCTTCGGGGCATGCTGGAGTAGATCATTC | 1082 |
| Qy | 228 | ProSerThrIle-----CysAlaGlyLeuSerPheGln | 238 |
| Db | 1083 | CCCTTCCCGGGTCATTCTGTGTCTACTGTGCTCCCAAGTACGTGTGTGGAGGGGCTTTTA | 1142 |
| Qy | 239 | ValValValArgGlyAsnGlyPheArgHISAla | 249 |
| Db | 1143 | GCAAGGTCTGAG-----ATAAGACACAGT | 1166 |
| RESULT 6 | | | |
| US-10-821-234-182/c | | | |
| ; Sequence 182, Application US/10821234 | | | |
| ; Publication No. US20050255114A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Labat, Ivan | | | |
| ; APPLICANT: Stache-Crain, Birgit | | | |
| ; APPLICANT: Andermani, Susan | | | |
| ; APPLICANT: Tang, Y. Tom | | | |
| ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Precipitase | | | |
| ; FILE REFERENCE: 821A | | | |
| ; CURRENT APPLICATION NUMBER: US/10/821,234 | | | |
| ; CURRENT FILING DATE: 2004-04-07 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/462,047 | | | |
| ; PRIOR FILING DATE: 2003-04-07 | | | |
| ; NUMBER OF SEQ ID NOS: 1704 | | | |
| ; SOFTWARE: pc_seq_genes Version 1.0 | | | |
| ; SEQ ID NO 182 | | | |
| ; LENGTH: 2501 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapiens | | | |
| US-10-821-234-182 | | | |
| Alignment Scores: | | | |
| Pred. No.: 0.0157 Length: 2501 | | | |
| Score: 113.50 Matches: 66 | | | |
| Percent Similarity: 38.28% Conservative: 63 | | | |
| Best Local Similarity: 19.58% Mismatches: 109 | | | |
| Query Match: 5.93% Indels: 99 | | | |
| DB: 6 Gaps: 17 | | | |
| US-09-970-076-2 (1-368) x US-10-821-234-182 (1-2501) | | | |
| Qy | 28 | GInGIyGLyArgArgGlyAspGly---GlyProAla----- | 38 |
| Db | 1631 | GAAAGAGTCGATGCTGAAGAGTGGAGCGACGCCAGGGGAACAAGACGGAGATGCTC | 1572 |
| Qy | 39 | -----CysTyrgLyGlyPheAspLeuTyrrPheIleLeuAspLySerGlySerVal--- | 55 |
| Db | 1571 | CTGAGCCTTAGAGTCCATGATCAACTTCACTCCGTGCTCAAGTAGATGACAGCATTTGGG | 1512 |
| Qy | 56 | -----LeuHISerIleTyrPheGlnIleTyrrTyrrPheValGlnIleuAlaHis | 71 |
| Db | 1511 | GCCAGCAACTTCACAGAGCCAAAAGTCTCAGTCAACTTAATGAGAAAGGTGGCAAGT | 1452 |
| Qy | 72 | LysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThr | 91 |
| Db | 1451 | TATGTGTGTAACCA-----AGATATGTCTTAGTACATTTGCCACTTACCCAAATTT | 1398 |
| Qy | 92 | LeuMetLysLeuThrGlu-----AspArgGlnGlnIleArgGlnGlyLeuGlu | 107 |
| Db | 1397 | TGGCTCAAGTGTCTGGAAGACAGACAGCATATGACAGCTGGGTCAAGACAGCTCAAT | 1338 |
| Qy | 108 | GluLeu-----GlnLysValLeuProGlyGlyAspThrTyrrMetHisGlnGly | 123 |
| Db | 1337 | GAAATCATTTATGAAGACCAACAAGTTGAAGTCAAGGAGACTAACCC----- | 1293 |

| | | | |
|---|-----|---|-----|
| QY | 124 | phegiuaaglaaserglunglnlelytyryguaaanarg----- | 136 |
| Db | 122 | -----AAGAAAGCCCTCCAGACAGTACAGATGATGAGTGGCCAGATACGTCCTCT | 123 |
| QY | 137 | glnqlytyr---ArgThrlaserValllelealeuThrlAspGly----- | 151 |
| Db | 123 | GAAGGCTGAAACCGACCCGCGCATGTCAATCATGTAGTATGATGACAAACATG | 117 |
| QY | 152 | -----glueuHlsgluAspLeuPhePheTyserGlu | 162 |
| Db | 117 | GGCGGGGACCCAAATTACTGTCAATTGATAGATCCGGAGCTTGCTATACATTGGCAAGAT | 111 |
| QY | 163 | ArggluaLaanArgSerArgAspLeuglyalaileVallytyrCysValGly-----Val | 180 |
| Db | 111 | CGCAAAAACCCAAAGGAGAGATTATTCGATGTCTATGTGTTGGGCTCGGCGCTTTGGTG | 105 |
| QY | 181 | LysAspPheanqluThrglnLeuAlaargllealaAspSerLyAspHisValPhePro | 200 |
| Db | 105 | AACCAAGTGAACATCATGATCTTTGGCTTCCAAAGAAAGACAATAGACACATGTGTTCAAA | 996 |
| QY | 201 | ValaanaapGlyPheglnAlaleuglnGlylleleHiserlleleuLyalyserCys | 220 |
| Db | 995 | GTCAAGAGAT---ATCGAAACCTGGAAGATGTTTCTCAATGATCATGATAAGC--- | 942 |
| QY | 221 | llegluileuAlaagluPproserThrlleCysAlaaglyGluSerPheglnVal | 240 |
| Db | 941 | -----CAGCTCTGAGTCTCTT----- | 924 |
| QY | 241 | ValArgLyaaNglyPheArgHisAlaarganValaAspArgValleuCyserPheLys | 260 |
| Db | 923 | -----GGCATGTGTTGGGAACACAGAAAGGTACCGAT----- | 891 |
| QY | 261 | lleaanaapSerValThrlleuansgluLysProPheSerValGluAspThryTrleuLeu | 280 |
| Db | 890 | -----TACCACAGAGAACCATGAGCGAGCCAGAAATCTCACTC----- | 855 |
| QY | 281 | CysProAlaProlleLeuLysgluValaGlyMetLysAlaAlaLeuglnValserMetAen | 300 |
| Db | 854 | -----ATTGGCGCTTCAAGGACACAGACAGCTGATGGG----- | 819 |
| QY | 301 | AspGlyLeuSerPheIleSerSerSerValllelelThrThrlHisCys | 317 |
| Db | 818 | -----GCTGTGTGTCTGAGTACTTGTGCTGACAGCAGCACATTGT | 777 |
| RESULT 7 | | | |
| US-10-131-826A-293 | | | |
| / Sequence 293, Application US/10131826A | | | |
| / Publication No. US20050245730A1 | | | |
| / GENERAL INFORMATION: | | | |
| / APPLICANT: Baker, Kevin P. | | | |
| / APPLICANT: Beresini, Maureen | | | |
| / APPLICANT: Deforge, Laura | | | |
| / APPLICANT: Desnoyers, Luc | | | |
| / APPLICANT: Filvaroff, Ellen | | | |
| / APPLICANT: Gao, Wei-Qiang | | | |
| / APPLICANT: Gerritsen, Mary E. | | | |
| / APPLICANT: Goddard, Audrey | | | |
| / APPLICANT: Godowski, Paul J. | | | |
| / APPLICANT: Gurney, Ausetin L. | | | |
| / APPLICANT: Sherwood, Steven | | | |
| / APPLICANT: Smith, Victoria | | | |
| / APPLICANT: Stewart, Timothy A. | | | |
| / APPLICANT: Tumas, Daniel | | | |
| / APPLICANT: Watanabe, Colin K | | | |
| / APPLICANT: Wood, William | | | |
| / APPLICANT: Zhang, Zhen | | | |
| / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC | | | |
| / FILE OF INVENTION: ACIDS ENCODING THE SAME | | | |
| / FILE REFERENCE: P3330R1C128 | | | |
| / CURRENT APPLICATION NUMBER: US/10/131,826A | | | |
| / CURRENT FILING DATE: 2002-04-24 | | | |
| / PRIOR APPLICATION NUMBER: 60/049911 | | | |

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PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 293
LENGTH: 3449
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-293

Alignment Scores:
Pred. No.: 0.0263 Length: 3449
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 5.93% Indels: 35
DB: 6 Gaps: 13

US-09-970-076-2 (1-368) x US-10-131-826A-293 (1-3449)
QY 44 AapLeuTyRheileuAerlySerGlySerVal---LeuHisIstPnaengluile 62
DB 372 GACCTGGTTTCATCATGCACTCGGCACTGTCACACGCCATGACTGCAAGAGTCC 431
QY 63 TyTyRhe---ValGluInleuAlaHisLeuRheileSerProGluLeu---ArgMet 80
DB 432 AACGAGTTCATCGTGGACATCTTGCAATCTTGCACTGCTGATGTCACCCGAGTG 491
QY 81 SerPheleValaHeserThraGlyThrThleu-----MetIsvleu 95
DB 492 GGCCTGCTCCAAAT-----GGCAGCACTGTCAAGAAATGATTCTCCCTCAAGACC 542
QY 96 ThGluAerArgGluInleuArgGlnGlyLeuGluInleuGluValLeuProGly 115
DB 543 TTCACAGAGAAAGTCCAGGTGAGCGCTGTCAAGAGATGGCGCATCTGTCCAGCGGC 602
QY 116 GlAerThTyRheHisGluGlyRheGluAraGlaSerGluInleuTyTyGluAer 135
DB 603 ACCATGACTGGCTGGCCATCCAGAT-----GCCCTGAACATCGATCTCGAAG 653
QY 136 ArgGlnGlyTyTyRg-----ThraIaserVallelealeuThraP 150
DB 654 GCAGAGGGGGCCCGCCCTGAGGAGAAATGTCACGGGTCAAAATGATGTGACAGAT 713
QY 151 GlGluInleuHisLeuAerPheRheTySerGluArgGluAlaAerAgsSerAgsP 170
DB 714 GGGAGACCTCAGACATCCGTC-----GCCAGGTGGCTGTAAAGCAGCGGAC 761
QY 171 LeuGlyAlaIleValTyTyValGlyVal-----LysAerPheAerGluThraGlu 188
DB 762 ACCGGCATCTTAATCTTGCAATGTGTGGCCAGAGTCAACACCTTGAAGTCC 821
QY 189 AlaArgIleAlaAerSerTyAerPheValaPheProValaAerGlyRheGlnAla 208
DB 822 ATTGGAGTAGCCCATGAGACCATGTCTTCTTGTCGCAAT---TTCACGCAAGATT 878
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QY 209 GlnGlyIleleHisSerIleuTySerGlyleGluIleuAlaAerPro 228
DB 879 GAGACGCTGACCTCGGTTCAGAAAGTTGTCAGCGCCACATGTCAGCACCTTG 938
QY 229 SerThraIeCyAlaGlyGluSerPheGlnValaValaArgGlyAerGlyPheArgHis 248
DB 939 GAGCATTAAGTGGC-----CACTTGTGCATCAACATCCGTGCTCATAGCTTGCAGG 992
QY 249 AlaArg-----AerValaAerArgValaLeuCySerPheTyIleAerP 263
DB 993 TGCACACAGGCTACATTTCTCAATCGATCGATCAGAGACTTGC-----AGAAATCCAGAT 1046
QY 264 SerValThraLeuAerGlu 269
DB 1047 CTGTGTGCATGAGAGAC 1064

RESULT 8
US-10-601-368-20
Sequence 20, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lotz, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
PRIOR FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 3564
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.0558 Length: 3564
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.80% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-2 (1-368) x US-10-601-368-20 (1-3564)
QY 39 CyTyTyGlyGlyPheAerPheTyRheileuAerlySerGlySerValleuHis 58
DB 475 TGCAGACTTAATGACATCTGATCTTGAATGAGCTCCCAACAGCATC---TACCCC 531
QY 59 TrPnaGluIleTyTyRheValaGluInleuAlaHisLeuRhe---IleSerPro--- 76
DB 532 TGGGTGAGAGTCCACATCTTCTCATCATATCTCTCAAAAAGTTCAACNTTGGCCCGG 591
QY 77 GlnLeuAerMetSerPheIleValaPheSerThraGlyThrThleuMetIsvleuTh 96
DB 592 CAGATCCAGGTGCGAATAGTCCAGTATGGAAGAAATGCCGTGCATGATGTTCCACTT--- 648
QY 97 GlAerArgGluInleuArgGlnGlyLeuGluInleuGluValaLeuProGlyGly 116
DB 649 AATGATACAGGCTGTGTAAAGATGTGTGGAAGCCGCCAGCCACATTAAGCAGAGAG 708
QY 117 AepThTyRheHisGluGlyRheGlu-----ArgAlaserGluInleuTyTy 133
DB 709 GGGACAGAAAGCCCGCAGGCAATTTGGCATTTGAATTTGCAAGCTTCCAGAGCTTCCAGAG 768
QY 134 GlAerArgGlnGlyTyTyRgThraIaserVallelealeuThraPrglyGluLeu 153
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Db      769 GGTGAAAGAAAGGGGCCAAG-----AAAGTATGATTGTCATCAAGAGGGAAATCC 822
QY      154 H1ag1uaap----- 156
Db      823 CACGACACCCGACACTGTGAGAGAGGTATCCGCGACAGCGAAGAGACACTGACACAGA 882
QY      157 -----LeuphetherYsergluArglu1a1aenArySerArgsp1eu 171
Db      883 TACGCTGTGCGCTTTTGGGCTACTACAAACCGCAGGGGATCAATCCAGAGCTTTCTTA 942
QY      172 G1yAla1leValTYrCYeValglYAllylsAp-----Pha5nglu1nThrLn 187
Db      943 AATGAAATCAATATACATGCCACGACACCTGACGACAGCAACTTCTTCAACGTCAAGAT 1002
QY      188 Leu1aAArg1eAlaAspSerlyAspH1sVal1PheProValAsnAspGlyPheGln1a 207
Db      1003 GAGCGGGCGCTG-----AAGGACATTTGTTGATGCCCTTGGGGAAGAGATCTTCAGC 1055
QY      208 LeuGlnGly 210
Db      1054 TTGGAAGGC 1062

RESULT 9
US-10-601-368-19
; Sequence 19, Application US/10601368
; Publication No. US20050260702a1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lotz, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.0916 Length: 4858
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.80% Indels: 38
DB: Gaps: 9

US-09-970-076-2 (1-368) x US-10-601-368-19 (1-4858)
QY      39 CybTYrGlyGlyPheAspLeuTYrPhe1leuAspLySergLySerVal1euH1s 58
Db      502 TGCCAGACTTACATGACATGCTCATTTGCTTGAATGCTCAACAGCATC---TACC 558
QY      59 TrpAenGlu1leTYrTYrPheValGluGln1euAlaH1slyPhe---1leSerPro--- 76
Db      559 TGGGAGAGGTGCAACACTTCTCTCAATATCTTCAAAAGATTCTTACATTTGGCCCG 618
QY      77 Gln1euATgMetSerPhe1leValPheSerThrArgGlyTrh1r1euMetLyS1euThr 96
Db      619 CAGATCCAGGTCCGAAATAGTCACAGATGAGAAAGATGCCGTCATGATTCACACTT--- 675
QY      97 Glu1euPArgGluGln1leArgGlnGlyLeuGln1leuGln1lyVal1euProGlyGly 116

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Db      676 AATGACTACAGCTCTGTAAAGATGTGGTGAAGCCGCCAGCCACATTGACGAGAGAGA 735
Qy      117 AspThrTyMetHisgluGlyPheGlu-----ArgAlaSerGluGlnIleTyTy 133
           |||
Db      726 GGGACAGAGACCCCGCAGCGCATTTGGCATTTGAATTGTGACCGCTCGAGGCTTTCCAGAG 795
Qy      134 GluAlaArgGlnGlyTyArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeu 153
           |||
Db      796 GGTGGAAAMAAAGGGGCCAAG-----AAAGTAGATTGTTCATCAGCAGCGGGAATCC 849
Qy      154 HisGluAsp----- 156
           |||
Db      850 CACGACAGCCCGACCTTGAGAGAGTATCCGCGACGACGAGAGAGACATGTCACACAGA 909
Qy      157 -----LeuPhePheTySerGluArgGlnAlaAsnArgSerArgAspLeu 171
           |||
Db      910 TACGCTGTGGCCGCTTTTGGGCTACTACAACCGCAGGGGAGATCAATCCAGAGACTTTCTGA 969
Qy      172 GlyAlaIleValTyTyCysValGlyValIlyAsp-----PheAsnGluThrGln 187
           |||
Db      970 AATGAAATCAATATCATGCGCCAGCCAGCCCTGCGACGACAGCACTTCTTCAACGTCACAGAT 1022
Qy      188 LeuAlaArgIleAlaAspSerTyAspHisValPheProValAsnAspGlyPheGlnAla 207
           |||
Db      1030 GAGCGCGCCCTG-----AAGGACATGTGTGATGCCCTTGGGACAGAGATCTTCAGC 1088
Qy      208 LeuGlnGly 210
           |||
Db      1081 TTGGAGAGC 1089

RESULT 10
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.123 Length: 3175
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 5.62% Indels: 45
DB: 6 Gaps: 9

US-09-970-076-2 (1-368) x US-10-995-561-464 (1-3175)

Qy      45 LeuTyPheIleLeuAspLysSerGlySerVal----- 55
           |||
Db      243 GTGATCTCGTGGTGGACACTCGGAGAGCGTCACATGACAGTCCCGCAGGACATCTGTG 302
Qy      56 LeuHisHisThrPheAsnGlu---IleTyTyThrPheValGluGlnIleuAlaHisIlyPheIle 74
           |||
Db      303 CTCCTTCACATGAAGCAAGCTTGTCGCCGCGCATTCATCAAGCCAGCTGACAGAAAGATTCTAC 362
Qy      75 SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 90
           |||
Db      363 CTGACACCAAGGTGGCGGTACGCTGGCGCGTAATYAGGCGGCGTCACTTCTTGACCAAGGTGAG 422
Qy      91 ThrIleuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGluGlnIleuGln 110

```

```
Db 423 GGTTCAGCCACCGGCGACGCGCTCTTCATCAAGAACTGACGGGCATCACG 482
Qy 111 LysValLeuProGlyLysAspThrTyrMetHisGluGlyPheGluArgLysSerGluGln 130
Db 483 TCCTTCGCGCGCGGCG-----ACCTTCACCGCACTGGCGCGCTGGCCAACTGACGGAGCAG 536
Qy 131 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAsp 150
Db 537 ATCCGGCAGAGACCGGACGAAAGGCG-----ACGTCACACTGGCGCGCTGGCATCACCGAC 590
Qy 151 GlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 170
Db 591 GGCACAGTCACCGGCGACCGCCCTGGGAGGAGCATCAAGCTGACGAGCGGCGCGCGAG 650
Qy 171 LeuGlyAlaIleValTyrCysVal-----GlyValLys 181
Db 651 GAGGCGATCCGGCTCTTCGCGCGTGGCGCCCAACCAAGACTGAAAGACGAGGCGCTGGCG 710
Qy 182 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 199
Db 711 GACATCGCAGACCGCGCGACGAGCTTACCGC-----AACGACTACGCGCACG 758
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 216
Db 759 ATGCTGCCYGACTCCACCGAGATCRAACAGACCATCAACCGCATCATCAAGATCATG 818
Qy 217 -----LysLysSerCysIleGluIle 223
Db 819 AAACAGAAAGCTTACGAGAGAGTGTCTACAGGTGAGCTGCTGGAATTC 866
```

```
RESULT 11
US-10-995-561-465
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 3464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-465
```

```
Alignment Scores:
Pred. No.: 0.142 Length: 3464
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 5.62% Indels: 45
DB: Gaps: 9
```

US-09-970-076-2 (1-368) x US-10-995-561-465 (1-3464)

```
Qy 45 LeuTyrPheIleLeuAspLysSerGlySerVal----- 55
Db 243 GTGTACTTGTGCTGTGACACCTCGAGAGAGCTACCATGCAAGTCCCGCCACGACATCTCG 302
Qy 56 LeuHisIleTrpAsnGlu---IleTyrTyrPheValGlnGlnLeuAlaHisLysPheIle 74
Db 303 CTCTTCACATGAAGAGATTGTCGCGCAGTTCATCAGCCAGTGAAGACGAGTTCTAC 362
Qy 75 SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 90
Db 363 CTGACACAGGTGCGCTGAGCTGCGCTTAAGCGCGCTGCACTTCTTGAACAGGTGAG 422
```

```
Qy 91 ThrLeuMetLysLeuThrGlnAspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGln 110
Db 423 GGTTCAGCCACCGGCGACGCGCGCTCTTCATCAAGAACTGACGGGCATCACG 482
Qy 111 LysValLeuProGlyLysAspThrTyrMetHisGluGlyPheGluArgLysSerGluGln 130
Db 483 TCCTTCGCGCGCGGCG-----ACCTTCACCGCACTGGCGCGCTGGCCAACTGACGGAGCAG 536
Qy 131 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAsp 150
Db 537 ATCCGGCAGAGACCGGACGAAAGGCG-----ACGTCACACTGGCGCGCTGGCATCACCGAC 590
Qy 151 GlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 170
Db 591 GGCACAGTCACCGGCGACCGCCCTGGGAGGAGCATCAAGCTGACGAGCGGCGCGCGAG 650
Qy 171 LeuGlyAlaIleValTyrCysVal-----GlyValLys 181
Db 651 GAGGCGATCCGGCTCTTCGCGCGTGGCGCCCAACCAAGACTGAAAGACGAGGCGCTGGCG 710
Qy 182 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 199
Db 711 GACATCGCAGACCGCGCGACGAGCTTACCGC-----AACGACTACGCGCACG 758
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 216
Db 759 ATGCTGCCYGACTCCACCGAGATCRAACAGACCATCAACCGCATCATCAAGATCATG 818
Qy 217 -----LysLysSerCysIleGluIle 223
Db 819 AAACAGAAAGCTTACGAGAGAGTGTCTACAGGTGAGCTGCTGGAATTC 866
```

```
RESULT 12
US-10-995-561-466
; Sequence 466, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-466
```

```
Alignment Scores:
Pred. No.: 0.142 Length: 3468
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 5.62% Indels: 45
DB: Gaps: 9
```

US-09-970-076-2 (1-368) x US-10-995-561-466 (1-3468)

```
Qy 45 LeuTyrPheIleLeuAspLysSerGlySerVal----- 55
Db 243 GTGTACTTGTGCTGTGACACCTCGAGAGAGCTACCATGCAAGTCCCGCCACGACATCTCG 302
Qy 56 LeuHisIleTrpAsnGlu---IleTyrTyrPheValGlnGlnLeuAlaHisLysPheIle 74
Db 303 CTCTTCACATGAAGAGATTGTCGCGCAGTTCATCAGCCAGTGAAGACGAGTTCTAC 362
Qy 75 SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 90
Db 363 CTGACACAGGTGCGCTGAGCTGCGCTTAAGCGCGCTGCACTTCTTGAACAGGTGAG 422
```


Qy 91 ThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGluGln 110
Db 423 GTGTTCAGCCCAACGGGCGAGCGGCGCTTCATCAAGAACTGCGAGGGCATGAC 482
Qy 111 LysValLeuProGlyGlyAspThrTyMetMetIleGluGlyPheGluArgAlaSerGluGln 130
Db 483 TCCTTCGCGCGCGCGC-----ACCTTCACGAGCTGCGCGCGTGCACATGACGAGACAG 536
Qy 131 IleTyArgLysLeuAspArgGlnGlyTyArgThrAlaSerValIleIleAlaLeuThrAsp 150
Db 537 ATCCGGAGGACCGCGACAGAGGCGC-----ACCTTCACCTTCGCGCGTGCATCACCAGAC 590
Qy 151 GluGluLeuMetIleGluAspLeuPhePheTySerGluArgGluAlaAspArgSerArgAsp 170
Db 591 GGGCAGCTTCACCGGCGAGCCCTGCGGGGCGATCAAGCTGACGCGGAGCGGCGGAG 650
Qy 171 LeuGlyValIleValIleTyArgValIle-----GlyValIle 181
Db 651 GAGGGCATCGCGGCTCTCGCGCGTGCAGCCCAACGAACTGAAAGAGAGCGGCGCTGCGG 710
Qy 182 AspPheAspGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 199
Db 711 GACATCGCGACGACGCGCGACGAGCTTACCGC-----AACGACTACGCGCAC 758
Qy 200 ProValAspAspArgLysPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 216
Db 759 ATCTGCTCCGATCTCCACGAGATTCACGAGACCACTCAACCGCATCATCAAGTCAATG 818
Qy 217 -----LysLysSerCysIleGluIle 223
Db 819 AAACAGCAAGCTTACGAGAGTGTCTACAGGTAGTGCCTCGGAAATC 866

RESULT 13
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ. ID NOS: 40
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ. ID NO. 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2

Alignment Scores:
Pred. No.: 0.171 length: 3564
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.59% Indels: 38
DB: Gaps: 9

US-09-970-076-2 (1-368) x US-10-601-368-2 (1-3564)
Qy 39 CysTyArgLysGlyPheAspLeuTyArgPheIleLeuAspLysSerGlySerValLeuHisHis 58
Db 475 TGCACAGACTACATGACATGCTGCTGCTGATGATGCTCAACAGCATC---TACCC 531

Qy 59 TrpAsnGluIleTyArgPheValGluGlnIleAlaHisLysPhe---IleSerPro--- 76
Db 532 TGGGTGAGGTTCAGACCTTCATCAATCATCTGTAAGAAAGTTTATCATTTGCGCGAG 591
Qy 77 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 96
Db 592 CAGATCCAGGTGTGAGTGTGACATGAGTGGAGAGATGTGTCATGATGATTTACCTC--- 648
Qy 97 GluAspArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGly 116
Db 649 AACGACTACAGCTCTGTAAAGATGTGTGAGAGCTGCCAGCCACATTTGACAGAGAGA 708
Qy 117 AspThrTyMetMetIleGluGlyPheGlu-----ArgAlaSerGluGlnIleTyArg 133
Db 709 GGAACAGAGACCGGAGCGGATTTGGCATTTGACAGCTTCAGAGGCTTCCAGAG 768
Qy 134 GluAspArgGlnGlyTyArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeu 153
Db 769 GGTGAAAGAAAGAGAGCAAG-----AAGGTATGATTTGTATCAGATGGGAGATCC 822
Qy 154 HisGluAsp----- 156
Db 823 CACGACAGCCCGACAGCTGGAAGAGTATCCAGCAAGCGAAAGACAACTGAACAGA 882
Qy 157 -----LeuPhePheTySerGluArgGluAlaAspArgSerArgAspLeu 171
Db 883 TATGCGGTGCGCTCTCGCGCTTCTACACCGAGGGGATCAATCCAGAACTTTCTA 942
Qy 172 GlyAlaIleValIleTyArgValGlyValLysAsp-----PheAsnGluThrGln 187
Db 943 AATGAATCAATATACATCCGCGATGACCTGATGACAGACATTTCTCAATGTCATGAT 1002
Qy 188 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAspArgLysPheGlnAla 207
Db 1003 GAGCTGCTCTG-----AAGGACATTTGTGATGATGCTGTGGGACAGAAATCTTCAGC 1053
Qy 208 LeuGlnGly 210
Db 1054 CTGGAAGGC 1062

RESULT 14
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aendi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NOVEL Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870

```

/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 574
/ LENGTH: 3967
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-000-463-574

Alignment Scores:
Pred. No.: 0.203 Length: 3967
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.59% Indels: 38
DB: Gaps: 9

US-09-970-076-2 (1-368) x US-11-000-463-574 (1-3967)
QY 39 CyeTyrGlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisHis 58
DB 524 TGGCAACCTACATGACATGATTCATTCCTGATGCTCCAAACGATC---TACCC 580
QY 59 TTPAsnGluIleTyrTyrPheValGluGlnLeuAlaHisIlePhe---IleSerPro--- 76
DB 581 TGGGTGAGGTTGACAGCTTCATCATCAATCTGAAAAAGTTTAACTTGGCCAGG 640
QY 77 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThr 96
DB 641 CAGATCAGGTTGGAGTTGGACATGCGAATGGCAAGATGTGTCATGATTCACCTC--- 697
QY 97 GluAspArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnIleuValLeuProGlyGly 116
DB 698 AACGACTACAGCTCTGTAAAGATGTGTGGAGCTGCCAGCACTTGACAGAGAG 757
QY 117 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyr 133
DB 758 GGAACAGAGACCCGACGCGCATTTGGCATTTGCAAGCTCCAGAGGCTTCCAGAG 817
QY 134 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleIleAlaLeuThrArgGlyGlu 153
DB 818 GGTGAAGGAAAGAGCCAAAG-----AAGTGATGATTTGTCAACAGTGGGAGTCC 871
QY 154 HisGluAsp----- 156
DB 872 CACGACAGCCACAGCTCGAAGAGTGATCCAGCAAGAGAAAGACAACGTAACAAG 931
QY 157 -----LeuPhePheTyrSerGluArgGlnAlaAsnArgSerArgAspLeu 171
DB 932 TATGCGGTGGCCGCTCGGCTACTACACCGAGGGGATCAATCCAGAACTTTTCTA 991
QY 172 GlyAlaIleValTyrCysValGlyValIleAsp-----PheAsnGluThrGln 187
DB 992 AATGAATCAAAATACATCGCCAGTACCTGTATGACAGACACTTCTCAATGTCACTGAT 1051
QY 188 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnArgGlyPheGlnAla 207
DB 1052 GAGGCTGGCTG-----AAGGACATGTGTGATGCCCTGGGGGAGCAAAATCTTACG 1102
QY 208 LeuGlnGly 210
DB 1103 CTGGAAGGC 1111

RESULT 15
US-11-000-463-102
/ Sequence 102, Application US/11000463
/ Publication No. US2005026423A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Maundi, Vinod
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Qian, Xiaohong B.

```

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/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhou, ping
/ APPLICANT: Cao, Yi-Cheng
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
/ FILE REFERENCE: 785CIPACN
/ CURRENT APPLICATION NUMBER: US/11/000,463
/ PRIOR FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: 10/291,265
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/922,279
/ PRIOR FILING DATE: 2001-06-03
/ PRIOR APPLICATION NUMBER: 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 09/617,746
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/631,451
/ PRIOR FILING DATE: 2000-06-03
/ PRIOR APPLICATION NUMBER: 09/633,870
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 102
/ LENGTH: 3969
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52) .. (3618)
US-11-000-463-102

Alignment Scores:
Pred. No.: 0.203 Length: 3969
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.59% Indels: 36
DB: Gaps: 9

US-09-970-076-2 (1-368) x US-11-000-463-102 (1-3969)
QY 39 CyeTyrGlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisHis 58
DB 526 TGGCAACCTACATGACATGATTCATTCCTGATGCTCCAAACGATC---TACCC 582
QY 59 TTPAsnGluIleTyrTyrPheValGluGlnIleuAlaHisIlePhe---IleSerPro--- 76
DB 583 TGGGTGAGGTTGACAGCTTCATCATCAATCTGAAAAAGTTTAACTTGGCCAGG 642
QY 77 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThr 96
DB 643 CAGATCAGGTTGGAGTTGTGAGTATGGCAAGATGTGTCATGATTCACCTC--- 699
QY 97 GluAspArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnIleuValLeuProGlyGly 116
DB 700 AACGACTACAGCTCTGTAAAGATGTGTGGAGCTGCCAGCACTTGACAGAGAG 759
QY 117 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyr 133
DB 760 GGAACAGAGACCCGACGCGCATTTGGCATTTGCAAGCTCCAGAGGCTTCCAGAG 819
QY 134 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleIleAlaLeuThrArgGlyGlu 153
DB 820 GGTGAAGGAAAGAGCCAAAG-----AAGTGATGATTTGTCAACAGTGGGAGTCC 873
QY 154 HisGluAsp----- 156
DB 874 CACGACAGCCACAGCTCGAAGAGTGATCCAGCAAGAGAAAGACAACGTAACAAG 933

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Qy 157 -----LeuphepHeTYrSerGluAArgGluAaenAArgSerArgAspLeu 171
Db 934 TATGCCGTGGCCGCTCTGGGCTACTACACCGCAGGGGATCAATCCAGAACTTTCTA 993
Qy 172 GlyAlaIleValTYrCysValGlyValLysAsp-----PheAenGluThrGln 187
Db 994 AATGAAATCAAAATACATCGCCAGTACCTGATGACAAGCAGCTTCTTCAATGTCACGTGAT 1053
Qy 188 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAenAAspGlyPheGlnAla 207
Db 1054 GAGGCTGCCTTG-----AAGGACATTGTGATGCCCTGGGGGACAGAAATCTTCAGC 1104
Qy 208 LeuGlnGly 210
Db 1105 CTGGAAGGC 1113

```

Search completed: December 19, 2005, 02:29:25
 Job time : 324.957 secB

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/ APPLICANT: Gallatin, W. Mich
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/286,889
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: P38,659
/ REFERENCE/DOCKET NUMBER: 27866/32168
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1155 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-286-889-46

Query Match      10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY      11 PACYGFGLDYFYLIDKSGSV-LHHWNEIYFVFEQLAHKFTSPQLRMSFIVFSTRGTTLMK 68
DB      144 PECPGEMDIALFIDSGSIDQSDFTQMKDFYKALMGQLASTSTSLMGYSILTKHTFT 203
QY      69 LTEDR-----EQIRGLBELQKVLPGGDTYMHGFEFASQIYYENRQGYRTA-SVITIAL 122
DB      204 FTEFKSSLSPQSLVDATVQLQ-----GLTYTASGIQKVVELPHSKNGARKSAKKILIVY 258
QY      123 TGEIHEDLFFYSE--REANRSRDGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
DB      259 TGGQKRDLERLHVHVIPEAKA---GIIRYAGVGDAFREPFLAQELNLTIGSAPSGDHVF 315
QY      174 PVNDGFQALQGIHHSILKSCIEILAAPESTICAGSFQVYVYVNGFRHARNVD 227
DB      316 KVGNFVALRSIQRIQIEK-----IFAIEGTESRSSSSFOHEMSQEGFSALSMD 364

RESULT 3
US-08-485-618-46
/ Sequence 46, Application US/08485618
/ Patent No. 5728533
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
```

```

/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,618
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32797
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1155 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-485-618-46

Query Match      10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY      11 PACYGFGLDYFYLIDKSGSV-LHHWNEIYFVFEQLAHKFTSPQLRMSFIVFSTRGTTLMK 68
DB      144 PECPGEMDIALFIDSGSIDQSDFTQMKDFYKALMGQLASTSTSLMGYSILTKHTFT 203
QY      69 LTEDR-----EQIRGLBELQKVLPGGDTYMHGFEFASQIYYENRQGYRTA-SVITIAL 122
DB      204 FTEFKSSLSPQSLVDATVQLQ-----GLTYTASGIQKVVELPHSKNGARKSAKKILIVY 258
QY      123 TGEIHEDLFFYSE--REANRSRDGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
DB      259 TGGQKRDLERLHVHVIPEAKA---GIIRYAGVGDAFREPFLAQELNLTIGSAPSGDHVF 315
QY      174 PVNDGFQALQGIHHSILKSCIEILAAPESTICAGSFQVYVYVNGFRHARNVD 227
DB      316 KVGNFVALRSIQRIQIEK-----IFAIEGTESRSSSSFOHEMSQEGFSALSMD 364

RESULT 4
US-08-362-652-46
/ Sequence 46, Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
```

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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-46
```

Query Match 10.8%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 7,4e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

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QY 11 PACYG-GFDLYFTLDKSGSV-LHNMNRIYFVEQLAHKFTSPOLRMSEFVSTRGTTLMK 68
DB 144 PECPGQEMDIAFLIDSGSIDQSFQMKDFVXALMGQLASTSTSPIMQYSNLKTHFT 203
QY 69 LTEDR-----EQIRGLSEHLOKVLPGDPTMHGSEFASQIYENKQYRTA-SVIAL 122
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQKVVVELFHSKNGAKSAKKILIVI 258
QY 123 TDGELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 173
DB 259 TDGQKRPDPLEYRHVPEAKA---GIIRVAIGVDAFREPTALQELINTIGSAPSDHVF 315
QY 174 PVNDGFOALOGIHSILKSCIEILAAEPSTICAGSFQVYVVRNGFRHARNVD 227
DB 316 KVGN-FVALNSIQRIQIEK---IFAIEGTSRSSSSSFQHMGEQGFSSALSMD 364
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RESULT 5

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US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46
```

Query Match 10.8%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 7,4e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

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QY 11 PACYG-GFDLYFTLDKSGSV-LHNMNRIYFVEQLAHKFTSPOLRMSEFVSTRGTTLMK 68
DB 144 PECPGQEMDIAFLIDSGSIDQSFQMKDFVXALMGQLASTSTSPIMQYSNLKTHFT 203
QY 69 LTEDR-----EQIRGLSEHLOKVLPGDPTMHGSEFASQIYENKQYRTA-SVIAL 122
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQKVVVELFHSKNGAKSAKKILIVI 258
QY 123 TDGELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 173
DB 259 TDGQKRPDPLEYRHVPEAKA---GIIRVAIGVDAFREPTALQELINTIGSAPSDHVF 315
QY 174 PVNDGFOALOGIHSILKSCIEILAAEPSTICAGSFQVYVVRNGFRHARNVD 227
DB 316 KVGN-FVALNSIQRIQIEK---IFAIEGTSRSSSSSFQHMGEQGFSSALSMD 364
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RESULT 6

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US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46

Query Match 10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYGFGLDYIILDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRGTTLMK 68
DB 144 PEPGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMGQLASTSTSLMQYSIILKTHFT 203
QY 69 LTEDR-----EQIRGLBELQKVLPGDITYMHGFERASQIYYENRGYRTA-SVITIAL 122
DB 204 FTEFSSSLSPQSLVDAIVLQ-----GLTYTASGIQKVVELPHSKNGARKSKKILIV 258
QY 123 TGBELHEDLFFYSE--REANRSRLGAIYCVGVD-FNE-TQLARI-----ADSKDHVF 173
DB 259 TDGQKRDPLERHVIPEAKA---GIIRYAIQVGAFFEPYALQELNLTIGSAPSGDHVF 315
QY 174 PVNDGFQALQGIHSLIKKSCIEILAAPEPTICAGESFOVVVVGNGFRHARNVD 227
DB 316 KVGNFVALLRSIQRIQERK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 7

US-08-943-363-46
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seair Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:

CLASSIFICATION: 530
APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-46

Query Match 10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYGFGLDYIILDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRGTTLMK 68
DB 144 PEPGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMGQLASTSTSLMQYSIILKTHFT 203
QY 69 LTEDR-----EQIRGLBELQKVLPGDITYMHGFERASQIYYENRGYRTA-SVITIAL 122
DB 204 FTEFSSSLSPQSLVDAIVLQ-----GLTYTASGIQKVVELPHSKNGARKSKKILIV 258
QY 123 TGBELHEDLFFYSE--REANRSRLGAIYCVGVD-FNE-TQLARI-----ADSKDHVF 173
DB 259 TDGQKRDPLERHVIPEAKA---GIIRYAIQVGAFFEPYALQELNLTIGSAPSGDHVF 315
QY 174 PVNDGFQALQGIHSLIKKSCIEILAAPEPTICAGESFOVVVVGNGFRHARNVD 227
DB 316 KVGNFVALLRSIQRIQERK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 8

US-09-193-043-46
Sequence 46, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46


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Query Match      10.8% Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GFDLYFILDKGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVFSTRGTTLMK 68
DB 144 PECPCQMDIAFLIDSGSIDQSDFTQMKDFVKALMQALSTSTSFSLMQYSNLTKHTFT 203
QY 69 LTER-----EQIRGSELEOKVLPGDPTMHGFEFASQIYVENQGRTA-SVIAL 122
DB 204 FTERKSSLSPOSIVDAIVQIQ-----GLTYTASGIQVKELEFHSKNGARKSARKILLIVI 258
QY 123 TDGELHEDLFFYSE--REANRSRLGAIYVCVGVKD-FNE-TOLARI-----ADSKDHVF 173
DB 259 TDGOKRPDPLEYRIVIVEAEKA---GIIRYAIQVGDAFREPTLQELINTGSAFSDQHV 315
QY 174 PVNDGFOALQGIHSLKSCIEILAEPTICAGSFQVVVRNGFRHARNVD 227
DB 316 KVGK-FVALRSIQRIQIEK----IFALGTESSRSSSFQHEMSQEGFSSALSMD 364
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RESULT 9
US-09-688-307A-46
; Sequence 46, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46
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Query Match      10.8% Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GFDLYFILDKGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVFSTRGTTLMK 68
DB 144 PECPCQMDIAFLIDSGSIDQSDFTQMKDFVKALMQALSTSTSFSLMQYSNLTKHTFT 203
QY 69 LTER-----EQIRGSELEOKVLPGDPTMHGFEFASQIYVENQGRTA-SVIAL 122
DB 204 FTERKSSLSPOSIVDAIVQIQ-----GLTYTASGIQVKELEFHSKNGARKSARKILLIVI 258
QY 123 TDGELHEDLFFYSE--REANRSRLGAIYVCVGVKD-FNE-TOLARI-----ADSKDHVF 173
DB 259 TDGOKRPDPLEYRIVIVEAEKA---GIIRYAIQVGDAFREPTLQELINTGSAFSDQHV 315
QY 174 PVNDGFOALQGIHSLKSCIEILAEPTICAGSFQVVVRNGFRHARNVD 227
DB 316 KVGK-FVALRSIQRIQIEK----IFALGTESSRSSSFQHEMSQEGFSSALSMD 364
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RESULT 10
US-09-350-259-46
; Sequence 46, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-259-46
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Query Match      10.8% Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GFDLYFILDKGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVFSTRGTTLMK 68
DB 144 PECPCQMDIAFLIDSGSIDQSDFTQMKDFVKALMQALSTSTSFSLMQYSNLTKHTFT 203
QY 69 LTER-----EQIRGSELEOKVLPGDPTMHGFEFASQIYVENQGRTA-SVIAL 122
DB 204 FTERKSSLSPOSIVDAIVQIQ-----GLTYTASGIQVKELEFHSKNGARKSARKILLIVI 258
QY 123 TDGELHEDLFFYSE--REANRSRLGAIYVCVGVKD-FNE-TOLARI-----ADSKDHVF 173
DB 259 TDGOKRPDPLEYRIVIVEAEKA---GIIRYAIQVGDAFREPTLQELINTGSAFSDQHV 315
QY 174 PVNDGFOALQGIHSLKSCIEILAEPTICAGSFQVVVRNGFRHARNVD 227
DB 316 KVGK-FVALRSIQRIQIEK----IFALGTESSRSSSFQHEMSQEGFSSALSMD 364
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RESULT 11
US-08-485-618-53
; Sequence 53, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Bear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GPDLFYFLDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRTTLMK 68
DB 144 PBCPGQEMDIATLIDSGSIDSDFTQMKDFVAKLMGQLASTSTSLMOYSIILKTHRT 203
QY 69 LTEDR-----EQIROGLBELQKVLPGDITYMHEGFERASQIYENRQGYRTA-SVYIAL 122
DB 204 FTEFKSSLSQSLVDIAVLQ-----GLTYTASGIQKVVELFHSKNGARKSAKILIIYI 258
QY 123 TDGELHEDLFFYSE--REANRSRDGAIYVCYKQ-FNE-TOLARI-----ADSCDHYF 173
DB 259 TDGQKRPDLBYRHVYIPEAKA---GIRYAIQVGDAFREPTALQELINTIGSAPSDHYF 315
QY 174 PVNDGFOALQGIHSLIKKSCIEILAEPTICAGSFQVYVNGNGFRHARND 227
DB 316 KVGNI-FVALKSIQRIQK-----IPALGETSRSSSFQHEMSQEGFSSALSMD 364

RESULT 12
US-08-362-652-53
Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GPDLFYFLDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRTTLMK 68
DB 144 PBCPGQEMDIATLIDSGSIDSDFTQMKDFVAKLMGQLASTSTSLMOYSIILKTHRT 203
QY 69 LTEDR-----EQIROGLBELQKVLPGDITYMHEGFERASQIYENRQGYRTA-SVYIAL 122
DB 204 FTEFKSSLSQSLVDIAVLQ-----GLTYTASGIQKVVELFHSKNGARKSAKILIIYI 258
QY 123 TDGELHEDLFFYSE--REANRSRDGAIYVCYKQ-FNE-TOLARI-----ADSCDHYF 173
DB 259 TDGQKRPDLBYRHVYIPEAKA---GIRYAIQVGDAFREPTALQELINTIGSAPSDHYF 315
QY 174 PVNDGFOALQGIHSLIKKSCIEILAEPTICAGSFQVYVNGNGFRHARND 227
DB 316 KVGNI-FVALKSIQRIQK-----IPALGETSRSSSFQHEMSQEGFSSALSMD 364

RESULT 13
US-08-605-672-53
Sequence 53, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRGTLMK 68
DB 144 PECPGEMDIAPFLIDSGSIDQSDPTQMDKDFVAKMGQLASTSTSFSLMYSNLKTHFT 203
QY 69 LTEDR-----EQIRGQLEBLQKVLPGDPTMHGEPERASQIYENRGYRTA-SVIAL 122
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQKVVELPHSKNGAKSAKKILIVI 258
QY 123 TDGELHEDLFFYSE--REANRSDLGAIYVCVGVK--FNE-TOLARI-----ADSKDHF 173
DB 259 TDQKFRDPLEYHVIPEAKA--GIRYAIQVGDVFRPTALQELNTIGSAPSDQHF 315
QY 174 PVNDGFOALQGIHSILKSCIEILAEPTICAGSFQVVGNGGFRHARNVD 227
DB 316 KVGK-FVALRSIQRIQEK---IFAIEGTESSSSSFQHMGEQSGSALSMD 364

RESULT 14
US-08-482-293A-53
Sequence 53; Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRGTLMK 68
DB 144 PECPGEMDIAPFLIDSGSIDQSDPTQMDKDFVAKMGQLASTSTSFSLMYSNLKTHFT 203
QY 69 LTEDR-----EQIRGQLEBLQKVLPGDPTMHGEPERASQIYENRGYRTA-SVIAL 122
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQKVVELPHSKNGAKSAKKILIVI 258
QY 123 TDGELHEDLFFYSE--REANRSDLGAIYVCVGVK--FNE-TOLARI-----ADSKDHF 173
DB 259 TDQKFRDPLEYHVIPEAKA--GIRYAIQVGDVFRPTALQELNTIGSAPSDQHF 315
QY 174 PVNDGFOALQGIHSILKSCIEILAEPTICAGSFQVVGNGGFRHARNVD 227
DB 316 KVGK-FVALRSIQRIQEK---IFAIEGTESSSSSFQHMGEQSGSALSMD 364

RESULT 15
US-08-943-363-53
Sequence 53; Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652

; FILING DATE: 21-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.
 ; REGISTRATION NUMBER: 38,659
 ; REFERENCE/DOCKET NUMBER: 27866/32684
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1161 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-943-363-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
 Best Local Similarity 28.2%; Pred. No. 7.4e-09;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYQ-GPDLTYFLDSSGSV-LHNMNIIYFVEQLAHKFTSPQLRMSFIVFSTRGTTLMK 68
 DB 144 PECPPGQEMDIAFLIDSSGSDPTQMDPVKALMGQLASTSTSPSLMQYSNLIKTHFT 203
 QY 69 LTEDR-----EQIRQGLELELOKVLPGADTYMHGEPERASEQIYYENRQGYRTA-SVIAL 122
 DB 204 FTFEKSLSLSPQSLVDALVQLQ-----GLYTTASGIQKVVELFHSKNGAKSAKTLIYI 258
 QY 123 TDGELHEDLFFYSE--REANRSRDLGAIYVCVVKD-FNE-TOLARI-----ADSKDHYF 173
 DB 259 TDGQKFRDPLEYRHVIPLEAKA---GIIRYALGVGDAREPTALQELINTIGSAPSDHYF 315
 QY 174 PVNDGFOALOGIHSLIKKSCIEILABPSTICAGESFOVVVRGNGFRHARNVD 227
 DB 316 KVGN-FVALRSIQRIQEK---IFAIEGTESRSSSSFOHENSQEGFSSALSHND 364

Search completed: December 14, 2005, 11:21:05
 Job time : 27.6032 secs

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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:07 ; Search time 88.8744 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536

Sequence: 1 GCGGRREDGAPCYGDFLY.....GLSFSSVITTHCSDS 295

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA Main:
1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|--------------------|
| 1 | 1536 | 100.0 | 368 | 6 US-11-047-278-2 | Sequence 2, App1 |
| 2 | 1536 | 100.0 | 403 | 3 US-09-833-245-621 | Sequence 621, App |
| 3 | 1536 | 100.0 | 564 | 3 US-09-918-715-187 | Sequence 187, App |
| 4 | 1536 | 100.0 | 564 | 3 US-09-918-715-232 | Sequence 222, App |
| 5 | 1536 | 100.0 | 564 | 4 US-10-301-822-199 | Sequence 199, App |
| 6 | 1536 | 100.0 | 564 | 4 US-10-408-765A-1823 | Sequence 1823, App |
| 7 | 1536 | 100.0 | 564 | 4 US-10-474-794-187 | Sequence 187, App |
| 8 | 1536 | 100.0 | 564 | 4 US-10-474-794-232 | Sequence 232, App |
| 9 | 1536 | 100.0 | 564 | 5 US-10-979-159-187 | Sequence 187, App |
| 10 | 1536 | 100.0 | 564 | 5 US-10-979-159-232 | Sequence 232, App |
| 11 | 1536 | 100.0 | 564 | 6 US-11-047-278-6 | Sequence 6, App1 |
| 12 | 1532 | 99.7 | 551 | 4 US-10-038-307-18 | Sequence 18, App1 |
| 13 | 1532 | 99.7 | 551 | 4 US-10-201-292-18 | Sequence 18, App1 |
| 14 | 1524 | 99.2 | 403 | 3 US-09-833-245-620 | Sequence 620, App |
| 15 | 1520 | 99.0 | 333 | 3 US-09-786-753-12 | Sequence 12, App1 |
| 16 | 1520 | 99.0 | 333 | 4 US-10-038-307-2 | Sequence 2, App1 |
| 17 | 1520 | 99.0 | 333 | 4 US-10-201-292-2 | Sequence 2, App1 |
| 18 | 1520 | 99.0 | 333 | 6 US-11-047-278-8 | Sequence 8, App1 |
| 19 | 1520 | 99.0 | 345 | 4 US-10-038-307-24 | Sequence 24, App1 |
| 20 | 1520 | 99.0 | 345 | 4 US-10-201-292-24 | Sequence 24, App1 |
| 21 | 1520 | 99.0 | 564 | 4 US-10-038-307-20 | Sequence 20, App1 |
| 22 | 1520 | 99.0 | 564 | 4 US-10-201-292-20 | Sequence 20, App1 |
| 23 | 1519 | 98.9 | 562 | 3 US-09-918-715-194 | Sequence 194, App |
| 24 | 1519 | 98.9 | 562 | 3 US-09-918-715-194 | Sequence 194, App |
| 25 | 1519 | 98.9 | 562 | 4 US-10-474-794-194 | Sequence 194, App |
| 26 | 1519 | 98.9 | 562 | 4 US-10-474-794-194 | Sequence 194, App |
| 27 | 1519 | 98.9 | 562 | 5 US-10-979-159-194 | Sequence 194, App |

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| 28 | 1519 | 98.9 | 562 | 5 US-10-979-159-301 | Sequence 301, App |
| 29 | 1507 | 98.1 | 328 | 4 US-10-038-307-26 | Sequence 26, App1 |
| 30 | 1507 | 98.1 | 328 | 4 US-10-201-292-26 | Sequence 26, App1 |
| 31 | 1505.5 | 98.0 | 342 | 4 US-10-038-307-22 | Sequence 22, App1 |
| 32 | 1505.5 | 98.0 | 342 | 4 US-10-201-292-22 | Sequence 22, App1 |
| 33 | 1500 | 97.7 | 543 | 4 US-10-038-307-16 | Sequence 16, App1 |
| 34 | 1500 | 97.7 | 543 | 4 US-10-038-307-16 | Sequence 16, App1 |
| 35 | 1500 | 97.7 | 543 | 4 US-10-201-292-16 | Sequence 16, App1 |
| 36 | 1500 | 97.7 | 543 | 4 US-10-201-292-16 | Sequence 16, App1 |
| 37 | 1490 | 97.0 | 543 | 4 US-10-038-307-10 | Sequence 10, App1 |
| 38 | 1490 | 97.0 | 543 | 4 US-10-201-292-10 | Sequence 10, App1 |
| 39 | 1479 | 96.3 | 534 | 4 US-10-038-307-12 | Sequence 12, App1 |
| 40 | 1479 | 96.3 | 534 | 4 US-10-201-292-12 | Sequence 12, App1 |
| 41 | 1419 | 92.4 | 529 | 4 US-10-201-292-36 | Sequence 36, App1 |
| 42 | 1305.5 | 85.0 | 504 | 4 US-10-201-292-32 | Sequence 32, App1 |
| 43 | 1178 | 76.7 | 479 | 4 US-10-201-292-32 | Sequence 32, App1 |
| 44 | 1064 | 69.3 | 460 | 4 US-10-201-292-28 | Sequence 28, App1 |
| 45 | 1054 | 68.6 | 460 | 4 US-10-201-292-30 | Sequence 30, App1 |

ALIGNMENTS

RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: McGridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Query Match 100.0%; Score 1536; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 76-149;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 1 | GCGGRREDGAPCYGDFLYFLIDKSGSVLHNNELIYFVEQLAHKFIISPOLMSPFVFS | 60 |
| DB | 27 | GCGGRREDGAPCYGDFLYFLIDKSGSVLHNNELIYFVEQLAHKFIISPOLMSPFVFS | 86 |
| QY | 61 | TRGTTMLKLTEDREQIRQGLEIQLKYLPGSDIYMHGCFERASQIYYENQGRITASVIT | 120 |
| DB | 87 | TRGTTMLKLTEDREQIRQGLEIQLKYLPGSDIYMHGCFERASQIYYENQGRITASVIT | 146 |
| QY | 121 | ALTDGELHEDLFFYSREARSRSDLGATVYCVGVQFNFTQLARIDSKDHPVNDGFO | 180 |
| DB | 147 | ALTDGELHEDLFFYSREARSRSDLGATVYCVGVQFNFTQLARIDSKDHPVNDGFO | 206 |
| QY | 181 | ALGGIHSILKSCIBILAEPSTICAGSFQVYVNGFRHARNDVRLCSFKINDSVT | 240 |
| DB | 207 | ALGGIHSILKSCIBILAEPSTICAGSFQVYVNGFRHARNDVRLCSFKINDSVT | 266 |
| QY | 241 | LNKPPSVEDVTLLCPAPILKEVGMKALQVSNMDGLSFSSVITTTTHCSGS | 295 |
| DB | 267 | LNKPPSVEDVTLLCPAPILKEVGMKALQVSNMDGLSFSSVITTTTHCSGS | 321 |

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RESULT 2
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Query Match          100.0%; Score 1536; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 8e-149;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGRREDGGPACYGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFISPOLMSTIVS 60
    |||||||
DB 27 GCGGRREDGGPACYGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFISPOLMSTIVS 86
    |||||||

QY 61 TRGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRASEQIYENRQGRITASVII 120
    |||||||
DB 87 TRGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRASEQIYENRQGRITASVII 146
    |||||||

QY 121 ALTDGELHEDLPFYSEREARNRSDIGAIVYCVGKDFNETQLARIADSKDHVPVNDGFO 180
    |||||||
DB 147 ALTDGELHEDLPFYSEREARNRSDIGAIVYCVGKDFNETQLARIADSKDHVPVNDGFO 206
    |||||||

QY 181 ALOGIITHSLKSCIEIILAEPSSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 240
    |||||||
DB 207 ALOGIITHSLKSCIEIILAEPSSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 266
    |||||||

QY 241 LNEKPSVEDTYLLCPAPILKEVGKKAALQVSMNDGLSFISSVITTTTHGSDGS 295
    |||||||
DB 267 LNEKPSVEDTYLLCPAPILKEVGKKAALQVSMNDGLSFISSVITTTTHGSDGS 321
    |||||||

RESULT 3
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-918-715-187

Query Match          100.0%; Score 1536; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGRREDGGPACYGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFISPOLMSTIVS 60
    |||||||
DB 27 GCGGRREDGGPACYGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFISPOLMSTIVS 86
    |||||||

QY 61 TRGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRASEQIYENRQGRITASVII 120
    |||||||
DB 87 TRGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRASEQIYENRQGRITASVII 146
    |||||||

QY 121 ALTDGELHEDLPFYSEREARNRSDIGAIVYCVGKDFNETQLARIADSKDHVPVNDGFO 180
    |||||||
DB 147 ALTDGELHEDLPFYSEREARNRSDIGAIVYCVGKDFNETQLARIADSKDHVPVNDGFO 206
    |||||||

QY 181 ALOGIITHSLKSCIEIILAEPSSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 240
    |||||||
DB 207 ALOGIITHSLKSCIEIILAEPSSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 266
    |||||||

QY 241 LNEKPSVEDTYLLCPAPILKEVGKKAALQVSMNDGLSFISSVITTTTHGSDGS 295
    |||||||
DB 267 LNEKPSVEDTYLLCPAPILKEVGKKAALQVSMNDGLSFISSVITTTTHGSDGS 321
    |||||||

RESULT 4
US-09-918-715-232
; Sequence 232, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-232

Query Match          100.0%; Score 1536; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGRREDGGPACYGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFISPOLMSTIVS 60
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DB 27 GCGGRREDGGPACYGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFISPOLMSTIVS 86
    |||||||

QY 61 TRGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRASEQIYENRQGRITASVII 120
    |||||||
DB 87 TRGTTLMKLTEDREQIROGLELOKVLPGGDTYMHGFEFRASEQIYENRQGRITASVII 146
    |||||||

QY 121 ALTDGELHEDLPFYSEREARNRSDIGAIVYCVGKDFNETQLARIADSKDHVPVNDGFO 180
    |||||||
DB 147 ALTDGELHEDLPFYSEREARNRSDIGAIVYCVGKDFNETQLARIADSKDHVPVNDGFO 206
    |||||||

QY 181 ALOGIITHSLKSCIEIILAEPSSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 240
    |||||||
DB 207 ALOGIITHSLKSCIEIILAEPSSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 266
    |||||||
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! APPLICANT: TAYLOR, STEVEN W.

UD 2 / GUGGKREDDGGFH

1 GGGKREDGGPACYGFDLIFLDKSGSVLHMNEIIIFVEQLAHKFI SPQLKMSFVFS 80

1 GGGKREDGGPACYGFDLIFLDKSGSVLHMNEIIIFVEQLAHKFISFQDKMSFVFS 80

| | | | |
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| Qy | 61 | TRGTTLMKLTTEREOIROGLEELQKVLPGSGDPTMEHGFERASQIYYENRQGRKTASVIT | 120 |
| Db | 87 | TRGTTLMKLTTEREOIROGLEELQKVLPGSGDPTMEHGFERASQIYYENRQGRKTASVIT | 146 |
| Qy | 121 | ALTDGELHEDLFFYSEBRANRSRDGAIYYCVGVKDQFNETOLARIADSKDHVFPVNDGQ | 180 |
| Db | 147 | ALTDGELHEDLFFYSEBRANRSRDGAIYYCVGVKDQFNETOLARIADSKDHVFPVNDGQ | 206 |
| Qy | 181 | ALOGIITHSLKKSCIEIILAAEPSTICAGSSFOVVYVRGNGFRHARANDRYLCSFKINDSVT | 240 |
| Db | 207 | ALOGIITHSLKKSCIEIILAAEPSTICAGSSFOVVYVRGNGFRHARANDRYLCSFKINDSVT | 266 |
| Qy | 241 | INKEPFSVEDTYLLCPAPILKEGVKAAQVSNNDGLSFSSSVITTTTHCSFGS | 295 |
| Db | 267 | INKEPFSVEDTYLLCPAPILKEGVKAAQVSNNDGLSFSSSVITTTTHCSFGS | 321 |

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US-RESULT 8
US-10-474-794-232
Publication 232, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Bred
APPLICANT: Vogelstein, Bert
APPLICANT: Kindler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPR
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 232
LENGTH: 564
TYPE: prt
ORGANISM: Homo sapiens
US-10-474-794-232

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|-----------------------|---------|--|--------|---------------|
| Query Match | 100.0%; | Score 1536; | DB 4; | Length 564; |
| Best Local Similarity | 100.0%; | Pred. No. 1.3e+18; | | |
| Matches | 295; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |
| QY | 1 | GCGGRRENGCGPACCYCGFDLYFLIDKSGSYLHMNNTYFVEGLAKFTSPOLRMSTFYPS | 60 | |
| Db | 27 | GCGGRRENGCGPACCYCGFDLYFLIDKSGSYLHMNNTYFVEGLAKFTSPOLRMSTFYPS | 86 | |
| QY | 61 | TRGTTMLKLTEDREQIROGLELQVYLPGGDTYMHGGERASEQIYENRQGYRTASVLI | 120 | |
| Db | 87 | TRGTTMLKLTEDREQIROGLELQVYLPGGDTYMHGGERASEQIYENRQGYRTASVLI | 146 | |
| QY | 121 | ALTDSLEHEDLFYSEERENRNRSDI GAYCYGVNDPNETOLARLADSDNHFFPNDDQ | 180 | |
| Db | 147 | ALTDSLEHEDLFYSEERENRNRSDI GAYCYGVNDPNETOLARLADSDNHFFPNDDQ | 206 | |
| QY | 181 | ALQGIHSILKKSCIEIILAAEPSTICAGESFOVVVRGNGFRHARVNDVRLCSFKINDSVT | 240 | |
| Db | 207 | ALQGIHSILKKSCIEIILAAEPSTICAGESFOVVVRGNGFRHARVNDVRLCSFKINDSVT | 266 | |
| QY | 241 | INERKFSVEDTYLLCPAPILKEGVKKALQVSMNDGLSTISSVITTTTHCGDGS | 295 | |
| Db | 267 | INERKFSVEDTYLLCPAPILKEGVKKALQVSMNDGLSTISSVITTTTHCGDGS | 321 | |

RESULT 9
US-10-979-159-187
; Sequence 187, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix

```

1  APPLICANT: Bert Vogelstein
2  APPLICANT: Kenneth Kinzler
3  TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
4  FILE REFERENCE: 1107_00134
5  CURRENT APPLICATION NUMBER: US/10/979,159
6  CURRENT FILING DATE: 2004-11-03
7  PRIOR APPLICATION NUMBER: US/09/919,715
8  PRIOR FILING DATE: 2001-08-01
9  PRIOR APPLICATION NUMBER: 60/222,599
10 PRIOR FILING DATE: 2000-08-02
11 PRIOR APPLICATION NUMBER: 60/224,360
12 PRIOR FILING DATE: 2000-08-11
13 PRIOR APPLICATION NUMBER: 60/282,850
14 PRIOR FILING DATE: 2000-04-11
15 NUMBER OF SEQ ID NOS: 358
16 SOFTWARE: FastSeq for Windows Version 3.0
17 SEQ ID NO 187
18 LENGTH: 564
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-10-979-159-187

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| | | | | |
|-----------------------|--------|---|------|--------------------------------|
| Query Match | 100.0% | Score 1536 | DB 5 | Length 564 |
| Best Local Similarity | 100.0% | Pred. No. 1,3e-148 | | |
| Matches | 295 | Conservative | 0 | Mismatches 0; Indels 0; Gaps 0 |
| QY | 1 | G G G G R E D G G P A C Y G G F D L Y F I L D K S G S V L H N N E I Y F V N Q L A H K F I S P O L R M S F I Y F S | 60 | |
| Db | 27 | G G G R R E D D G G P A C Y G G F D L Y F I L D K S G S V L H N N E I Y F V N Q L A H K F I S P O L R M S F I Y F S | 86 | |
| QY | 61 | T R G T T L A K T L E D R E R Q I R Q G L E E L Q K V L P G G D T Y N H G E G E R A S E O I Y Y N R Q G Y R A S Y I I | 120 | |
| Db | 87 | T R G T T L A K T L E D R R Q I R Q G L E E L Q K V L P G G D T Y N H G E R A S E Q I Y Y E N R Q G Y R A S Y I I | 146 | |
| QY | 121 | A L T D G E L H E D L F F S E R E A N R S R O L G A I Y V C V G Y K D F N E T O L A I A D S K D H V F P N D G F Q | 180 | |
| Db | 147 | A L T D G E L H E D L F F S E R E A N R S R O L G A I Y V C V G Y K D F N E T O L A I A D S K D H V F P N D G F Q | 206 | |
| QY | 181 | A L G G I I H S I L K S C I E I L L A A P S T I C A G E S F Q V V V R G N G F P H A R N V D S L C S F K I N D S V T | 240 | |
| Db | 207 | A L G G I I H S I L K S C I E I L L A A P S T I C A G E S F Q V V V R G N G F P H A R N V D S L C S F K I N D S V T | 266 | |
| QY | 241 | L N E R P E S V E D T Y L L C P A P I L K E V G M K A L Q V S N D G S L F I S S V I I T T H C S D G S | 295 | |
| Db | 267 | L N E R P E S V E D T Y L L C P A P I L K E V G M K A L Q V S N D G S L F I S S V I I T T H C S D G S | 321 | |

```

RESULT 10-159-232
US-10-979-232
Sequence 232, Application US/10979159
Publication No. US20050142138A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Kenneth Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00134
CURRENT APPLICATION NUMBER: US/10/979, 159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918, 715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222, 599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224, 360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282, 850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRF
ORGANISM: Homo sapiens

```


US-10-979-159-232

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 100.0%; | Score 1536; | DB 5; | Length 564; |
| Best Local Similarity | 100.0%; | Pred. No. 1.3e-148; | | |
| Matches 295; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | |
|----|-----|--|
| Qy | 60 | GQGGRRDDGPACGCGDLYFLIDKSGSVLHMNNELYFVEQJLAKFISPOLRMSFVFS |
| Db | 86 | GQGGRRDDGPACGCGDLYFLIDKSGSVLHMNNELYFVEQJLAKFISPOLRMSFVFS |
| Qy | 120 | TRGTTLMKLTEDBEBOJIRQGLEELQKVLPGGDTYMHGFEFRASEOIYYENROGYRTASYII |
| Db | 146 | TRGTTLMKLTEDBEBOJIRQGLEELQKVLPGGDTYMHGFEFRASEOIYYENROGYRTASYII |
| Qy | 180 | ALTDGELHEBLLPFYSEBEANRSPDQIAYCYGVQDQFNEBTQIARJADSKDHVPVNNQFO |
| Db | 206 | ALTDGELHEBLLPFYSEBEANRSPDQIAYCYGVQDQFNEBTQIARJADSKDHVPVNNQFO |
| Qy | 240 | ALOGIIHSLIKSKSCIEILAEPESTICAGESFOVVYRNGNGFRHARNVDELCSFKINDSVT |
| Db | 266 | ALOGIIHSLIKSKSCIEILAEPESTICAGESFOVVYRNGNGFRHARNVDELCSFKINDSVT |
| Qy | 295 | LNKRPFEVEETYLILCAPILIKKEGMAQALQVSMNGLSFTSSVITTTTHCSDDG |
| Db | 321 | LNKRPFEVEETYLILCAPILIKKEGMAQALQVSMNGLSFTSSVITTTTHCSDDG |

RESULT 11
US-11-047-278-6

```

1  APPLICANT: Young, Kenneth A.
2  APPLICANT: Bradley, Kenneth A.
3  APPLICANT: Collier, Robert J.
4  APPLICANT: Morigg, Jeremy S.
5  TITLE OF INVENTION: Anthrax Toxin Receptor
6  FILE REFERENCE: 960296.97745
7  CURRENT APPLICATION NUMBER: US/11/047,278
8  CURRENT FILING DATE: 2005-01-31
9  PRIOR APPLICATION NUMBER: US/09/970,076
10 PRIOR FILING DATE: 2001-10-03
11 PRIOR APPLICATION NUMBER: 60/251,481
12 PRIOR FILING DATE: 2000-12-05
13 NUMBER OF SEQ ID NOS: 10
14 SOFTWARE: PatentIn Ver. 2.1
15 SEQ ID NO 6
16 LENGTH: 564
17 TYPE: FRT
18 ORGANISM: Homo sapiens
19 US-11-047-278-6

```

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 100.0%; | Score 1536; | DB 6; | Length 564; |
| Best Local Similarity | 100.0%; | Pred. No. 1.3e+148; | | |
| Matches 295; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| Qy | 1 | G G G R R E D D G P A C G G E D L Y F I L D K S G S V L H M N E L Y F V E O L A K F I S P O L M S F V F S | 60 |
| Db | 27 | G G G R R E D D G P A C G G E D L Y F I L D K S G S V L H M N E L Y F V E O L A K F I S P O L M S F V F S | 86 |
| Qy | 61 | T R G T T L M K L T E D R E Q I R Q G L E E L Q K L P G D T Y M H G E F R A S E Q I Y E N R Q G Y T A S Y I I | 120 |
| Db | 87 | T R G T T L M K L T E D R E Q I R Q G L E E L Q K L P G D T Y M H G E F R A S E Q I Y E N R Q G Y T A S Y I I | 146 |
| Qy | 121 | A L T D G E L H E D L F P Y S E R E A N R S R D L G A I Y C V G V D F N E T Q L A R I A D S K D H V F P V N D G F Q | 180 |
| Db | 147 | A L T D G E L H E D L F P Y S E R E A N R S R D L G A I Y C V G V D F N E T Q L A R I A D S K D H V F P V N D G F Q | 206 |
| Qy | 181 | A L G G I I H S I L K S C I E I L A A P S T I C A G S F O V V Y R G C G F R A R V A D V L S F K I N S V T | 240 |
| Db | 207 | A L G G I I H S I L K S C I E I L A A P S T I C A G S F O V V Y R G C G F R A R V A D V L S F K I N S V T | 266 |
| Qy | 241 | L N E K P F S V E D T Y L L C P A P I L K E G M K A A Q V S M N D G L S F I S S V I I T T T H C S D S | 295 |

Db 267 LNEKPFSEDTYLLCPAPILKEVGKALQVSMNDGLSFSSVITTTCHSDGS 321

RESULT 12
US-10-038-307-18
; Sequence 18, Application US/10038307

```

APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKANNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-507-18

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| | | | | |
|-----------------------|----------------|--------------------|----------|------------|
| Query Match | 99.7% | Score 1532 | DB 4 | Length 551 |
| Best Local Similarity | 100.0% | Pred. No. 3.3e-148 | | |
| Matches 294 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

| | | | |
|----|-----|--|-----|
| Qy | 1 | GQGRREDGSPACYGSGFDLYFLILDSGSYLHNMNIYYEYVQLAHKFSPLQJMSFLVFS | 60 |
| Db | 27 | GQGRREDGSPACYGSGFDLYFLILDSGSYLHNMNIYYEYVQLAHKFSPLQJMSFLVFS | 86 |
| Qy | 61 | TRGTTLMKLTEDREQIRQGLEELQVLPQGDYVHGEGERASEQIYYENRGYPTASVII | 120 |
| Db | 87 | TRGTTLMKLTEDREQIRQGLEELQVLPQGDYVHGEGERASEQIYYENRGYPTASVII | 146 |
| Qy | 121 | ALTDGELHEDLPFYSSREANRSBDIGALVYCVGYGDFNEQLAIIAISKDHVPFVNGFQ | 186 |
| Db | 147 | ALTDGELHEDLPFYSSREANRSBDIGALVYCVGYGDFNEQLAIIAISKDHVPFVNGFQ | 206 |
| Qy | 181 | ALQGIHSLILKSCIEIILAAEPSTICAGSEFQVVRNGGFRHANVDRVLCSFKINDSVT | 240 |
| Db | 207 | ALQGIHSLILKSCIEIILAAEPSTICAGSEFQVVRNGGFRHANVDRVLCSFKINDSVT | 266 |
| Qy | 241 | LNKRPSPVEDTYLLCAPILKEVGKAAIQVSNADGLSFISSVYITTTTHSDG | 294 |
| Db | 267 | LNKRPSPVEDTYLLCAPILKEVGKAAIQVSNADGLSFISSVYITTTTHSDG | 320 |

RESULT 13
US-10-201-292-18
; Sequence 18, Application US/10201292
; Publication No. US2003014193A1

```

APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKANNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-18

```

| | | | | |
|-----------------------|---------|---------------------|-------|-------------|
| Query Match | 99.7%; | Score 1532; | DB 4; | Length 551; |
| Best Local Similarity | 100.0%; | Pred. No. 3.3e-148; | | |

| | Matches | 294; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|---------|------|--------------|----|------------|----|--------|----|------|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|---|---|---|---|---|----|---|---|---|---|---|-----|-----|-----|
| QY | 1 | G | G | G | R | R | E | D | G | G | A | C | G | G | E | D | L | L | F | I | D | S | G | S | V | L | H | N | N | E | I | Y | F | V | E | L | A | K | T | S | P | O | L | R | M | S | F | I | S | 60 | | | | | | | | |
| Db | 27 | G | G | G | R | R | E | D | G | G | A | C | G | G | E | D | L | L | F | I | D | S | G | S | V | L | H | N | N | E | I | Y | F | V | E | L | A | K | T | S | P | O | L | R | M | S | F | I | S | 86 | | | | | | | | |
| QY | 61 | T | R | G | T | T | L | M | K | L | T | D | R | E | D | R | E | O | I | R | O | G | L | E | L | O | K | V | L | P | G | D | T | V | M | E | G | E | R | A | S | E | O | I | Y | E | N | R | O | G | T | R | A | S | V | I | 120 | |
| Db | 87 | T | R | G | T | T | L | M | K | L | T | D | R | E | D | R | E | O | I | R | O | G | L | E | L | O | K | V | L | P | G | D | T | V | M | E | G | E | R | A | S | E | O | I | Y | E | N | R | O | G | T | R | A | S | V | I | 146 | |
| QY | 121 | A | L | T | O | G | E | L | H | E | D | I | F | E | Y | S | E | R | E | N | R | S | R | D | G | A | I | V | C | V | G | V | D | F | M | E | T | O | L | A | R | I | A | D | S | K | D | H | F | P | N | D | E | F | O | 180 | | |
| Db | 147 | A | L | T | O | G | E | L | H | E | D | I | F | E | Y | S | E | R | E | N | R | S | R | D | G | A | I | V | C | V | G | V | D | F | M | E | T | O | L | A | R | I | A | D | S | K | D | H | F | P | N | D | E | F | O | 206 | | |
| QY | 181 | A | L | O | G | I | H | S | I | L | K | K | S | C | I | E | I | L | A | A | B | P | S | T | I | C | A | G | S | P | O | V | V | R | G | N | G | F | R | I | A | R | N | D | R | V | L | C | S | F | K | I | N | D | S | V | T | 240 |
| Db | 207 | A | L | O | G | I | H | S | I | L | K | K | S | C | I | E | I | L | A | A | B | P | S | T | I | C | A | G | S | P | O | V | V | R | G | N | G | F | R | I | A | R | N | D | R | V | L | C | S | F | K | I | N | D | S | V | T | 266 |
| QY | 241 | L | N | E | K | P | S | V | E | D | I | L | C | P | A | P | L | K | E | V | G | K | A | L | O | V | M | N | G | S | P | I | S | S | V | I | T | T | H | C | S | D | G | 294 | | | | | | | | | | | | | | |
| Db | 267 | L | N | E | K | P | S | V | E | D | I | L | C | P | A | P | L | K | E | V | G | K | A | L | O | V | M | N | G | S | P | I | S | S | V | I | T | T | H | C | S | D | G | 320 | | | | | | | | | | | | | | |

| QY | DB | Query Match | Best Local Similarity | Matches | Conservative | Indels | Gaps |
|----|----|---|--------------------------------------|---------|--------------|--------|------|
| QY | DB | 1 GGGGRRDGGPACYGFPDIYFLIDSGSVLHHMNEIYYVEQLANKFISPOLRMSFIYVS 60 | 99.2%; Score 1524; DB 3; Length 403; | | | | |
| QY | DB | 27 GGGGRRDGGPACYGFPDIYFLIDSGSVLHHMNEIYYVEQLANKFISPOLRMSFIYVS 86 | 99.2%; Score 1524; DB 3; Length 403; | | | | |
| QY | DB | 61 TRGTTLMKLTBEREOIRQGLLELQKVLPGGDTYMHGGEFRASEQIYYENRQGRTPASVIT 120 | 99.2%; Score 1524; DB 3; Length 403; | | | | |
| QY | DB | 87 TRGTTLMKLTBEREOIRQGLLELQKVLPGGDTYMHGGEFRASEQIYYENRQGRTPASVIT 146 | 99.2%; Score 1524; DB 3; Length 403; | | | | |
| QY | DB | 121 ALTDDELHEDLFYFSEREANRSDIGAIVYCVGVNDNETQIARIADSKDHFVPVNDGQ 180 | 99.2%; Score 1524; DB 3; Length 403; | | | | |

| | | | |
|----|-----|--|-----|
| Db | 147 | ALDGLSLHEDLFFYSREANRNRDGLAXCYGVVDENETGLARIADSKOHVFPVNDGQ | 206 |
| Qy | 181 | ALGGIITHSLIKSCIEIILAEPSTTCAGSEFOVYVRNGGFHARNVDRLCSFKINDSVT | 240 |
| Db | 207 | ALGGIITHSLIKSCIEIILAEPSTTCAGSEFOVYVRNGGFHARNVDRLCSFKINDSVT | 266 |
| Qy | 241 | LNKRPSEVDYTLCPAPILKEVGKAKALQVSMNDGLSFISSVIITTHCSDS | 295 |
| Db | 267 | LNKRPSEVDYTLCPAPILKEVGKAKALQVSMNDGLSFISSVIITTHCSDS | 321 |

```

1      RESULT 15
2      US-09-796-753-12
3      ; Sequence 12, Application US/09796753
4      ; Publication No. US20030027998A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: McCarthy, Sean A.
7      ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
8      ; FILE REFERENCE: 7853-227-999
9      ; CURRENT APPLICATION NUMBER: US/09/796,753
10     ; CURRENT FILING DATE: 2001-03-01
11     ; PRIOR APPLICATION NUMBER: 09/183,175
12     ; PRIOR FILING DATE: 1998-10-30
13     ; PRIOR APPLICATION NUMBER: 09/223,094
14     ; PRIOR FILING DATE: 1998-12-30
15     ; PRIOR APPLICATION NUMBER: 09/223,546
16     ; PRIOR FILING DATE: 1998-12-30
17     ; PRIOR APPLICATION NUMBER: 09/224,246
18     ; PRIOR FILING DATE: 1998-12-30
19     ; PRIOR APPLICATION NUMBER: 09/259,388
20     ; PRIOR FILING DATE: 1999-02-26
21     ; PRIOR APPLICATION NUMBER: 60/122,458
22     ; PRIOR FILING DATE: 1999-03-01
23     ; PRIOR APPLICATION NUMBER: 09/312,359
24     ; PRIOR FILING DATE: 1999-05-14
25     ; PRIOR APPLICATION NUMBER: 09/336,536
26     ; PRIOR FILING DATE: 1999-06-10
27     ; PRIOR APPLICATION NUMBER: 09/342,687
28     ; PRIOR FILING DATE: 1999-06-29
29     ; PRIOR APPLICATION NUMBER: 09/345,464
30     ; PRIOR FILING DATE: 1999-06-30
31     ; PRIOR APPLICATION NUMBER: 09/365,164
32     ; PRIOR FILING DATE: 1999-07-30
33     ; PRIOR APPLICATION NUMBER: 09/399,723
34     ; PRIOR FILING DATE: 1999-09-20
35     ; PRIOR APPLICATION NUMBER: 09/409,634
36     ; PRIOR FILING DATE: 1999-09-30
37     ; PRIOR APPLICATION NUMBER: 09/471,179
38     ; PRIOR FILING DATE: 1999-12-23
39     ; PRIOR APPLICATION NUMBER: 09/474,071
40     ; PRIOR FILING DATE: 1999-12-29
41     ; PRIOR APPLICATION NUMBER: 09/474,072
42     ; PRIOR FILING DATE: 1999-12-29
43     ; PRIOR APPLICATION NUMBER: 09/514,010
44     ; PRIOR FILING DATE: 2000-02-25
45     ; PRIOR APPLICATION NUMBER: 09/516,745
46     ; PRIOR FILING DATE: 2000-03-01
47     ; PRIOR APPLICATION NUMBER: 09/572,002
48     ; PRIOR FILING DATE: 2000-05-14
49     ; PRIOR APPLICATION NUMBER: 09/597,993
50     ; PRIOR FILING DATE: 2000-06-19
51     ; PRIOR APPLICATION NUMBER: 09/599,596
52     ; PRIOR FILING DATE: 2000-06-22
53     ; PRIOR APPLICATION NUMBER: 09/630,334
54     ; PRIOR FILING DATE: 2000-07-31
55     ; PRIOR APPLICATION NUMBER: 09/606,565
56     ; PRIOR FILING DATE: 2000-06-29
57     ; PRIOR APPLICATION NUMBER: 09/606,317
58     ; PRIOR FILING DATE: 2000-06-29
59     ; PRIOR APPLICATION NUMBER: 09/665,666
60     ; PRIOR FILING DATE: 2000-09-20
61     ; PRIOR APPLICATION NUMBER: 09/677,751

```

; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12

Query Match 99.0%; Score 1520; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.7e-147;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | G G G R R E D G G P A C Y G F D L Y F I L D K S G S V L H M N E I Y F V E Q L A H K F I S P Q L R M S F I V F S | 60 |
| Db | 27 | G G G R R E D G G P A C Y G F D L Y F I L D K S G S V L H M N E I Y F V E Q L A H K F I S P Q L R M S F I V F S | 86 |
| Qy | 61 | T R G T T L M K L T E D R E Q I R Q G L E L O K V L P G G D T Y M H E G F E R A S E Q I Y Y E N R Q G R T A S V I I | 120 |
| Db | 87 | T R G T T L M K L T E D R E Q I R Q G L E L O K V L P G G D T Y M H E G F E R A S E Q I Y Y E N R Q G R T A S V I I | 146 |
| Qy | 121 | A L T D G E L H E D L F F Y S E R E A N R S R D L G A I V Y C V G K D F N E T Q L A R I A D S K D H V F P V N D G F Q | 180 |
| Db | 147 | A L T D G E L H E D L F F Y S E R E A N R S R D L G A I V Y C V G K D F N E T Q L A R I A D S K D H V F P V N D G F Q | 206 |
| Qy | 181 | A L O G I I H S I L K K S C I E I L A A P S T I C A G E S F Q V V V R N G F R H A N V D R V L C S F K I N D S V T | 240 |
| Db | 207 | A L O G I I H S I L K K S C I E I L A A P S T I C A G E S F Q V V V R N G F R H A N V D R V L C S F K I N D S V T | 266 |
| Qy | 241 | L N E K P F S V E D T Y L I C P A P I L K E V G M K A A L Q V S M N D G L S F I S S V I T T H C S | 292 |
| Db | 267 | L N E K P F S V E D T Y L I C P A P I L K E V G M K A A L Q V S M N D G L S F I S S V I T T H C S | 318 |

Search completed: December 14, 2005, 11:58:59
Job time : 90.0411 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 4.33534 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536
Sequence: 1 GGGRRDDGGPACYGGFGLY.....GLSFSSSVITTTTCSDDG 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA New:
1: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB pep: *
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB pep: *
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB pep: *
4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB pep: *
5: /cgn2_6/prodata/1/pubpaa/PCR_NEW_PUB pep: *
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB pep: *
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB pep: *
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1 | 1536 | 100.0 | 564 | US-11-186-284-199 | Sequence 199, App |
| 2 | 145.5 | 9.5 | 1152 | US-11-080-026-4 | Sequence 4, Appl |
| 3 | 131 | 8.5 | 3063 | US-11-186-284-26 | Sequence 26, Appl |
| 4 | 113.5 | 7.4 | 739 | US-11-057-047-2 | Sequence 2, Appl |
| 5 | 113.5 | 7.4 | 764 | US-11-057-047-1 | Sequence 1, Appl |
| 6 | 113.5 | 7.4 | 798 | US-10-821-234-1034 | Sequence 1034, Ap |
| 7 | 113.5 | 7.4 | 915 | US-10-131-826A-294 | Sequence 294, App |
| 8 | 113.5 | 7.4 | 956 | US-11-113-424-39 | Sequence 39, Appl |
| 9 | 111 | 7.2 | 1141 | US-10-601-368-24 | Sequence 24, Appl |
| 10 | 111 | 7.2 | 1166 | US-10-601-368-22 | Sequence 22, Appl |
| 11 | 111 | 7.2 | 1188 | US-10-601-368-21 | Sequence 21, Appl |
| 12 | 110.5 | 7.2 | 761 | US-11-057-047-6 | Sequence 6, Appl |
| 13 | 107 | 7.0 | 1141 | US-10-601-368-6 | Sequence 6, Appl |
| 14 | 107 | 7.0 | 1166 | US-10-601-368-4 | Sequence 4, Appl |
| 15 | 107 | 7.0 | 1188 | US-10-601-368-3 | Sequence 3, Appl |
| 16 | 107 | 7.0 | 1188 | US-11-000-463-338 | Sequence 338, App |
| 17 | 107 | 7.0 | 1188 | US-11-000-463-810 | Sequence 810, App |
| 18 | 104.5 | 6.8 | 828 | US-10-995-561-983 | Sequence 983, App |
| 19 | 104.5 | 6.8 | 918 | US-10-995-561-981 | Sequence 981, App |
| 20 | 104.5 | 6.8 | 1019 | US-10-995-561-982 | Sequence 982, App |
| 21 | 103.5 | 6.7 | 182 | US-10-601-368-25 | Sequence 25, Appl |
| 22 | 100 | 6.5 | 678 | US-11-102-240-34 | Sequence 34, Appl |
| 23 | 99.5 | 6.2 | 182 | US-10-601-368-7 | Sequence 7, Appl |
| 24 | 95.5 | 6.2 | 1179 | US-11-097-125-1 | Sequence 1, Appl |
| 25 | 95.5 | 6.2 | 1196 | US-10-995-561-921 | Sequence 921, App |

| | | | | | |
|----|------|-----|------|--------------------|-------------------|
| 26 | 95 | 6.2 | 1167 | US-11-097-125-2 | Sequence 2, Appl |
| 27 | 94 | 6.1 | 353 | US-11-137-465-44 | Sequence 44, Appl |
| 28 | 94 | 6.1 | 448 | US-11-137-465-45 | Sequence 45, Appl |
| 29 | 91.5 | 6.0 | 627 | US-10-467-657-5432 | Sequence 5432, Ap |
| 30 | 91 | 5.9 | 1167 | US-10-601-368-18 | Sequence 18, Appl |
| 31 | 91 | 5.9 | 1062 | US-10-513-786-2 | Sequence 2, Appl |
| 32 | 82 | 5.3 | 1804 | US-10-513-786-2 | Sequence 2, Appl |
| 33 | 81 | 5.3 | 3704 | US-10-513-786-1 | Sequence 1, Appl |
| 34 | 79.5 | 5.2 | 904 | US-10-507-275-5 | Sequence 5, Appl |
| 35 | 77.5 | 5.0 | 319 | US-10-793-626-1040 | Sequence 1040, Ap |
| 36 | 77.5 | 5.0 | 415 | US-10-763-712A-25 | Sequence 25, Appl |
| 37 | 77.5 | 5.0 | 436 | US-10-763-712A-5 | Sequence 5, Appl |
| 38 | 76.5 | 5.0 | 1798 | US-10-995-561-1003 | Sequence 1003, Ap |
| 39 | 76.5 | 5.0 | 1798 | US-10-995-561-1033 | Sequence 1034, Ap |
| 40 | 76 | 4.9 | 469 | US-10-467-657-4370 | Sequence 4370, Ap |
| 41 | 75.5 | 4.9 | 1933 | US-10-523-912-2 | Sequence 2, Appl |
| 42 | 74 | 4.8 | 384 | US-10-510-386-158 | Sequence 158, App |
| 43 | 74 | 4.8 | 509 | US-10-793-626-2880 | Sequence 2880, Ap |
| 44 | 74 | 4.8 | 619 | US-10-999-886-3 | Sequence 3, Appl |
| 45 | 74 | 4.8 | 640 | US-10-999-886-4 | Sequence 4, Appl |

ALIGNMENTS

| | |
|--|--|
| RESULT 1 | |
| US-11-186-284-199 | |
| Sequence 199, Application US/11186284 | |
| Publication No. US2005026493A1 | |
| GENERAL INFORMATION: | |
| APPLICANT: Millennium Pharmaceuticals, Inc. | |
| APPLICANT: Berger, Allison | |
| APPLICANT: Guillemette, Tracy L. | |
| APPLICANT: Kametkar, Shubhanga | |
| APPLICANT: Schlegel, Robert | |
| APPLICANT: Monahan, John E. | |
| APPLICANT: Thibodeau, Stephen N. | |
| APPLICANT: Burgart, Lawrence J. | |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND | |
| METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND | |
| THERAPY OF COLON CANCER | |
| FILE REFERENCE: MEMO1-029P2RM | |
| CURRENT APPLICATION NUMBER: US/11/186,284 | |
| CURRENT FILING DATE: 2005-07-21 | |
| PRIOR APPLICATION NUMBER: US/10/301,822 | |
| PRIOR FILING DATE: 2002-11-21 | |
| PRIOR APPLICATION NUMBER: US 60/339,971 | |
| PRIOR FILING DATE: 2001-12-10 | |
| PRIOR APPLICATION NUMBER: US 60/361,978 | |
| PRIOR FILING DATE: 2002-03-05 | |
| PRIOR APPLICATION NUMBER: US 60/381,988 | |
| PRIOR FILING DATE: 2002-05-20 | |
| NUMBER OF SEQ ID NOS: 228 | |
| SOFTWARE: FastSeq for Windows Version 4.0 | |
| SEQ ID NO 199 | |
| LENGTH: 564 | |
| TYPE: PRT | |
| ORGANISM: Homo Sapiens | |
| US-11-186-284-199 | |
| Query Match | |
| Best Local Similarity 100.0%; Score 1536; DB 7; Length 564; | |
| Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 GGGRRDDGGPACYGGFGLYFLIDKSGSVLHNNELIYFVEQLAHKFIISPOLMSFIVFS 60 |
| DB | 27 GGGRRDDGGPACYGGFGLYFLIDKSGSVLHNNELIYFVEQLAHKFIISPOLMSFIVFS 86 |
| QY | 61 TRGTTMLKLTEDNEQIRGIEELQKYLPGDDTYMHGCFEASQIYYENQGRITASVIT 120 |
| DB | 87 TRGTTMLKLTEDNEQIRGIEELQKYLPGDDTYMHGCFEASQIYYENQGRITASVIT 146 |
| QY | 121 ALTDGELHEDLFYSEBENRSDLAIVYCVGKDFNFRQLARIADSKDHVPVNDGFQ 180 |

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Db 147 ALDGLHEDLPFYSESRANRSDLAIVYCVKDFNETQLARIADSKDHVPVNDGQ 206
|||
Qy 181 ALOGIHSLIKKSCITIIAEPSTICAGSEFOVYVNGNGRRARNDRVLCSEKINDSVT 240
|||
Db 207 ALOGIHSLIKKSCITIIAEPSTICAGSEFOVYVNGNGRRARNDRVLCSEKINDSVT 266
|||
Qy 241 LNEKPSVEDTYLCCAPILKEVGMKAALOVSNNDGLSFISSEVITTTTHCSDGS 295
|||
Db 267 LNEKPSVEDTYLCCAPILKEVGMKAALOVSNNDGLSFISSEVITTTTHCSDGS 321
|||

RESULT 2
US-11-080-026-4
; Sequence 4, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CFBP-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-026-4

Query Match 9.5%; Score 145.5; DB 7; Length 1152;
Best Local Similarity 26.2%; Pred. No. 1.1e-05;
Matches 60; Conservative 45; Mismatches 81; Indels 43; Gaps 12;

Qy 18 DLYFIIDKSGSV-LHNMNIYFVEQLAKHP-ISPQLRMSFIVSTRTGTLMLKLTED- 72
|||
Db 150 DIAFLIDGSGSIIPIHPRRKKEFVST-----VMEQLKSKSLRPS-----LMQSESEFRH 199
|||
Qy 73 -----RQIQGLELEOKVLP-GSDTYMHGEPERASEQIYYENRQGYTA-SVITIALT 123
|||
Db 200 FTPEKQNNPNPRLSLVLPITQLL--GRTHTATGIRKVRRELFNITNGARKNAFKILVIT 257
|||
Qy 124 DGEIHEDLPFYSE--REANRSRDLAGIVYCVKDFNETQLAR-----IADS--KDHVPF 174
|||
Db 258 DGEKFDPLGEYEDVPEADRE--GVIRYVIGVDAPRSKSKQELANTISKPEPRDHFQ 314
|||
Qy 175 VNDGFOALOGIHSILIKKSCITIIAEPSTICAGSEFOVYVNGNGRRHA 223
|||
Db 315 VNN-FEALKTQIQNLRK-----IFAIRGTQTGSSSSPSEHMSQEGFSA 358
|||

RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangt
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
```

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; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Query Match 8.5%; Score 131; DB 7; Length 3063;
Best Local Similarity 29.8%; Pred. No. 0.00099;
Matches 59; Conservative 38; Mismatches 75; Indels 26; Gaps 13;

Qy 18 DLYFIIDKSGSV-LHNMNIYFVEQLAKHP-ISPQLRMSFIVSTRTGTLMLKLTB 71
|||
Db 440 DIVFLVDGSYSIGIANFVVKRAFLVLYKSFESIPRVQISLVQVSRDPDTEFTLKKFTK 499
|||
Qy 72 DGEIQGLELEOKVLP--GSDTYMHGEPERASEQIYYENRQGYR--ASVITIALDDEL 127
|||
Db 500 VEDII-----EAINTFPYRGSTNGKANTYVREKLFVSK-GSRNVPRKWLITDGR- 552
|||
Qy 128 HEDLPFYSESRANRSDLAIVYCVKDFNETQLARIAD--SKDHVPVNDGFOALOGI 185
|||
Db 553 SSDAF---RDPALKLRNSVVEIFAVGVKDAVASELEAISPPAEHTVFTVED-FDAFQRI 608
|||
Qy 186 IHSILIKKSCIEI--LAA 200
|||
Db 609 SFELTQSLCLRIEQELAA 626
|||

RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-047-2

Query Match 7.4%; Score 113.5; DB 7; Length 739;
Best Local Similarity 19.6%; Pred. No. 0.006;
Matches 66; Conservative 63; Mismatches 109; Indels 99; Gaps 17;
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0Y      2 OGGREDG-GPA-----CYGPFILFLIDSGSV-----LHMNEIYFVEOLAH 45
Db      218 EGVADBDHGHPGEOOKRKIVLDPSGSMMIYVLVDSDSIGASNFTGAKKCLVNLIEKAS 277
0Y      46 KFI$POLMSFVIF$TRGTTLMKLT-----DREOIRQOLEEL-----OKVLPGSDTYMHG 97
Db      278 YGVK--RYGLVTVATYPIKWIKVSEAOSSNADWTKOLNEINETHDKLKGSTYT----- 330
0Y      98 FERASEQIYENR-----OGY-RTASVITIALTDG-----ELHEDLFPFYSE 136
Db      331 -KKAQVAYVSMMSWPDVBPPEGMRNTRVITILMTDGLHNMGGDPITVIDELRDLYIGKD 389
0Y      137 REARNSRDLGAIYVYG--VKDFNETOLARIADSDOHVPYNDGFOALQGIHSLTKKSC 194
Db      390 RKNPREDYLDVYFVGVGLVNOVINNALASKKDNQOHFKYKD--MENLEDVFOYOMIDES- 447
0Y      195 IEILAA$PTICAGESFOVVVRGNGFRHARHVRDRLG$PKINDSVTLNEKRF$VEDPYLL 254
Db      448 -----Q$LSLJC-----GMWVERRKGD-----YHKOPWAKTISV- 476
0Y      255 CPAPILKEVGMKALQVSMNDGL$FIS$SVIITTHC 291
Db      477 -----IRPSKGH$SCMG-----AV$SEYFVITAAHC 502

```

```

RESULT 5
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-047-1

Query Match          7 4*: Score 113.5; DB 7; Length 764;
Beet Local Similarity 19.6%; Fred. No. 0.0062;
Matches 66; Conservative 63; Mismatches 109; Indels 99; Gaps 17;

QY      2  QGGRREDS-GPA-----CYGGFDLYFLDKSGSV-----LHHNNEIYYFVEQLAH 45
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      243 EGVADAEHDHGEGEQQRKIVLDPGSGMWIYLVLOSSDSIGASNFTGAKKCLVNIIEKVAS 302
QY      46  KPIISQILMSPIVSTRTGTTLMKLT---DREQIRQGLEL---QKVLFGSGDTYMHG 97
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      303 YGVAK--RYGLVYATYATYPRKIWKVSEADSSNADWYTKQLININEDHKLKSGTWT----- 355
QY      98  FERASEQIYENR-----QGY-RTASVITIALFDG-----ELHEDLFFYSE 136
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      356 -KKALQAYYSMMSWPDDVPRPEGKMRITRIVIIIMTDGGLHNMGGDPITVIDEIRDLILYIKD 414
QY      137 REANRSRLGAIIVCVG--VKDFNETQIARIADSKDHVFPVNDGFRQALQGIINSLKSC 194
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

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Db      415 RKRPRADYLDVVYFGVGLPQVNNALASKKQNEQHFKYKD-MENLEDVFYQIMDES- 4724
Qy      195 IETLAAPSTICAGSFQVVYVNGNGFRHARNDVRLGSEFKINDSVTNNKPFSEDDYLL 254
Db      473 -----QSLSLC-----GMWHEIRKGD-----YHKQWQAKISV-- 501
Qy      255 CPAPILKEVGMKRALQVMSNDGLSTISSVITTHC 291
Db      502 ----IRPSKHESCMG-----AVSEYFVTLAHC 527

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```

RESULT 6
US-10-821-234-1034
; Sequence 1034, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1034
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1034

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Query Match      7.4%; Score 113.5; DB 6; Length 798;
Best Local Similarity 19.6%; Pred. No. 0.0066;
Matches 66; Conservative 63; Mismatches 109; Indels 99; Gaps 17;

QY      2 QCGRRBDG-GPA-----CYGFDLYFLIDKSGSV-----LHHMNEYFYVEQLAH 45
           ||| | | | | | : : : | | | : : | : |
DB      277 EGVDAEDHGHDGEQQKKRIVLDPGSGNNIYLVLDGSDSIGASNFTGAKCCLVNLIERVAS 336
           ||| | | | | | : : : | | | : : | : |
QY      46 KFIISPOLRMSEFYFSTGTTLMKLTE---DREDIRQGLEEL---OKVLPGSDTYMHEG 97
           : : : : : : : : : : : : : : : :
DB      337 YGVNP--RYGLVTATYATPKIMVKVSEADSSNAPWTVTKQLNEINVEDHKLSGNT----- 389
           : : : : : : : : : : : : : : : :
QY      98 FERRASEDIYYENR-----QG-Y-RTASVILALTDG-----ELHEDLFYSYE 136
           : : : : : : : : : : : : : : : :
DB      390 -KKRLQAVVMYSMMSPDDVPPEGMWRIRHYIIILMTGDGHANNGBDEITVIDEIRDLVYGKD 448
           : : : : : : : : : : : : : : : :
QY      137 REANRSRDLAGIAYCVG--VKDFNETOLAIADSKDVFPVNDGFQALOGIIHSILKSC 194
           | : | : | : | : | : | : | : | : | : |
DB      449 RKNREBYLDVIVPVGVELVNQNINMLASKDNCEGVHFVKD-METLEDVFQIMDES- 506
           : : : : : : : : : : : : : : : :
QY      195 IEIIAAEPSTICAGESFOVVVRNGNFHAARVDVLCFSKINDSVTINEKPFSEVEDTYLL 254
           : : : : : : : : : : : : : : : :
DB      507 -----QSLSLC-----GWVMEHRKGTD-----YHKPMQAKTSV-- 535
           : : : : : : : : : : : : : : : :
QY      255 CPAPILKEVGMKALQVSMNDGSFLISSYIIITTHC 291
           : : : : : : : : : : : : : : : :
DB      536 ----IRPSKGHEGCMG-----AAYSEYFVLTPAAC 561
           : : : : : : : : : : : : : : : :

RESULT 7
US-10-131-826A-294
; Sequence 294, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Deenoyez, Luc
; APPLICANT: Filvaroff, Ellen
```

```
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerltse, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining prior application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 294
/ LENGTH: 915
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-294

Query Match      7.4%; Score 113.5; DB 6; Length 915;
Best Local Similarity 22.4%; Pred. No. 0.008;
Matches 55; Conservative 53; Mismatches 103; Indels 35; Gaps 13;

QY 18 DLYFIIDKSGSV-LHHMNEIYVF-VEQLAHKFIISPOL-RMSFVIFSTRTGTL-----MKL 69
DB 57 DLVFIIDSSRSVNTHYAKKEFIYDILQFLDIGPVTYVGLQY---GSTVKNBSLKT 113
QY 70 TEDREQIQGLELEQVLPQGDITYMEGFERASEQIYYENRQYR-----TASVITALTLD 124
DB 114 FKXKSEVERAVKMRHLSTGWTGLAIQY---ALNTAFSEAGARPLRENVPRVIMVTD 170
QY 125 GEIHEDLFFYSEERARSRLDGAIVYCVGV--KDFNETQLARLADSKDHFPPVNDGQAL 182
DB 171 GRPQDSV---AEVAAKARDTGILIFAIQGVQVDFNTLKSIGSEPHEDHVFVLAN--FSQI 225
QY 183 QGIHHSILKKSCTEILAAEPSTICAGESFOVWVRGNGFRHAR-----NVDRLCSFKIND 237
DB 226 ETLTSVFOKKLCTRAHMCSTLEHNC--HFCINIPGSYVCRCKQGYILNSQDTTC--RIQD 281
QY 238 SVTLNE 243
DB 282 LCAMED 287

RESULT 8
US-11-113-424-39
/ Sequence 39, Application US/11113424
```

```
/ Publication No. US20050260713A1
/ GENERAL INFORMATION:
/ APPLICANT: Gangolli et al.
/ TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-225
/ CURRENT APPLICATION NUMBER: US/11/113,424
/ PRIOR FILING DATE: 2005-04-21
/ PRIOR APPLICATION NUMBER: 60/256,704
/ PRIOR FILING DATE: 2000-12-19
/ PRIOR APPLICATION NUMBER: 60/311,590
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/257,314
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 60/311,613
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/315,617
/ PRIOR FILING DATE: 2001-08-29
/ PRIOR APPLICATION NUMBER: 60/307,506
/ PRIOR FILING DATE: 2001-07-24
/ PRIOR APPLICATION NUMBER: 60/322,358
/ PRIOR FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: 60/294,075
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 60/288,153
/ PRIOR FILING DATE: 2001-05-02
/ NUMBER OF SEQ ID NOS: 190
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 956
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-113-424-39

Query Match      7.4%; Score 113.5; DB 7; Length 956;
Best Local Similarity 22.4%; Pred. No. 0.0085;
Matches 55; Conservative 53; Mismatches 103; Indels 35; Gaps 13;

QY 18 DLYFIIDKSGSV-LHHMNEIYVF-VEQLAHKFIISPOL-RMSFVIFSTRTGTL-----MKL 69
DB 57 DLVFIIDSSRSVNTHYAKKEFIYDILQFLDIGPVTYVGLQY---GSTVKNBSLKT 113
QY 70 TEDREQIQGLELEQVLPQGDITYMEGFERASEQIYYENRQYR-----TASVITALTLD 124
DB 114 FKXKSEVERAVKMRHLSTGWTGLAIQY---ALNTAFSEAGARPLRENVPRVIMVTD 170
QY 125 GEIHEDLFFYSEERARSRLDGAIVYCVGV--KDFNETQLARLADSKDHFPPVNDGQAL 182
DB 171 GRPQDSV---AEVAAKARDTGILIFAIQGVQVDFNTLKSIGSEPHEDHVFVLAN--FSQI 225
QY 183 QGIHHSILKKSCTEILAAEPSTICAGESFOVWVRGNGFRHAR-----NVDRLCSFKIND 237
DB 226 ETLTSVFOKKLCTRAHMCSTLEHNC--HFCINIPGSYVCRCKQGYILNSQDTTC--RIQD 281
QY 238 SVTLNE 243
DB 282 LCAMED 287

RESULT 9
US-10-601-368-24
/ Sequence 24, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ CURRENT APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
```


NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1141
TYPE: PRT
ORGANISM: Mus musculus
US-10-601-368-24

Query Match 7.2%; Score 111; DB 6; Length 1141;
Best Local Similarity 24.1%; Pred. No. 0.019;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 13 CYGFDLYFLIDKSGSVLHMNEIYFVEQLAHKF-ISP-QLRMSFVSTRTGTTLMKLT 70
DB 159 CQYMDIVYLDGNSI-YPMVEVQHFLINILKKFYIGPQIQVGIQYGEDAVHERFL- 216
QY 71 EDREQIRQGLEBLQKVLPGSDTYMHGFE--RASEQIYYENRGYRTASVIALTDGEL 127
DB 217 NDYRSVQDVVEASHIEQRGTEFRTAFGIEFARSEAFQKGRKAK--KVMIVITDGS 274
QY 128 HED-----LFFYSERANRSDGAIYVCVVD---FNETQ 161
DB 275 HDSPDLEKVIROSEKDNVTRYAVAVLGYNRRGINPETFLNEIKYIASDPDKHFFNVTD 334
QY 162 LARIADSKDHVPVNDGFOALOG 184
DB 335 EAML---KDIVDALGDRIFSLG 354

RESULT 10
US-10-601-368-22
Sequence 22; Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 1166
TYPE: PRT
ORGANISM: Mus musculus
US-10-601-368-22

Query Match 7.2%; Score 111; DB 6; Length 1166;
Best Local Similarity 24.1%; Pred. No. 0.019;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 13 CYGFDLYFLIDKSGSVLHMNEIYFVEQLAHKF-ISP-QLRMSFVSTRTGTTLMKLT 70
DB 137 CQYMDIVYLDGNSI-YPMVEVQHFLINILKKFYIGPQIQVGIQYGEDAVHERFL- 194
QY 71 EDREQIRQGLEBLQKVLPGSDTYMHGFE--RASEQIYYENRGYRTASVIALTDGEL 127
DB 195 NDYRSVQDVVEASHIEQRGTEFRTAFGIEFARSEAFQKGRKAK--KVMIVITDGS 252
QY 128 HED-----LFFYSERANRSDGAIYVCVVD---FNETQ 161
DB 253 HDSPDLEKVIROSEKDNVTRYAVAVLGYNRRGINPETFLNEIKYIASDPDKHFFNVTD 312
QY 162 LARIADSKDHVPVNDGFOALOG 184
DB 313 EAML---KDIVDALGDRIFSLG 332

RESULT 11
US-10-601-368-21
Sequence 21; Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 1188
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-21

Query Match 7.2%; Score 111; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.02;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 13 CYGFDLYFLIDKSGSVLHMNEIYFVEQLAHKF-ISP-QLRMSFVSTRTGTTLMKLT 70
DB 159 CQYMDIVYLDGNSI-YPMVEVQHFLINILKKFYIGPQIQVGIQYGEDAVHERFL- 216
QY 71 EDREQIRQGLEBLQKVLPGSDTYMHGFE--RASEQIYYENRGYRTASVIALTDGEL 127
DB 217 NDYRSVQDVVEASHIEQRGTEFRTAFGIEFARSEAFQKGRKAK--KVMIVITDGS 274
QY 128 HED-----LFFYSERANRSDGAIYVCVVD---FNETQ 161
DB 275 HDSPDLEKVIROSEKDNVTRYAVAVLGYNRRGINPETFLNEIKYIASDPDKHFFNVTD 334
QY 162 LARIADSKDHVPVNDGFOALOG 184
DB 335 EAML---KDIVDALGDRIFSLG 354

RESULT 12
US-11-057-047-6
Sequence 6; Application US/11057047
Publication No. US20050260198A1
GENERAL INFORMATION:
APPLICANT: Holers, Vernon
APPLICANT: Thurman, Joshua
APPLICANT: Taube, Christian
APPLICANT: Gelfand, Erwin
APPLICANT: Gillespie, Gary
TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
FILE REFERENCE: 2848-66
CURRENT APPLICATION NUMBER: US/11/057,047
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,594
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/636,239
PRIOR FILING DATE: 2004-12-14
PRIOR APPLICATION NUMBER: US04/015040
PRIOR FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 761
TYPE: PRT

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/ ORGANISM: Mus musculus
US-11-057-047-6

Query Match
Best Local Similarity 20.5%; Score 110.5; DB 7; Length 761;
Matches 71; Conservative 59; Mismatches 99; Indels 117; Gaps 20;

QY 2 OGGRRDG-----GPACYGFDLYLDKSGSV-----LHNNETIY 37
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 EGADADGHSRPGQKRIYLDPS--GSNNIYVLDGSDSISGNSFTGAKRCITN----- 292
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 38 YVEQIAHKFISPOLRMSPIVSTRTGTTMLKLTEDR-----EQIRGLEELQKVLPG 89
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 -LEKVASVGRB--RYGLITVATVPKVLAVRVEDSSDDADWTETKLNQISYEDHKLKSG 349
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 90 GDTYMEGPERASEQIYY-----ENRQCY-RTASVITALTGELH-----EDL 131
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 350 TNT-----KRALQAVYSMMWAGDAPPEGMNTRHVIITMDG-LHNNGNFVTVIODI 402
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 132 FFYSE--REANRSD--LGAIVYCVG--VKDFNETQLARIADSKDHVPVNDGFOALQGI 185
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 403 RALDDIGRDPKNREYLDVYVGVGPBYDSVAINALASKDNEHVFKYKD--MEDLENV 461
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 186 IHSILKKSCEILAAEPSTICAGESFOVVVNGGFPHARNVDVLCSEFKINDSVTLNEKP 245
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 462 FYQMIDET-----KSLSLC-----GMVWEHKKGNDYHKQPMQAKISVT---RP 501
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 246 FSVEDYTLCPAPILKEVKGKALQVSMNDGLSFSSVITTTTC 291
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 502 LKGHET---CMGAV-----VSEFVLTIAHC 524
   | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-10-601-368-6
/ Sequence 6, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 1141
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-6

Query Match
Best Local Similarity 7.0%; Score 107; DB 6; Length 1141;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 13 CYGSPDYLYLDKSGSVLHNNETIYVEQLAHKF--ISP-QLRMSFIVSTRTGTTMLKLT 70
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 CQYMDIVYLDGNSNI--YPMVEVQHFLNLIKKFYIGQIQGVGVQGEDVNHFEHL- 216
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 71 EDREQIRGLEIELQKVLPGDITYMEGFE--RASEQIYYENRQGYRTASVITALTDEL 127
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 217 NDYRSVQDVVEAASHIEQRGTETRTAFGIEPARSEAFQGGKRGAK--KVMIVITDGS 274
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 HED-----LFFYSERANRSDIGAIVYCVGVKD---FRETQ 161
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 275 HDSPDLEKVIQOGERDNTVRVAVAVLGYNRRGINPETPLNEIKYIASPDDDKHFFNVTD 334
   | | | | | | | | | | | | | | | | | | | | | | | |
```

```
QY 162 LARIADSKDHVPVNDGFOALQG 184
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 335 EAAL---KDIVDALGDRIFSLBG 354
   | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
US-10-601-368-4
/ Sequence 4, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 1166
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-601-368-4

Query Match
Best Local Similarity 7.0%; Score 107; DB 6; Length 1166;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 13 CYGSPDYLYLDKSGSVLHNNETIYVEQLAHKF--ISP-QLRMSFIVSTRTGTTMLKLT 70
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 CQYMDIVYLDGNSNI--YPMVEVQHFLNLIKKFYIGQIQGVGVQGEDVNHFEHL- 194
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 71 EDREQIRGLEIELQKVLPGDITYMEGFE--RASEQIYYENRQGYRTASVITALTDEL 127
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 195 NDYRSVQDVVEAASHIEQRGTETRTAFGIEPARSEAFQGGKRGAK--KVMIVITDGS 252
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 HED-----LFFYSERANRSDIGAIVYCVGVKD---FRETQ 161
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 253 HSPDLEKVIQOGERDNTVRVAVAVLGYNRRGINPETPLNEIKYIASPDDDKHFFNVTD 312
   | | | | | | | | | | | | | | | | | | | | | | | |
QY 162 LARIADSKDHVPVNDGFOALQG 184
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 313 EAAL---KDIVDALGDRIFSLBG 352
   | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
US-10-601-368-3
/ Sequence 3, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 1188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
```

LOCATION: (1) ... (22)
US-10-601-368-3

Query Match 7.0%; Score 107; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.046;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

```

QY 13 CYGFDLYFILDKSGSVLHMHNEIYFVEQLAHKF-ISP-QLNMFIVFSTRGTTLMKLT 70
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 159 CQYMDIIVIVLDGNSNI-YFWVEVQHFLINILKKFYIGPGIQGVGVQGEDVHHEFHL- 216
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 71 EDREQIRQGLEELQKVLPGSDTYMHGFE--RASEQIYYENRQGYRTASVIALTDGEL 127
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 217 NDYRSVADVVEAASHIEQRGTEFRTAFGEFARSEAFQKGRKAK--KMIIVITDGES 274
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 128 HED-----LFFYSERANRSRDIGAIYVCVGD---FNETQ 161
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 275 HDSPDLEKVIQSERDNTRYAVAVLGYNRRGINPETFLNEIKYIASDPDDKHFFVVTD 334
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 162 LARIADSKDHVPFVNDGFOALOG 184
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 335 EAML---KDIYDALGDRIFSLEG 354
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Search completed: December 14, 2005, 11:59:27
Job time : 5.33534 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37 ; Search time 207.111 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536
Sequence: 1 GCGGREDGEGACGCGFDLY.....GLSFSSVITTTTCSGDS 295

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 88870828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.epool/US0970076/runat_14122005_11850_20999/app_query.fasta_1.2410
-DB=Issued_Patents_NA -OPMT=fastcap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=humana40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPR=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0970076_@CGN_1_1_535 @runat_14122005_11850_20999 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/1.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RB.COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1263 | 82.2 | 1609 | 3 | US-09-620-312D-8 |
| 2 | 790.5 | 51.5 | 2234 | 3 | US-10-104-047-669 |
| 3 | 709 | 46.2 | 1492 | 3 | US-09-774-528-297 |
| 4 | 709 | 46.2 | 1492 | 3 | US-10-120-988-297 |
| 5 | 662 | 43.1 | 3981 | 3 | US-09-799-451-250 |
| 6 | 166 | 10.8 | 3519 | 2 | US-08-286-889-45 |
| 7 | 166 | 10.8 | 3519 | 2 | US-08-485-618-45 |
| 8 | 166 | 10.8 | 3519 | 2 | US-08-362-652-45 |
| 9 | 166 | 10.8 | 3519 | 2 | US-08-605-672-45 |

| | | | | | | |
|----|-------|------|------|---|-------------------|-------------------|
| 10 | 166 | 10.8 | 3519 | 2 | US-08-482-293A-45 | Sequence 45, Appl |
| 11 | 166 | 10.8 | 3519 | 2 | US-08-943-363-45 | Sequence 45, Appl |
| 12 | 166 | 10.8 | 3519 | 3 | US-09-193-043-45 | Sequence 45, Appl |
| 13 | 166 | 10.8 | 3519 | 3 | US-09-688-307A-45 | Sequence 45, Appl |
| 14 | 166 | 10.8 | 3519 | 3 | US-09-350-259-45 | Sequence 45, Appl |
| 15 | 166 | 10.8 | 3803 | 2 | US-08-485-618-52 | Sequence 52, Appl |
| 16 | 166 | 10.8 | 3803 | 2 | US-08-362-652-52 | Sequence 52, Appl |
| 17 | 166 | 10.8 | 3803 | 2 | US-08-605-672-52 | Sequence 52, Appl |
| 18 | 166 | 10.8 | 3803 | 2 | US-08-482-293A-52 | Sequence 52, Appl |
| 19 | 166 | 10.8 | 3803 | 2 | US-08-943-363-52 | Sequence 52, Appl |
| 20 | 166 | 10.8 | 3803 | 3 | US-09-193-043-52 | Sequence 52, Appl |
| 21 | 166 | 10.8 | 3803 | 3 | US-09-688-307A-52 | Sequence 52, Appl |
| 22 | 166 | 10.8 | 3803 | 3 | US-09-350-259-52 | Sequence 52, Appl |
| 23 | 159.5 | 10.4 | 3528 | 2 | US-08-286-889-36 | Sequence 36, Appl |
| 24 | 159.5 | 10.4 | 3528 | 2 | US-08-485-618-36 | Sequence 36, Appl |
| 25 | 159.5 | 10.4 | 3528 | 2 | US-08-362-652-36 | Sequence 36, Appl |
| 26 | 159.5 | 10.4 | 3528 | 2 | US-08-605-672-36 | Sequence 36, Appl |
| 27 | 159.5 | 10.4 | 3528 | 2 | US-08-482-293A-36 | Sequence 36, Appl |
| 28 | 159.5 | 10.4 | 3528 | 2 | US-08-943-363-36 | Sequence 36, Appl |
| 29 | 159.5 | 10.4 | 3528 | 3 | US-09-193-043-36 | Sequence 36, Appl |
| 30 | 159.5 | 10.4 | 3528 | 3 | US-09-688-307A-36 | Sequence 36, Appl |
| 31 | 159.5 | 10.4 | 3528 | 3 | US-09-350-259-36 | Sequence 36, Appl |
| 32 | 159.5 | 10.4 | 3528 | 2 | US-08-485-618-54 | Sequence 54, Appl |
| 33 | 159.5 | 10.4 | 3528 | 2 | US-08-362-652-54 | Sequence 54, Appl |
| 34 | 159.5 | 10.4 | 3528 | 2 | US-08-605-672-54 | Sequence 54, Appl |
| 35 | 159.5 | 10.4 | 3528 | 2 | US-08-482-293A-54 | Sequence 54, Appl |
| 36 | 159.5 | 10.4 | 3528 | 2 | US-08-943-363-54 | Sequence 54, Appl |
| 37 | 159.5 | 10.4 | 3528 | 3 | US-09-193-043-54 | Sequence 54, Appl |
| 38 | 159.5 | 10.4 | 3528 | 3 | US-09-688-307A-54 | Sequence 54, Appl |
| 39 | 159.5 | 10.4 | 3528 | 3 | US-09-350-259-54 | Sequence 54, Appl |
| 40 | 156 | 10.2 | 2499 | 2 | US-08-485-618-96 | Sequence 96, Appl |
| 41 | 156 | 10.2 | 2499 | 2 | US-08-605-672-96 | Sequence 96, Appl |
| 42 | 156 | 10.2 | 2499 | 2 | US-08-482-293A-96 | Sequence 96, Appl |
| 43 | 156 | 10.2 | 2499 | 2 | US-08-943-363-96 | Sequence 96, Appl |
| 44 | 156 | 10.2 | 2499 | 3 | US-09-193-043-96 | Sequence 96, Appl |
| 45 | 156 | 10.2 | 2499 | 3 | US-09-688-307A-96 | Sequence 96, Appl |

ALIGNMENTS

RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jjian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_Fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 6.92e-154 Length: 1609
Score: 1263.00 Matches: 241
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.18% Mismatches: 0
Query Match: 82.23% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-09-620-312D-8 (1-1609)

QY 1 G1yG1ng1yG1yArgrgrgluArgrglYg1ProAlCyErYrG1yG1yPheArpLeuYr 20
Db 387 GGGCAAGGGGAGCGAGGAGGAGTGGGGTCCAGCCTGACCGCGATTGACCTGTAC 446
QY 21 PheIleuArpYserGlySerValLeuHiEtrpAnGluIleYrYrYrPheVal 40
Db 447 TTCATTTTGGCAAAATCAGAGAGTGTGCTGACCACTGGAATGAAATCTATTCTTGTG 506
QY 41 GluGluLeuAlaHiEtrpPheIleSerProGluLeuArpMeSerPheIleValPheSer 60
Db 507 GAACAGTTGGCTCAAAATTCATCAGCCACAGTGAAGATGCTTTATGTTTCTCC 566
QY 61 ThrArG1yThrThreuMeTyLeuThrGluArpArgrgluInIleArgrG1ng1yLeu 80
Db 567 ACCCGAGAAACACTTAATGAACCTGACAGAAAGACAGAAACAAATCCCTCAAGCCTA 626
QY 81 GluGluLeuGluInIleYrYrYrGluArpArgrG1ng1yYrArgrThrAlaSerValIleIle 120
Db 627 GAAGAAGTCCAGAAAGTTCTGACAGAGGAGACACTTACATGATGAAGATTGAAAG 686
QY 101 AlaSerGluGluInIleYrYrYrGluArpArgrG1ng1yYrArgrThrAlaSerValIleIle 120
Db 687 GCCAGTGAAGCATTTATTTATGAAACAGCAAGGATGACAGACAGCAGCTATCAT 746
QY 121 AlaLeuThrArpGlyGluLeuHiEtrpArpLeuPheThrYrSerGluArG1ua1AaSn 140
Db 747 GCTTGACTGATGGAAGACTCCATGAAGACTCTTTTTCATTCAGAGAGGAGCTAAT 806
QY 141 ArgSerArpArpLeuGlyAlaIleValTYrCYsValG1yValIySArpPheAnGluThr 160
Db 807 AGGTCTCGAATCTTGGTGCATTTGTTACTGTGTGTGTAAGATTTCATATGAGACA 866
QY 161 GluLeuAlaArpG1leAlaArpSerTyLeuArpHiEtrpPheProValaArpArgrlyPheGlu 180
Db 867 CAGCTGCGCGAATGCGGACAGTAAGATCATGTGTTCCCGTAATGACGCTTTCAG 926
QY 181 AlaLeuGluG1yIleIleHiSerIleLeuYlySerCYsIleGluIleLeuAlaA1a 200
Db 927 GCTCTGAAGCATCATCACTCAATTTTGAAGAGCTCGCATCGAAATTCAGAGAGCT 986
QY 201 GluProSerThrIleCYsAlaG1yG1uSerPheGluInValValArgrG1yAnG1yPhe 220
Db 987 GAACATCCACATATGTGACAGAGAGTCAATTCATCAATGTCGTAAGAGGAAACGCGCTTC 1046
QY 221 ArgHiEtrpArpArpValaArpArpValLeuCYsSerPheYlyIleAaArpSerValThr 240
Db 1047 CGACATGCCGCAACGTGACAGAGGTCTCTGACAGTTCAAGATCAATGACTCGGTACA 1106
QY 241 LeuAnGlu 243
Db 1107 CTCAGTAAG 1115

RESULT 2
US-10-104-047-669
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/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. 6943241el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIORITY FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 3.77e-92 Length: 2234
Score: 790.50 Matches: 157
Percent Similarity: 71.53% Conservative: 54
Best Local Similarity: 53.22% Mismatches: 81
Query Match: 51.46% Indels: 3
DB: 3 Gaps: 2

US-09-970-076-2_COPY_27_321 (1-295) x US-10-104-047-669 (1-2234)

QY 1 G1yG1ng1yG1y---ArgrgrgluArpGlyG1yProAlCyErYrG1yG1yPheArpLeu 19
Db 604 GGTCCCGGGGGCTGTGTGGCCGCCAGAGAGCCCTCTGCAAGAAACCTTGTATCTC 663
QY 20 YrPheIleuArpYserGlySerValLeuHiEtrpAnGluIleYrYrYrPhe 39
Db 664 TACTTGCTCTGACAGAGCTGTGAGATGTGGCAAAATCACTGATTAATTTATTTTC 723
QY 40 ValGluGluLeuAlaHiEtrpPheIleSerProGluLeuArpMeSerPheIleValPhe 59
Db 724 GTACAGCAACTTGGCGAGATTTTGAGCCCTGAAATGATATCTTCAATTTGTTT 783
QY 60 SerThrArG1yThrThreuMeTyLeuThrGluArpArgrgluInIleArgrG1ng1y 79
Db 784 TCTTCCAGCAACTATTTATTTTGGCCATTACTGAGACAGAGCAAAATCACTAAAGC 843
QY 80 LeuGluGluLeuGluInIleYrYrYrGluArpArgrG1yYrArgrThrAlaSerValIle 99
Db 844 TTGAGAGATTTTAAAGCTGTAGTCCAGTAAGAGACATATATCCATGAAGACATAAG 903
QY 100 ArgAlaSerGluGluInIleYrYrYrGluArpArgrG1ng1yYrArgrThrAlaSerValIle 119
Db 904 CTAGCGAATGAACAAATTT-----CAGAAAGCAGAGGCTTGAAACCTCCAGTATCATTA 957
QY 120 IleAlaLeuThrArpGlyGluLeuHiEtrpArpLeuPheThrYrSerGluArG1ua1A 139
Db 958 ATTGCTCTGACAGATGCAAGATTGACGCTGTGCTCCATCATATGACAGAAAGAGCA 1017
QY 140 AaArpSerArpArpLeuGlyAlaIleValTYrCYsValG1yValIySArpPheAnGlu 159
Db 1018 AAGATATCCAGAGCACTTGGGGTACTGATTTATGTGTGTGCTCTGATTTTGAACA 1077
QY 160 ThrGluLeuAlaArpG1leAlaArpSerTyLeuArpHiEtrpPheProValaArpArgrlyPhe 179
Db 1078 GCACAGCTTGAAGAAATGCTGTATTCAGAGAGCAAGATTTTCCCTGCAAAAGGTGATTT 1137
QY 180 GluAlaLeuGluG1yIleIleHiSerIleLeuYlySerCYsIleGluIleLeuAlaA1a 199
Db 1138 CAGGCTCTTAAAGGAATTAATTTATTAATCACTGACAGTCACTGAATCTTGAAGAA 1197
QY 200 AlaGluProSerThrIleCYsAlaG1yG1uSerPheGluInValValArgrG1yAnG1y 219
Db 1198 TTGCAAGCCCTCAAGATGTGTGTGTGGGAGAGAAATTTCAATTTCTTTAACTGGAAGAGA 1257
QY 220 PheArG1leAlaArpArpValaArpArpValLeuCYsSerPheYlyIleAaArpSerVal 239
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Db      1258 TTGATGCTGGGAGTCCGGAATGGAGTCTTCTCGCACTTACCTGTAATAAGAAACATAT 1317
Qy      240 ThrleuabnglulyspropheServalGluabpThrlyrleuLeuCyseProAlProile 259
Db      1318 ACAACGAGTGTAAACCGATAGGTGTACAGCTTAATCTTAATCTTGTGCTCGACCTATTC 1377
Qy      260 LeuylsegIuValGlymeclValAlaLeuclnValSerMetAanpBglyLeuSerPhe 279
Db      1378 CTGAATTAAGCTGGAAGAACTCTTGATGTTCAGAGGCTTTAATGAGAGAAATCTGTC 1437
Qy      280 IleserServalIleIleThrThrHisCyseSerApBgly 294
Db      1438 ATTTCAGATCATTAATTCATGTCACAGCCACAGATGTTCTAACGGG 1482

RESULT 3
US-09-974-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyen
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-09-774-528-297

Alignment Scores:
Pred. No.: 7,98e-82 Length: 1492
Score: 709.00 Matches: 139
Percent Similarity: 72.35% Conservative: 52
Best Local Similarity: 52.65% Mismatches: 71
Query Match: 46.16% Gaps: 2
DB: 3

US-09-970-076-2_COPY_27_321 (1-295) x US-09-774-528-297 (1-1492)
Qy      31 HleHleThpabnglulietYrTy-rPheValGluGlnleuAlaHlelypPheIleSerPro 50
Db      16 AATAACTGAGATTGAATTTATTAATTTCTGACAGCACTTGCGAGAGATTGTGAGCCCT 75
Qy      51 GlnleuArGMeSerPheIleValpPheSerThraRglYThrThrleuMetlyleuThr 70
Db      76 GAATGAGATTAATCTTTCATGCTGTTTCTCTCAGAGAACTATTAATTTGCCATTACT 135
Qy      71 GluabpArgGlnGlnIleArgGlnGlyLeuGlnGluLeuGlnlyValleuProGlyGly 90
Db      136 GGAACAGAGGCGAAATCAGTAAAGGCTTGAGAGATTAAACCTGTTAGTCCAGTGA 195
Qy      91 AspThrlyrMetHleGluGlyPheGluArgAlaSerGlnIleYrTyGluAbnArg 110
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Db      196 GAGCATATATCCATGAGAGCTAAAGCTAAGCTAGCGATGAACAATTT-----CAGAAAGCA 249
Qy      111 GlnGlyTyraRgThraIaSerValIleIleAlaLeuThraRgGlyGluLeuHiGluasp 130
Db      250 GAGGCTTGAACCTCAGATATCATATTCCTCTGACAGATGCGAAGTTGAGCGCTGTG 309
Qy      131 LeuPheTherlyrSerGluArgGluAlaAbnArgSerArgAspLeuGlyAlaIleValTy 150
Db      310 GTGCCATCATATGCAAGAAAGAGGCAAGATATCCAGGTCACCTTGAGGCTAGTGTAT 369
Qy      151 CyseValGlyVallyAspPheasngluThrGlnleuAlaRglIleAlaAspSerlyAsp 170
Db      370 TGCTTGCGGATCCTTGATTTTGAACAAGCAGCAGCTTAAGAATTCGATTCAGAGAG 429
Qy      171 HleValpPheProValaanaBglyPheGlnAlaLeuGlnGlyIleHleSerIleleu 190
Db      430 CAAGTTTCCCTGCAAGAGGAGATTCAGGCTCTTAAGAGATTAATTAATTCATCTA 489
Qy      191 LyblySerCyseIleGluIleleuAlaGluabpSerThrIleCyseAlaGlyGluSer 210
Db      490 GCTAGTCATGTAAGTGAATCTTAAGATTGAGCCCTCAAGTGTCTGTGCGGAGGAA 549
Qy      211 PheGlnValValaArgGlyAenglyPheArgHisAlaArgaenValaAspArgValleu 230
Db      550 TTTCAAGATTCCTTAAGTGAAGAGATTCATGCTGGGCGAGTCGGAATGGCAGTCTCTC 609
Qy      231 CyseRPhelysIleAanaBgServalThrleuabnglulyspropheServalGluasp 250
Db      610 TGCACTTAACCTGTAATGAACATATATACAGAGTGTAAACACAGTAAGTGTACACTT 669
Qy      251 ThrlyrleuLeuCyseProAlProIleleuLyblyGluValGlymeclValAlaLeuGln 270
Db      670 AATTCTATGCTTGTCTGCACTTAATCTTAATTAACCTGAGAACTCTTGATGTTCA 729
Qy      271 ValSerMetAanpBglyLeuSerPheIleSerServalIleIleThrThrHis 290
Db      730 GTAGACTTAAATGAGAGAAATCTGTCAATTTCAAGATCATTAATTCACAGCACGAA 789
Qy      291 CyseSerApBgly 294
Db      790 TGTCTTAACGG 801

RESULT 4
US-10-120-988-297
; Sequence 297, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyen
; APPLICANT: Wang, Dumnui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; PRIOR APPLICATION NUMBER: 09/774,528
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-10-120-988-297

Alignment Scores:
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Pred. No.: 7,98e-82 Length: 1492
Score: 709.00 Matches: 139
Percent Similarity: 72.35% Conservative: 52
Best Local Similarity: 52.65% Mismatches: 71
Query Match: 46.16% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_COPY_27_321 (1-295) x US-10-120-988-297 (1-1492)

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QY 31 HnHtTbAsnGluIleTyrrPheValGluGluLeuAlaHisLysPheIleSerPro 50
DB 16 AATAACTGGAGATTGAAATTAAATTTCGACAGCACTTGAGAGATTGGAGCCCT 75
QY 51 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrXleuMetLysLeuThr 70
DB 76 GAAATGAGATTATCTTTCATTGTTGTTTCTTCCAGCACTATTATTGTCATTAACT 135
QY 71 GluAspArgGluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGly 90
DB 136 GGAGACAGAGGCAAAATCAGTAAAGCCTTGAGGATTAAACGTTTACTCCAGTACGA 195
QY 91 AspThrTyrrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrrTyrrGluAsnArg 110
DB 196 GAGACATATATCCATGAGAGCTAAGCTAAGCTGAGATGACAAATL-----CAGAAAGCA 249
QY 111 GlnGlyTyrrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 130
DB 250 GAGAGGCTTGAAAACCTCCATCATATATTGCTGTGACATGGAAGTTGGACGGCTGC 309
QY 131 LeuPhePheTyrrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrr 150
DB 310 GTCCCATCATATATCAGAGAAAGGCAAAAGATATCCGCTGCTGGGCTGAGTGTATT 369
QY 151 CysValGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAsp 170
DB 370 TGGTTGGGGTCTCTGATTGTAACAACAGCTTGAAAGAAATGCTGATCCAGAGAG 429
QY 171 HisValPheProValAsnAspGlyPheGlnAlaLeuGlnIleIleHisSerIleLeu 190
DB 430 CAAGTTTCCCTGCAAGGTGATTTCAAGCTCTTAAAGAAATTAATTCTATATCTA 489
QY 191 LysLysSerCysIleGluIleLeuAlaGluProSerThrIleCysAlaGlyGluSer 210
DB 490 GCTCAGCATGTACTGAAATCTTGAATTCAGGCCCTCAAGTGTCTGTGGGGGAGAA 549
QY 211 PheGluValValAlaArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeu 230
DB 550 TTTCAAGTTTGTCTTAACTGGAAGAGATTCATGCTGGGCACTGGAAATGGCACTGTTCTC 609
QY 231 CysSerPheLysIleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAsp 250
DB 610 TGCACCTTACACTGTAAATGAAACATATACACAGAGCTTAAACCAAGTAATGTACAGCTT 669
QY 251 ThrTyrrLeuLeuCysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGln 270
DB 670 AATTCTATGCTTTGTCTGCACTATCTGAATTAACCTGAGAACTCTTGATGTTTCA 729
QY 271 ValSerMetAsnAspGlyLysSerPheIleSerSerSerValIleIleThrThrHis 290
DB 730 GTAGAGCTTAAATGAGGAAAAATCTGTCATTTCAAGATCATTAATTGTACAGCCACAGAA 789
QY 291 CysSerAspGly 294
DB 790 TGTTCCTAACGG 801
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RESULT 5
US-09-799-451-250
; Sequence 250, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, RyLe

```
/ APPLICANT: Asundi, Vinod  
/ APPLICANT: Ren, Feiyan  
/ APPLICANT: Zhang, Jie  
/ APPLICANT: Xue, Aidong J.  
/ APPLICANT: Zhao, Qing A.  
/ APPLICANT: Wang, Jian-Rui  
/ APPLICANT: Ma, Yungting  
/ APPLICANT: Yamazaki, Victoria  
/ APPLICANT: Chen, Rui-hong  
/ APPLICANT: Wang, Zhiwei  
/ APPLICANT: Wang, Dunrui  
/ APPLICANT: Yang, Yonghong  
/ APPLICANT: Wehrman, Tom  
/ APPLICANT: Ghosh, Reena  
/ APPLICANT: Drmanac, Radoje T.  
/ TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and  
/ FILE OF INVENTION: Polypeptides  
/ FILE REFERENCE: 803  
/ CURRENT APPLICATION NUMBER: US/09/799,451  
/ CURRENT FILING DATE: 2001-03-05  
/ SOFTWARE: pt_FL_genes Version 2.0  
/ SEQ ID NO 250  
/ LENGTH: 3981  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (287)..(1118)  
US-09-799-451-250
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Alignment Scores:
Pred. No.: 5.11e-75 Length: 3981
Score: 662.00 Matches: 129
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.10% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-09-799-451-250 (1-3981)

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QY 167 AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnIleIle 186
DB 3 GACAGTAGAGATCATGTGTTCCCGTGAATGACGGCTTTCAAGCTGTGCAAGCATCATC 62
QY 187 HisSerIleLeuLysLysSerCysIleGluIleLeuAlaGluProSerThrIleCys 206
DB 63 CACTCAATTTTGAAGAAATCTGCAATCGAAATTCAGACTGAACCATTCACCATATGT 122
QY 207 AlaGlyLysSerPheGlnValValAlaArgGlyAsnGlyPheArgHisAlaArgAsnVal 226
DB 123 GCGAGAGATGATCTTCAAGTTGCGTGAAGGAAAGGGCTTCGACATGCCCAAGCTG 182
QY 227 AspArgValLeuCysSerPheLysIleAsnAspSerValThrLeuAsnGluLysProPhe 246
DB 183 GACAGGGTCTCTGCACTTCAAGATCAATGACTCGCTCACTCATATGAGAAAGCCCTTT 242
QY 247 SerValGluAspThrTyrrLeuLeuCysProAlaProIleLeuLysGluValGlyMetLys 266
DB 243 TCTGTGAAGATATCTTATTTACTGTGTCCAGCCCTTATCTTAAAGAAAGTTGGCATGAA 302
QY 267 AlaAlaLeuGlnValSerMetAsnAspGlyLysSerPheIleSerSerSerValIleIle 286
DB 303 GCTGCACTCCAGGTGAGCATGAAAGATGGGCTCTCTTTATATCCAGTTCTGTCAATCATC 362
QY 287 ThrThrThrHisCysSerAspGlySer 295
DB 363 ACCACCACACACTGTCTGACGGTTC 389
```

RESULT 6
US-08-286-889-45
; Sequence 45, Application US/08286889
; Patent No. 5470953

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-286-889-45
Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: 2 Gaps: 12
US-09-970-076-2_COPY_27_321 (1-295) x US-08-286-889-45 (1-3519)
Qy 11 ProhlaCyeryrGly--GlyPheAspleuTyRphelLeuAplySeGlySeVal 29
Db 481 CCAGAGTGTCCAGACAGAGATGACATTCCTTCTGATTAAGCTCCGGCAGCAT 540
Qy 30 ---LeuH1sh1strPaengluileTyTyRphValgluInleuA1sh1slyPhe1le 48
Db 541 GATCAAGTACCTTACCCAGATGAGAGCTTCTGCAAGCTTTGATGGCGCACTT 600
Qy 49 SerProglInleuAgtMetSerPheileValPheSerThrArgGlyThrLeuMeclys 68
Db 601 AGCACGACGACCTGCTCTCCCTGATGCAATCAACATCTGAAGACTCATTTTACC 660
Qy 69 LeuThrgluAparG-----gluInleAargGluInglyLeuGluGluLeu 83
Db 661 TTCACGAAATTCAGACAGACGCTGAGCCCTCAGAGCTGGATGCCATGCTCAGCTC 720
Qy 84 GluIyValleuProglIyAparThrTyRMecl1sgluIyPheGluArgAlaSerGlu 103
Db 721 CAA-----GGCCTGACGTACACAGCTCGGCGCATCCAGAAAGTGGTGAAA 765

Qy 104 GluileTyTyrgluAenArgGluInglyTyArgThrala---SerValile1Alaleu 122
Db 766 GAGCTATTTCATTCAGAAAGATGGGGCCGAAAGTCCAGAAAGATTCATTCATTC 825
Qy 123 ThrApgIygluLeuH1sh1slyApleuPhePheTySerGlu-----ArgGluAlaSn 140
Db 826 ACAGATGGCGAAATTCAGAGACCCCTGGAGATATGACATGTCATCCCTGAAAGCAG 885
Qy 141 ArgSerArgApleuGlyAla1leValTyRcyValGlyValysAap---PheAsglu 159
Db 886 AAAGCT-----GGATCATTCGCTATGATGAGGGGTGGAGATGCCCTCCGGGAA 936
Qy 160 ---ThrgluA1laArgle-----AlaApseryAapPhe1ValPhe 173
Db 937 CCACATCCCTACGAGAGCTGAAACCATTTGGCTCAGCTCCCTGCAGACCATGTTT 996
Qy 174 ProValAaApgIyPheGluAlaLeuGluIngly1le1sh1ser1leuTylySer 193
Db 997 AAGGTGGGCAT---TTGTAGACATTCGACGATCCAGGGCGCAATTCAGAGAAA--- 1050
Qy 194 CysIleGluileuA1aAlaGluProSerThrIleCysAlaGlyIuSerPheGluVal 213
Db 1051 -----ATCTTGCCATTTGAAGGAACCGAATCAAGTCAAGTACTGCTTTACAGCAC 1101
Qy 214 ValValArgGlyAaNgIyPheArgH1eAlaArgAaValAap 227
Db 1102 GAGATGTACAGAGATTCACGCTCAGCTCTCTCAATGAT 1143
RESULT 7
US-08-485-618-45 Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

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/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
US-08-485-618-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-485-618-45 (1-3519)
QY 11 ProAlaCyetyrGly---GlyPheAspLeuTyPheIleLeuAspLysSerGlySerVal 29
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QY 30 ---LeuHiHiHiETrpAnGluIleTyTyPheValGluGlnLeuAlaHisLysPheIle 48
DB 541 GATCAAGTGACTTACCCAGATGAAGGACTTGTCAAAAGCTTGTATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArGmetSerPheIleValPheSerThrArgGlyThrPheLeuMetLys 68
DB 601 AGCACCAGACCTGTTCTCTCCGTATGCAATACTCAAAACCTCTGAAGACTCATTTTACC 660
QY 69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 83
DB 661 TTACCGGAATTCAAGAGCAGCCTGAGCCCTCAGAGCTGTGATGCCATCGTCCAGCTC 720
QY 84 GlnLysValLeuProGlyIleAspThrTyPheMetHisGluGlyPheGluArgAlaSerGlu 103
DB 721 CAA-----GGCCTGACGTTACACAGCCTCGGGCATCCAGAAAGTGTGTA 765
QY 104 GlnIleTyTyGlnLysAsnArgGlnGlyTyPheArgThrAla---SerValIleIleAlaLeu 122
DB 766 GAGCTATTTCATGACAGAAATGGGGCCGAAAAGTGCAGAAAGATTAATTGTTCATC 825
QY 123 ThrAspGlyGluLeuHisGluAspLeuPhePheTyPheSerGlu-----ArgGluAlaAsn 140
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATATGACATGTCATCCTCGAAAGCAGAG 885
QY 141 ArgSerArgAspLeuGlyAlaIleValTyTyCysValGlyValLysAsp---PheAsnGlu 159
DB 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGGAGATGCTTCCGGGAA 936
QY 160 ---ThcGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
DB 937 CCCACTGCCCCCTTACAGAGAGTGAACACCATGCTCACCTCCCTGCGAGCACAGTGTTC 996
QY 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 193
DB 997 AAGGTGGGCAAT---TTTGTAAGCATTCGCGAGCATTCAGCGGCAAAATTCAGAGAAA--- 1050
QY 194 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnVal 213
DB 1051 -----ATCTTGCCATTGAAAGAACCAAGATCAAGTCAAGTACTCTTTACAGCAC 1101
QY 214 ValValArgGlyAsnGlyPheAspHisAlaArgAsnValAsp 227
DB 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 8
US-08-362-652-45
/ Sequence 45: Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
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/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ. ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
US-08-362-652-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-362-652-45 (1-3519)
QY 11 ProAlaCyetyrGly---GlyPheAspLeuTyPheIleLeuAspLysSerGlySerVal 29
DB 481 CCAGAGTGTCCAGAGACAGAGAGATGACATTGCTTCTGTATGATGGCTCCGACAGATT 540
QY 30 ---LeuHiHiHiETrpAnGluIleTyTyPheValGluGlnLeuAlaHisLysPheIle 48
DB 541 GATCAAGTGACTTACCCAGATGAAGGACTTGTCAAAAGCTTGTATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArGmetSerPheIleValPheSerThrArgGlyThrPheLeuMetLys 68
DB 601 AGCACCAGACCTGTTCTCTCCGTATGCAATACTCAAAACCTCTGAAGACTCATTTTACC 660
QY 69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 83
DB 661 TTACCGGAATTCAAGAGCAGCCTGAGCCCTCAGAGCTGTGATGCCATCGTCCAGCTC 720
QY 84 GlnLysValLeuProGlyIleAspThrTyPheMetHisGluGlyPheGluArgAlaSerGlu 103
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Db 721 CAA-----GCGCTGACGTACACAGCTCGCGCATCCAGAAAGTGTA 765
Qy 104 GlnIleTyTyrGluAsnArgGlnGlyTyrArgThra---SerValIleIleAlaLeu 122
Db 766 GAGCTATTTCATTACCAAGATGGGCGCCGAAAGAGTCCAGAAAGATTAATGTCATC 825
Qy 123 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 140
Db 826 ACAAGATGGGCAAGAAATTCAGAGACCCCTGGAGATATACACTGTCAATCCCTGAAGCAGAG 885
Qy 141 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValysAsp---PheAsnGlu 159
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGCGGTGGAGATCCCTTCGCGGAA 936
Qy 160 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
Db 937 CCCACTGCTCCCTACGAGAGCTGAAACCACTTGGCTCAGCTCCCTCGCAGAGACAGTGTTC 996
Qy 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 193
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGACAGCATCCAGCGGCAAAATTCAGAGAAA--- 1050
Qy 194 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 213
Db 1051 -----ATCTTGGCATTTGAAAGAAACCAAGTCAAGTCAAGTCTTCTTACAGCAC 1101
Qy 214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db 1102 GAGATGTACAAAGAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 9
US-08-605-672-45
; Sequence 45, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seair Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856

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; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..3519
; US-08-605-672-45

Alignment Scores:
Pred. No.: 154e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-605-672-45 (1-3519)
Qy 11 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 29
Db 481 CCAGAGTGTCCAGGACAAAGATGAGATGATGCTTCTGATTAATGAGCTCCGCGACAT 540
Qy 30 ---LeuHisIleTyrAsnGlyIleTyrTyrPheValGluGlnLeuAlaHisLysPheIle 48
Db 541 GATCAAGATGACTTATCCAGATGAGATGAGACCTTCTGCAAACTTGTATGGGCGAGTGGCG 600
Qy 49 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 68
Db 601 AGCACACGACCTCTGTTCTCTCTGATCAATTAATCAACATCTGAAGACTCATTTTACC 660
Qy 69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluLeu 83
Db 661 TTACCGGAATTCAAAGACAGACCTGAGCCCTGAGAGCTGGTGAATGCCATGTCACATC 720
Qy 84 GlnLysValLeuProGlyIleAspThrTyrMetHisGluGlyPheGlnArgAlaSerGlu 103
Db 721 CAA-----GCGCTGACGTACACAGCCCTGGGCAATCCAGAAAGTGTA 765
Qy 104 GlnIleTyTyrGluAsnArgGlnGlyTyrArgThra---SerValIleIleAlaLeu 122
Db 766 GAGCTATTTCATTACCAAGATGGGCGCCGAAAGAGTCCAGAAAGATTAATGTCATC 825
Qy 123 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 140
Db 826 ACAAGATGGGCAAGAAATTCAGAGACCCCTGGAGATATAGACATGTCATCCCTGAAGCAGAG 885
Qy 141 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValysAsp---PheAsnGlu 159
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGCGGTGGAGATGCTTCGCGGAA 936
Qy 160 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
Db 937 CCCACTGCTCCCTACGAGAGCTGAAACCACTTGGCTCAGCTCCCTCGCAGAGACAGTGTTC 996
Qy 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 193
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGACAGCATCCAGCGGCAAAATTCAGAGAAA--- 1050
Qy 194 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 213
Db 1051 -----ATCTTGGCATTTGAAAGAAACCAAGTCAAGTCAAGTCTTCTTACAGCAC 1101
Qy 214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db 1102 GAGATGTACAAAGAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 10
US-08-482-293A-45
; Sequence 45, Application US/08482293A

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REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45

Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
Gaps: 12
DB:

US-09-970-076-2_COPY_27_321 (1-295) x US-08-943-363-45 (1-3519)

QY 11 ProAlaCyArTyGly--GlyPheArLeuTyPheIleLeuArLySeRgLySeRVal 29
DB 481 CCAGAGTGTCAGAGCAAGATGACATTCCTTCCGATGATGATGCTCCGGCAGCAT 540
QY 30 ---LeuH1h1tPraEngIuIeTyTyPheValGluGlnLeuAlaH1sLyvPheIle 48
DB 541 GATCAAAAGTACCTTACCCAGATGAAGACTTCGTCAAAGCTTTGATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArGMeSerPheIleValPheSerThArGlyThrThrLeuMetLyS 68
DB 601 AGACCCAGCACTGCTTCCTCCGATGACATACCAAAATCCGAAGACTCATTTTACC 660
QY 69 LeuThGlnArPArG-----GluGlnIleArGlnGlyLeuGlnGluLeu 83
DB 661 TTCACGGAAATTCAGAGCAGCTGAGCCCTCAGAGCTGGATGATGCATGTCACAGCTC 720
QY 84 GlnLyvAlLeuPProGlyGlyArPThrTyMeH1sGlyGlyPheGlnArGAlaSerGlu 103
DB 721 CAA-----GGCTGACGTACACAGCTCGGAGCATCCGAAAGTGGTAA 765
QY 104 GlnIleTyTyGlnuArGlnGlyTyArGThAla---SerValIleIleAlaLeu 122
DB 766 GAGCTATTTCATGCAAGATGGGCCCCGAAAGTCCCAAGAAATCTAATTGTCATC 825
QY 123 ThrArGlyGlyLeuH1sGlyArLeuPhePheTySerGlu-----ArgGlnAlaAr 140
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATGACATGTCATCCCTGAAGCAGAG 885
QY 141 ArgSerArGArPLeuGlyAlaIleValTyTyCyvAlaGlyAlaArP---PheArGln 159
DB 886 AAAGCT-----GGATCATTCGCTATGATAGGGGTGGAGATGCTTCGGGAA 926
QY 160 ---ThGlnLeuAlaArGlyle-----AlaArSerLyvArPHeIleValPhe 173
DB 937 CCCACTGCTTACAGAGCTGACACATTCGCTGAGCTCCCTGCGAGACACAGCTTTC 996
QY 174 ProValArPArGlyPheGlnAlaLeuGlnGlyIleIleH1sSerIleLeuLyvSer 193
DB 997 AAGGTGGGCAAT---TTGTAGACATTCGCAAGATCCAGCGCAAAATTCAGGAA--- 1050
QY 194 CyvIleGlnIleuAlaIleGlnPProSerThrIleCyvAlaGlyGlnSerPheGlnVal 213
DB 1051 -----ATCTTGGCATTTGAAGGACCAAGATCAAGTCAAGTACTCTTCACAGAC 1101
QY 214 ValIleArGlyLeuEngIyPheArGTh1sAlaArGArPAlaArP 227
DB 227

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DB 1102 GAGATGTCACAAAGGTTTCAGCTCAGCTCTCTCATATGAT 1143
RESULT 12
US-09-193-043-45
Sequence 45, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT FILING DATE: 1998-11-16
EARLIER FILING DATE: 1998-12-23, 497
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 45
LENGTH: 3519
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3516)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-45

Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
Gaps: 12
DB:

US-09-970-076-2_COPY_27_321 (1-295) x US-09-193-043-45 (1-3519)

QY 11 ProAlaCyArTyGly--GlyPheArLeuTyPheIleLeuArLySeRgLySeRVal 29
DB 481 CCAGAGTGTCAGAGCAAGATGACATTCCTTCCGATGATGATGCTCCGGCAGCAT 540
QY 30 ---LeuH1h1tPraEngIuIeTyTyPheValGluGlnLeuAlaH1sLyvPheIle 48
DB 541 GATCAAAAGTACCTTACCCAGATGAAGACTTCGTCAAAGCTTTGATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArGMeSerPheIleValPheSerThArGlyThrThrLeuMetLyS 68
DB 601 AGACCCAGCACTGCTTCCTCCGATGACATACCAAAATCCGAAGACTCATTTTACC 660
QY 69 LeuThGlnArPArG-----GluGlnIleArGlnGlyLeuGlnGluLeu 83
DB 661 TTCACGGAAATTCAGAGCAGCTGAGCCCTCAGAGCTGGATGATGCATGTCACAGCTC 720
QY 84 GlnLyvAlLeuPProGlyGlyArPThrTyMeH1sGlyGlyPheGlnArGAlaSerGlu 103
DB 721 CAA-----GGCTGACGTACACAGCTCGGAGCATCCGAAAGTGGTAA 765
QY 104 GlnIleTyTyGlnuArGlnGlyTyArGThAla---SerValIleIleAlaLeu 122
DB 766 GAGCTATTTCATGCAAGATGGGCCCCGAAAGTCCCAAGAAATCTAATTGTCATC 825
QY 123 ThrArGlyGlyLeuH1sGlyArLeuPhePheTySerGlu-----ArgGlnAlaAr 140
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATGACATGTCATCCCTGAAGCAGAG 885
QY 141 ArgSerArGArPLeuGlyAlaIleValTyTyCyvAlaGlyAlaArP---PheArGln 159
DB 159

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Db      886  AAAGCT-----GGGATCATTCCTATGCTATAGGGGTGGAGATGCTCCGGGAA 936
Qy      160  ---ThGlnLeuAlaArgIle-----AlaAspSerIysAspHisValPhe 173
Db      937  CCCACGTCCCTACAGAGCAAGAACACCACTGGCTCAGCTCCCTCGAGAGCACAGTGTTC 996
Qy      174  ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSer 193
Db      997  AAGTGGGCAAT---TTTGTAGCACTTCGAGCATTCAGCGGCAATTTCAGGAA--- 1050
Qy      194  CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 213
Db      1051  -----ATCTTGGCCATTGGAAGAACCAATCAAGTCAAGTAGTCTCTTCAGCAC 1101
Qy      214  ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db      1102  GAGATGTCAACAAGAGTTTCAGCTCAGCTCTCTCAATGSAAT 1143

RESULT 13
US-09-688-307A-45
; Sequence 45, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-09-688-307A-45 (1-3519)
Qy      11  ProAlaCysArgIly---GlyPheAspLeuTyrrPheIleLeuAspIysSerGlySerVal 29
Db      481  CCAGAGGTCCAGGACAAGAGATGACATTCCTTCGTGATGATGCTCCGGGAGCATT 540
Qy      30  ---LeuHisThrPasnGluIleTyrrPheValGluGlnLeuAlaHisIysPheIle 48
Db      541  GATCAAAAGTACCTTACCCAGATGAAGACTTCGTCAAGAGTTGATGGCGAGTTGGCG 600
Qy      49  SerProGlnLeuArgMetSerPheIleValPheSerThrArgIlyThrThrLeuMetIys 68
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Db      601  ACCACAGCAGCCTCGTTCTCCCTGATGCATCTCAAAATCCTGAAAGCTCATTTTACC 660
Qy      69  LeuThrGluAspArgI-----GluGlnIleArgGlnIlyLeuGluGluLeu 83
Db      661  TTCAGAGAAATTCAAGAGCAGCAGCCTCGAGCCTCGAGAGCTGTGGATGCCATCTCCAGCTC 720
Qy      84  GlnIysValLeuProGlyGlyAspThrTyrrMetHisGluGlyPheGluArgAlaSerGlu 103
Db      721  CAA-----GGCTGACGTACACAGCCTCGGGCATCCAGAAAGGTGGA 765
Qy      104  GlnIleTyrrTyrrGluAsnArgGlnIlyTyrrArgThrAla---SerValIleIleAlaLeu 122
Db      766  GAGCTAATTCATAGCAAGAAAGTGGGCCCGAAAAGTCCCAAGAGATCAATATTGTCAATC 825
Qy      123  ThrAspGlyGluLeuHisGluIleAspLeuPhePheTyrrSerGlu-----ArgGluAlaAsn 140
Db      826  ACGATGGGCAAAATTCCAGAGACCCCGGAGTATGACATGTATCCCTTAAGAGAGAG 885
Qy      141  ArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyValIysAsp---PheAsnGlu 159
Db      886  AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTCCGGGAA 936
Qy      160  ---ThGlnLeuAlaArgIle-----AlaAspSerIysAspHisValPhe 173
Db      937  CCCACGTCCCTACAGAGCAAGAACCACTGGCTCAGCTCCCTCGAGAGCACAGTGTTC 996
Qy      174  ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSer 193
Db      997  AAGTGGGCAAT---TTTGTAGCACTTCGAGCATTCAGCGGCAATTTCAGGAA--- 1050
Qy      194  CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 213
Db      1051  -----ATCTTGGCCATTGGAAGAACCAATCAAGTCAAGTAGTCTCTTCAGCAC 1101
Qy      214  ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db      1102  GAGATGTCAACAAGAGTTTCAGCTCAGCTCTCTCAATGSAAT 1143

RESULT 14
US-09-350-259-45
; Sequence 45, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-45
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Alignment Scores:

Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-09-350-259-45 (1-3519)

QY 11 ProbaLeuTyrGly---GlyPheAerLeuTyrPheileuAerLysSerGlySerVal 29
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QY 30 ---LeuHieHieTPAengLuiLeuTyrTyrPheValGluGluLeuAhiLysPheile 48
DB 541 GATCAAGATGACATTACCAAGATGAGATGACATTGCTTCTGATGATGAGCTCCGGAGCAT 600
QY 49 SerProGluLeuAerMetSerPheileValPheSerThrArgLysThrLeuMetLys 68
DB 601 AGCACAGACACCTGCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 69 LeuThrGluAerArg-----GluGluLeuArgGluGluLeuGluLeu 83
DB 661 TTCACGGAATTCAGAGACAGACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 720
QY 84 GlnLysValLeuProGlyAerThrTyrMechieGluGluPheGluAerGlu 103
DB 721 CAA-----GGCTGACGTACACAGCTCGGGCATCCAGAAAGTGAGAA 765
QY 104 GlnLysTyrGluAerArgGluGluTyrArgThrAla---SerValileileu 122
DB 766 GAGCTATTTCATACAGAAATGGGGCCGAAAGTCCAGAAAGATGATGATGATGATGAT 825
QY 123 ThrAerGluLeuHieGluAerLeuPhePheTyrSerGlu-----ArgGluAla 140
DB 826 ACAGATGGGCGCAATTCAGAGACCCCTGAGTATGACATGTCATCCCTGAAAGCAG 885
QY 141 ArgSerThrAerLeuGluAlaileValTyrCysValGlyValLysAer---PheAerGlu 159
DB 886 AAGCT-----GGATCATTCGCTATGCTATGAGGGGAGAGATGCTTCGGGAA 936
QY 160 ---ThrGlnLeuAlaArgLys-----AlaAerSerLysAerPheileVal 173
DB 937 CCCACTCCCTACAGAGCTGAGACATGAGCTGAGCTCCCTGAGAGACAGCTGATTC 996
QY 174 ProValAerAerGluPheGluAlaLeuGluGlyLeileHieSerileuLysSer 193
DB 997 AAGTGGGCAAT---TTGTAGCACTTCGAGCATCCAGCGGCAATTCAGAGAA--- 1050
QY 194 CysileuLuiLeuAlaLysGluPheSerThrileCysAlaGluLysPheGluVal 213
DB 1051 -----ATCTTGGCATTTGAGAGAACCAATCAAGGTCATGATCTCTTCAGACAC 1101
QY 214 ValValArgLysAerGluPheAerGluAlaAerAerValAer 227
DB 1102 GAGATGTCACAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 15
US-08-485-618-52
Sequence 52, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 3803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3486
US-08-485-618-52

Alignment Scores:
Pred. No.: 1.74e-10 Length: 3803
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-485-618-52 (1-3803)

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QY 30 ---LeuHieHieTPAengLuiLeuTyrTyrPheValGluGluLeuAhiLysPheile 48
DB 490 GATCAAGATGACATTACCAAGATGAGATGACATTGCTTCTGATGATGAGCTCCGGAGCAT 549
QY 49 SerProGluLeuAerMetSerPheileValPheSerThrArgLysThrLeuMetLys 68
DB 550 AGCACAGACACCTGCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 609
QY 69 LeuThrGluAerArg-----GluGluLeuArgGluGluLeuGluLeu 83
DB 610 TTCACGGAATTCAGAGACAGACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 669
QY 84 GlnLysValLeuProGlyAerThrTyrMechieGluGluPheGluAerGlu 103
DB 670 CAA-----GGCTGACGTACACAGCTCGGGCATCCAGAAAGTGAGAA 714
QY 104 GlnLysTyrGluAerArgGluGluTyrArgThrAla---SerValileileu 122
DB 715 GAGCTATTTCATACAGAAATGGGGCCGAAAGTCCAGAAAGATGATGATGATGATGAT 774

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    |||||:::
QY 141 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp--PheAsnGlu 159
    :::::
Db 835 AAAGCT-----GGGATCATTCGCTATGTATAGGGGTGGAGATGCTTCGGGAA 885
    |||||:::
QY 160 ---ThrGluLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
    |||||:::
Db 886 CCCACTGCCCTTACAGAGAGCTGAACACCATTTGGCTCAGCTCCCTCGCAGAGCACGTGTTTC 945
    |||||:::
QY 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 193
    |||||:::
Db 946 AAGGTGGGCAAT---TTGTAGCACTTCGAGCATCCAGCGGCAAAATTCAGAGAAA--- 999
    |||||:::
QY 194 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnVal 213
    |||||:::
Db 1000 -----ATCTTGGCATTGAAGGAAACCGAATCAAGTCAAGTATTCTTTTCAGCAC 1050
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QY 214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
    :::::
Db 1051 GAGATGTACACAGAAAGGTTTCAGCTCAGCTCTCTCAATGAT 1092
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Search completed: December 18, 2005, 07:34:00
Job time : 225.111 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:35:12 ; Search time 945.104 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

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| Ygapop 10.0 , Ygapext 0.5 | |
| Fgapop 6.0 , Fgapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA_Main -OPMT=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsun62
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published_Applications_NA_Main:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1536 | 100.0 | 1454 | 6 | US-10-133-937-58 |
| 3 | 1536 | 100.0 | 1454 | 6 | US-10-159-563-58 |
| 4 | 1536 | 100.0 | 5540 | 3 | US-09-918-715-176 |
| 5 | 1536 | 100.0 | 5540 | 3 | US-09-918-715-231 |
| 6 | 1536 | 100.0 | 5540 | 6 | US-10-301-822-198 |
| 7 | 1536 | 100.0 | 5540 | 8 | US-10-474-794-176 |
| 8 | 1536 | 100.0 | 5540 | 8 | US-10-474-794-231 |

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| 9 | 1536 | 100.0 | 5540 | 9 | US-10-979-159-176 | Sequence 176, App |
| 10 | 1536 | 100.0 | 5540 | 9 | US-10-979-159-231 | Sequence 231, App |
| 11 | 1536 | 100.0 | 5540 | 10 | US-11-047-278-5 | Sequence 5, Appl |
| 12 | 1532 | 99.7 | 1674 | 6 | US-10-038-307-17 | Sequence 17, Appl |
| 13 | 1532 | 99.7 | 1674 | 6 | US-10-201-292-17 | Sequence 17, Appl |
| 14 | 1521 | 99.0 | 1650 | 6 | US-10-038-307-13 | Sequence 13, Appl |
| 15 | 1521 | 99.0 | 1650 | 6 | US-10-038-307-15 | Sequence 15, Appl |
| 16 | 1521 | 99.0 | 1650 | 6 | US-10-201-292-13 | Sequence 13, Appl |
| 17 | 1521 | 99.0 | 1650 | 6 | US-10-301-822-15 | Sequence 15, Appl |
| 18 | 1520 | 99.0 | 1056 | 6 | US-10-038-307-23 | Sequence 23, Appl |
| 19 | 1520 | 99.0 | 1056 | 6 | US-10-201-292-23 | Sequence 23, Appl |
| 20 | 1520 | 99.0 | 1713 | 6 | US-10-038-307-19 | Sequence 19, Appl |
| 21 | 1520 | 99.0 | 1713 | 6 | US-10-201-292-19 | Sequence 19, Appl |
| 22 | 1520 | 99.0 | 2112 | 10 | US-11-047-278-7 | Sequence 7, Appl |
| 23 | 1520 | 99.0 | 2272 | 3 | US-09-796-153-11 | Sequence 11, Appl |
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| 25 | 1520 | 99.0 | 2272 | 6 | US-10-201-292-1 | Sequence 1, Appl |
| 26 | 1520 | 99.0 | 2233 | 5 | US-10-198-846-9957 | Sequence 9957, Ap |
| 27 | 1519 | 98.9 | 5220 | 3 | US-09-918-715-186 | Sequence 186, App |
| 28 | 1519 | 98.9 | 5220 | 3 | US-09-918-715-300 | Sequence 300, App |
| 29 | 1519 | 98.9 | 5220 | 8 | US-10-474-794-186 | Sequence 186, App |
| 30 | 1519 | 98.9 | 5220 | 8 | US-10-474-794-300 | Sequence 300, App |
| 31 | 1519 | 98.9 | 5220 | 9 | US-10-979-159-186 | Sequence 186, App |
| 32 | 1519 | 98.9 | 5220 | 9 | US-10-979-159-300 | Sequence 300, App |
| 33 | 1511 | 98.4 | 1650 | 6 | US-10-038-307-9 | Sequence 9, Appl |
| 34 | 1511 | 98.4 | 1650 | 6 | US-10-201-292-9 | Sequence 9, Appl |
| 35 | 1507 | 98.1 | 1008 | 6 | US-10-038-307-25 | Sequence 25, Appl |
| 36 | 1507 | 98.1 | 1008 | 6 | US-10-201-292-25 | Sequence 25, Appl |
| 37 | 1505.5 | 98.0 | 1047 | 6 | US-10-038-307-21 | Sequence 21, Appl |
| 38 | 1505.5 | 98.0 | 1047 | 6 | US-10-201-292-21 | Sequence 21, Appl |
| 39 | 1500 | 97.7 | 1623 | 6 | US-10-038-307-11 | Sequence 11, Appl |
| 40 | 1500 | 97.7 | 1623 | 6 | US-10-201-292-11 | Sequence 11, Appl |
| 41 | 1419 | 92.4 | 1608 | 6 | US-10-201-292-35 | Sequence 35, Appl |
| 42 | 1391 | 90.6 | 2397 | 6 | US-10-062-674-1757 | Sequence 1757, Ap |
| 43 | 1294 | 84.2 | 1534 | 6 | US-10-201-292-33 | Sequence 33, Appl |
| 44 | 1263 | 82.2 | 1436 | 10 | US-11-047-278-9 | Sequence 9, Appl |
| 45 | 1263 | 82.2 | 1609 | 5 | US-10-037-270-8 | Sequence 8, Appl |

ALIGNMENTS

RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: McGridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Alignment Scores:
Pred. No.: 3,24e-186
Score: 1536.00
Length: 1414
Matches: 295
Percent Similarity: 100.00%
Conservative: 0

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Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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QY 21 PheIleLeuAspLysSerGlySerValLeuHisIleTyrAsnGluIleTyrTyrPheVal 40
DB 242 TTCATTTTGGACAATTCAGAGAGTGTCTGCACACCTGGAATGAAATCTATTCTTTG 301
QY 41 GluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSer 60
DB 302 GAACAGTTGGCTCAAAATTCATCAGCCACAGTTGGAATGTCCTTTATTGTTTCTCC 361
QY 61 ThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlnIleArgGlnGlyLeu 80
DB 362 ACCCGAGAACCACTTAAATGAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCTTA 421
QY 81 GluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArg 100
DB 422 GAAGAACTCCAGAAAGTTCTGCCAGAGAGACCTTACATGATGAAAGATTGAAAGG 481
QY 101 AlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIle 120
DB 482 GCCAGTGAAGCATTTATTATGAAACAGACAGGGTACAGACAGCCAGCTCATCATTT 541
QY 121 AlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsn 140
DB 542 GCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGAGAGGCTAAT 601
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DB 602 AGGTCTCGAATCTTGTGTGCAATTGTTACTGTGTGTGTGAAGATTTTCAATGAGACA 661
QY 161 GluLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGln 180
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QY 181 AlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIleGluIleLeuAlaAla 200
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DB 1022 TTCAGTTCTGTCAATCATCACCAACACACTGTTCTGACGGTTCC 1066
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APPLICANT: Peterson, Carsten
APPLICANT: Melzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
FILE REFERENCE: 11613.56US01
CURRENT APPLICATION NUMBER: US/10/133,937
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-133-937-58
Alignment Scores:
Pred. No.: 3,396-186 Length: 1454
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Beet Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 1 GlyGlnGlyValArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyr 20
DB 222 GGGCAAGGGGAGCGCAGGAGATGGGGGTCCAGCGCTGACGGCGATTGACCTGTAC 281
QY 21 PheIleLeuAspLysSerGlySerValLeuHisIleTyrAsnGluIleTyrTyrPheVal 40
DB 282 TTCATTTTGGACAATTCAGAGAGTGTCTGCACACCTGGAATGAAATCTATTCTTTG 341
QY 41 GluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSer 60
DB 342 GAACATTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTTATTGTTTCTCC 401
QY 61 ThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlnIleArgGlnGlyLeu 80
DB 402 ACCCGAGAACCACTTAAATGAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCTTA 461
QY 81 GluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArg 100
DB 462 GAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAAGATTGAAAGG 521
QY 101 AlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIle 120
DB 522 GCCAGTGAAGCATTTATTATGAAACAGACAGGGTACAGACAGCCAGCTCATCATTT 581
QY 121 AlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsn 140
DB 582 GCTTTACTGATGAGAACTCCATGAAGATCTTTTCTATTCAAGAGAGAGGCTAAT 641
QY 141 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAspPheAsnGluThr 160
DB 642 AGGTCTCGAATCTTGTGTGCAATTGTTACTGTGTGTGTGAAGATTTTCAATGAGACA 701
QY 161 GluLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGln 180
DB 702 CAGCTGCCCCGACAGTGAACAGTGAAGATCATGTGTTCCCGTAATGACGGCTTTCAG 761
QY 181 AlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIleGluIleLeuAlaAla 200
DB 762 GCTCTGAGAGCATCATCCACTCAATTTTGAAGAATCTCTGATCGAAATTTCTAGACGCT 821
QY 201 GluProSerThrIleCysAlaGlyLysSerPheGlnValValAlaArgGlyAsnGlyPhe 220
DB 822 GAACATTCACCATATGTGACAGAGATCATTTCAAGTGTGTGAGAGAAACGGCTTC 881
QY 221 ArgHisAlaArgAsnValaAspArgValLeuCysSerPheLysIleAsnAspSerValThr 240
DB 882 CGACATGCCCGACAGTGAACAGGGTCTCTGACGCTTCAGATCAATGACTGGGTACACA 941
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QY      241 LEUANGULYEPROBHESEVALGUAERTTYLEUENUCYPROALAEPULEU    260
DB      942 CTCATGAGAACGCCCTTTTCTGTGGAAAGACATTATTACTGTGTCCAGCGCTTATCTTA    1001
QY      261 IYEGJUALVIGLYMELYSVAIAALEUGINVAISEMECAANAPGYLUSERPHELLE    280
DB      1002 AAGAAGATTGGCATAAAGCTGCACCTCAAGGTGAGCATGAACATGGCCCTCTTTTATC    1061
QY      281 SERSESERVAIIIELEHETHRTTHRHACVSERAEOPYLER    295
DB      1062 TCCAGTTCGTCAATCATCACACACACTGTTCTGACGGTTC    1106

RESULT 3
US-10-159-563-58
Sequence 58, Application US/10159563
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Melzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
FILE REFERENCE: 11613.56US11
CURRENT APPLICATION NUMBER: US/10/159,563
PRIORITY FILING DATE: 2002-12-09
PRIOR FILING DATE: US 10/133,937
NUMBER OF SEQ ID NOS: 444
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:
Pred. No.:          3,39e-186           Length:          1454
Score:             1536.00              Matches:            295
Percent Similarity: 100.00%              Conservative:        0
Best Local Similarity: 100.00%             Mismatches:         0
Query Match:       100.00%                Indels:             0
DB:               6                      Gaps:               0

US-09-970-076-2_COPY_27_321 (1-295) x US-10-159-563-58 (1-1454)
QY      1 GIYGINGLYGVYARGRGGLUABPGIYGIYPCOALCYSTYISGLYPHEAPLEUYR    20
DB      222 GGCGAAGGGGAGCGCAGGAGGATGGGGGTCCAGCGTGCTACGGCGATTGACCTGTAC    281
QY      21 PHELLLEUABPYSESERGISERVALLLEUHIIHTPAENGILULETYTPRYEVAL    40
DB      282 TTCATTTTGGACAACATCAGAAAGTGTGTGCACACCTGGAAATGATTAATCTTTGTG    341
QY      41 GIUGINLEUALHIHLYBPHELLIESERPGRGINLEUARWGESERPHELLIEVALPHESER    60
DB      342 GAACACTTGCGTCACAAATTCATCAGCCCACTTGAGAAATGTCCTTTATGTTTTCTCC    401
QY      61 THIRARGLYTHRTRLEUMECILEYLSLEUTHRGIUASPARGLUNIIIEARGINGLYLEU    80
DB      402 ACCCGAGNAACAACCTTAATGAAACTGACAGAAAGACAGAAACAAATCCGTCAGGCGCTA    461
QY      81 GIUGIULEUGILLYVALLEUPROGIVGYIAPERTHYTMETCHAGIUNGIPHEGIUARY    100
DB      462 GAAGAACTCCAGAAATCTCTGCCAGGAGGAGACACTTACATGATAGATAAGGATTGAAAGG    521
QY      101 ALASERGULGINILETYTRYGIUAENARVGINGLYTRYARTGHRAIASERVALLIELE    120
DB      522 GCCAGTGACAGATTATTATTAAGAAACAGACMAAGGTACAGACACCGACGTCATCATTT    581
QY      121 ALALEUTHRAPGILYGLIUEHHISGLIUBAPLEUPHERPHYTSERGILUARGLIUALEN    140

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| | | | |
|--|------|--|------|
| Db | 582 | GCTTTGATCTGATNGAGAACTCCATGAAGATCTCTTTTCTTTTACAGAGAGGAGCTAAT | 641 |
| Qy | 141 | ARGSERAAAGAPLEUGLYALAIILEVALTYTCYSAIGLYVALIYVSAAPHASNGIUTHR | 160 |
| Db | 642 | AGGTCCTCAGATCTCTTGAGCAATGTTTAACTGTGTGTGTGGAAGAATTTCAATGAGACA | 701 |
| Qy | 161 | GLINLEUALAAGIIEALIASPSELYSAPHISVALPHEPROVALASNAASPGIYPHEGIN | 180 |
| Db | 702 | CAGCTGCGCCCGATTTGGCGACAGTBAAGATCATGTGTTTCCCGTGAATGACGGCTTCAG | 761 |
| Qy | 181 | ALALEUNGINGLYIIEIIEHIESERTILEULYSIYSSERYSIIIEGULIELEUALAALA | 200 |
| Db | 762 | GCTCGGAAGGCATCATCTCACTCAATTTTGAAGAAGTCTCGCATCGAAATTCCTAGACACT | 821 |
| Qy | 201 | GLUPROSETHRTIIECYSAIIGLYIUSERPHEGINVALVALIVALARGLYIASNGLYPHE | 220 |
| Db | 822 | GAACCATTCACCAATATGACAGAGAGAGCATTTTCAAGTGTGCGAGAGGAAAGGGCTTC | 881 |
| Qy | 221 | ARGHSALIAAGYANVALASPAHVAlLEUCYSSERPHELYSIIIEANASPSERVALTHR | 240 |
| Db | 882 | CGACATGCGCCGACAGTGAAGAGGGTCTCTGCGAGCTTCAGATCAATGATCGGTCACA | 941 |
| Qy | 241 | LEUBENGILIYSPROPHESERVALGILUASPTHRTYRIEULEUCYSPROALAPROILEUEN | 260 |
| Db | 942 | CTCATATGAGAAAGCCCTTTCTGTGTGAAGACACTTATTTCATCTGTCTCAGCGCCATCTTA | 1001 |
| Qy | 261 | LYSGILUVALIglyMETLYSALIALALEUNGIVALSERMECAANASPGIYLEUSERPHEILE | 280 |
| Db | 1002 | AAAGAAAGTTGGCAGTGAAGAGTGCACTCCAGGTCAGATGAAACGATGGCCCTCTTTTATC | 1061 |
| Qy | 281 | SERSESERVALIIEIIEIETHRTTHRTIIECYSSERASPGIYSER | 295 |
| Db | 1062 | TTCAGATTCTGTCATCATCATCACACACACACATGTTCTGACGGGTCC | 1106 |
| RESULT 4 | | | |
| US-09-918-715-176 | | | |
| Sequence 176, Application US/09918715 | | | |
| Publication No. US20030017157A1 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Brad St. Croix | | | |
| APPLICANT: Bert Vogelstein | | | |
| APPLICANT: Kenneth Kinzler | | | |
| TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS | | | |
| FILE REFERENCE: 1107.00134 | | | |
| CURRENT APPLICATION NUMBER: US/09/918.715 | | | |
| CURRENT FILING DATE: 2001-08-01 | | | |
| PRIOR APPLICATION NUMBER: 60/222,599 | | | |
| PRIOR FILING DATE: 2000-08-02 | | | |
| PRIOR APPLICATION NUMBER: 60/224,360 | | | |
| PRIOR FILING DATE: 2000-08-11 | | | |
| PRIOR APPLICATION NUMBER: 60/282,850 | | | |
| PRIOR FILING DATE: 2000-04-11 | | | |
| NUMBER OF SEQ ID NOS: 358 | | | |
| SOFTWARE: FastSeq for Windows Version 3.0 | | | |
| SEQ ID NO 176 | | | |
| LENGTH: 5540 | | | |
| TYPE: DNA | | | |
| ORGANISM: Homo sapiens | | | |
| US-09-918-715-176 | | | |
| Alignment Scores: | | | |
| Pred. No.: 2.87e-185 | | | |
| Score: 1536.00 | | | |
| Percent Similarity: 100.00% | | | |
| Best Local Similarity: 100.00% | | | |
| Query Match: 100.00% | | | |
| DB: 3 | | | |
| Gaps: 0 | | | |
| US-09-970-076-2_COPY_27_321 (1-295) x US-09-918-715-176 (1-5540) | | | |
| Qy | 1 | GLIYGLNGIYGLYAAGATGGLUASPGIYGLYPROALACYSTRYGLYGLYPHEASPLEUTHR | 20 |
| Db | 222 | GGGCAAGGGGAGCGAGGAGGAAATGGGGGTCCAGCCTGCTACGGCGGATTTGACCTTGAC | 281 |

| | | | |
|--|------|---|------|
| Qy | 21 | PhellleleuaplybSerglySerValleuhtshstppamgullleTyrTrPheVal | 40 |
| Db | 282 | TYCATTTTGGCAAAATCAGAAAGTGCTGCACCACTGAAATGAATCTATTACTTGTG | 341 |
| Qy | 41 | GIUGIuLeuAlaHlelyPheHleSerProGluLeuAzmctSerPheHleValPheSer | 60 |
| Db | 342 | GAACTGTGGCTCAAAATTCATCATCGCCACAGTTGAGAAATGCTTTATTTGTTTCTCC | 401 |
| Qy | 61 | ThArnglyThrThrLeuMetyleuThrgluAparagIugInleargGInglyLeu | 80 |
| Db | 402 | ACCGAGGAACAACCTTATGAACTGACAGAAAGCAGAAACAAATCCGTCAAGGCTTA | 461 |
| Qy | 81 | GIUGIuLeuGInlybValleuProGlyglyAspThrTyrMetHleagluclyPhegluArg | 100 |
| Db | 462 | GAAAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACATGCAAGAAAGATTGAAAGG | 521 |
| Qy | 101 | AlaSerGIUGInlleTyrTrGluAparagInglyTyrArgThrAlaSerValHlelle | 120 |
| Db | 522 | GCCACTGACCAATTTATTAATGAAACAGACAGAGGTACAGAGACGCCACTCATCTT | 581 |
| Qy | 121 | AlaLeuthraSpGlygluLeuHleaglulAspleuPhePheTyrSerGIuArgGluAlaAn | 140 |
| Db | 582 | GCTTGACTGATGAGAACTTCATGAAGTCTCTTTTCTATTGAGAGGAGGCTTAT | 641 |
| Qy | 141 | ArgSerArGaSpLeuglyAlaHleValTyrCybValglyValLybAspPheAsnGluThr | 160 |
| Db | 642 | AGGTCTCGAGATCTTGGTGCAATGTTTAACTGTGTGTGGTGAGAAATTTCATGTAGACA | 701 |
| Qy | 161 | GIuLeuAlaArgIleAlaAspSerLybAspHleValPheProValAsnAspGlyPheGln | 180 |
| Db | 702 | CAGCTGGCCCGATGGCGAGACGTAAGATCATGTGTTCCTGGTAATGACGGCTTTCAG | 761 |
| Qy | 181 | AlaLeuGInglyHleHleHleSerIleuLysLybSerCybHleGluHleuAlaAla | 200 |
| Db | 762 | GCTCGCAAGGATCATCATCACTCATTTTGAAGAAGCTCTGATGAAATTCATGCACT | 821 |
| Qy | 201 | GIuProSerThrTleCybAlaglyGluSerPheGlnValValArgGlybAsnGlyPhe | 220 |
| Db | 822 | GAACCATCCACCATATGTGTCAGAGAAAGTCATTTCAAGTGTGCTGAGAGAAACCGCTTC | 881 |
| Qy | 221 | ArgHleAlaArgAsnValAspArgValleuCybSerPheLybHleAsnAspSerValThr | 240 |
| Db | 882 | CGACATGCCCGCAAGCTGACAGGGGTCTCTGCACCTTCAGATCAATGAATCTCGGTCA | 941 |
| Qy | 241 | LeuAsnGluLybProPheSerValGluAspThrTyrLeuLeuCybProAlaProIleLeu | 260 |
| Db | 942 | CTCATATGAAAGCCCTTTTCTGTGAAAGTACTTATTTTACTGTGTCCAGCGCTTACTTA | 1001 |
| Qy | 261 | LybGIuValGlyMetLybAlaHleuGlnValSerMetAsnAspGlyLeuSerPheHle | 280 |
| Db | 1002 | AAAGAAAGTTGGCATGAAAGCTGCATCCAGGTCACACATGAAGAGATGGCTCTCTTTATTC | 1061 |
| Qy | 281 | SerSerSerValHleHleThrThrThrHsCybSerAspGlySer | 295 |
| Db | 1062 | TCCAGTCTGTATCATCATCACCACTGTCTTCTGACGGTTCC | 1106 |
| RESULT 5 | | | |
| US-09-918-715-231 | | | |
| / Sequence 231, Application US/09918715 | | | |
| / Publication No. US20030017157A1 | | | |
| / GENERAL INFORMATION: | | | |
| / APPLICANT: Brad St. Croix | | | |
| / APPLICANT: Bert Vogelstein | | | |
| / APPLICANT: Kenneth Kinzler | | | |
| / TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS | | | |
| / FILE REFERENCE: 1107.00134 | | | |
| / CURRENT APPLICATION NUMBER: US/09/918,715 | | | |
| / CURRENT FILING DATE: 2001-08-01 | | | |
| / PRIOR APPLICATION NUMBER: 60/222,599 | | | |
| / PRIOR FILING DATE: 2000-08-02 | | | |
| / PRIOR APPLICATION NUMBER: 60/224,360 | | | |
| / PRIOR FILING DATE: 2000-08-11 | | | |

[illegible]

Db 1002 AAGAGTGGCATGAAAGTCGACCTCCAGGTGACGATGAAAGTGGCTCTTTATC 1061
Qy 281 SerSerValIleIleThrThrThiAcYSerAspGlySer 295
Db 1062 TCCAGTTCTGTCTATCATCATCACCAACACACTGTTCTGACGGTTCC 1106

RESULT 6

US-10-301-822-198
; Sequence 198, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P22RM
; CURRENT APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144) ... (1838)
US-10-301-822-198

Alignment Scores:
Pred. No.: 2,87e-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_copy_27_321 (1-295) x US-10-301-822-198 (1-5540)

Qy 1 G1yG1ng1yG1yA9gAG1uAPG1yG1yPro1aCyEYrG1yG1yPheA9PLeuYr 20
Db 222 GCGCAAGGGGAGCCGAGGAGATGGGGTCTCAGCTCTGACGGATTTGACCTGTAC 281
Qy 21 PheIleuA9PLeuS9rG1ySerValIeuhIshIstrPa9ngIuIleYrTYrPheVal 40
Db 282 TTCATTTTGGACAATCATGAGAGTGTCTGCACACATGGAATGAAATCTATTACTTTGTG 341
Qy 41 G1uG1n1euh1A9IleYrPheIleS9rProG1n1euhYrGmetSerPheIleValPheSer 60
Db 342 GAACAGTTGGCTCAAAATTCATGAGCCACAGTTGAAAGTCTTATATGTTTCTCC 401
Qy 61 ThrArg1yThrThrLeuMetLeuThrG1uA9PArgG1uG1n1leArgG1nG1yLeu 80
Db 402 ACCGAGAGAAACACTTAATGAACTGACAGAGACAGAGAAACAAATCCGTCAAGCCTTA 461
Qy 81 G1uG1u1euh1n1yValIeuhProG1yG1yA9PThrTYrMetH9g1uG1yPheG1uA9g 100
Db 462 GAAGAACTCCAGAAAGTTCTGCGAGAGAGAGACACTTATCATGATGAAGATTTGAAAG 521

Qy 101 AlAs9rG1uG1n1leYrTYrG1uA9nArgG1nG1yTYrArgThrAlAs9rValIle 120
Db 522 GCGATGACGAGATTTTATTTGAAAACAGACAGAGGATACAGACAGCGATCATATT 581
Qy 121 AlAleuThrA9PGLyG1uLeuhI9g1uA9PLeuPheTYrSerG1uA9G1uAlA9n 140
Db 582 GCTTGACATGAGAGAACTCCATGAAGATCTCTTTTCTATTATCAGAGAGGAGCTTAAT 641
Qy 141 ArgSerThrA9PLeuG1yAlIleValTYrCy9ValG1yValIyA9PLeuA9nG1uThr 160
Db 642 AGGTCTGAAGATCTTGGTGAATTTTACTGTGTGTGTGAAAGATTTCAATGAAGACA 701
Qy 161 G1uLeuh1A9rG1leAlA9PSeTYrA9PShI9ValPheProValA9nA9PGLyPheG1n 180
Db 702 CAGCTGCCCGGATGTGGGACAGTACATGTGTTCCCGTAATGACGCTTTCAAG 761
Qy 181 AlAleuG1nG1yIleIleIshSerIleLeuh1yA9PSeTYrS9rIleG1uIleuAlA9a 200
Db 762 GCTTGCAAGGACATCATCCACTCAATTTTGAAGAGTCCGATCGAAATTTCTAGCAGCT 821
Qy 201 G1uA9PSeThrIleCy9AlI9g1yG1uSerPheG1n1yAlI9ValA9rG1yA9nG1yPhe 220
Db 822 GAACATCCACCATATGTGAGAGAGAGTCAATTCAGTTGTCTGTGAGAGAGAAAGGCTTC 881
Qy 221 ArgH1sAlA9rA9nValA9PArgValIleuCy9SerPheIyS9rIleA9nA9PSeValThr 240
Db 882 CGACATCCCGCAACGTCGACAGGTCCTCTGACGCTTCAAGATCATGATCGCTACACA 941
Qy 241 LeuA9nG1uYrPProPheSerValG1uA9PThrTYrLeuLeuCy9ProAlA9rIleu 260
Db 942 CTCAATGAGAGAGCCCTTTCTGTGAGAGATCTTAATTAATGATGTCCAGGCGCTATCTTA 1001
Qy 261 Ly9G1uValG1yMetLy9AlA9leuG1nValI9SerMetA9nA9PGLyLeuSerPheIle 280
Db 1002 AAGAAAGTTGACATGAAGCTGCACTCCAGGTGACATGAAGATGAGATGGCTCTTTATC 1061
Qy 281 SerSerValIleIleThrThrThiAcYSerAspGlySer 295
Db 1062 TCCAGTTCTGTCTATCATCATCACCAACACACTGTTCTGACGGTTCC 1106

RESULT 7

US-10-474-794-176
; Sequence 176, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107,00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-176

Alignment Scores:
Pred. No.: 2,87e-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

```
US-09-970-076-2_copy_27_321 (1-295) x US-10-474-794-176 (1-5540)
QY 1 G1YGLNG1YGYARARGLUAPRG1YGLYPRALCYETRYG1YGLYPHEAPLEUTYR 20
| | | | |
DB 222 GGGCAAGGGGAGCGAGGAGATGGGGCTCCAGCTCGTACCGGGATTGACCTGTAC 281
QY 21 PHE1LEUAPLYSERGLYSERVALLEUHIH1ETPAANG1U1ETRYTPHEVAL 40
| | | | |
DB 282 TTCATTTTGGCAAAATCAGAGAGTGCTGCACCACTGGAATGAAATCTATTACTTTG 341
QY 41 G1UG1LEU1A1H1S1YSPHE1LESERPROG1LEU1A1RGMESERPH1E1VALPHE 60
| | | | |
DB 342 GAACAGTTGGCTCAAAATTCATCAGCCACAGTTGGAATGCTTTATTTGTTCTCC 401
QY 61 THRARG1YTHRTHREUMETLYLEU1A1RGMESERPH1E1VALPHE 80
| | | | |
DB 402 ACCCGAGGAACCACTTAATGAAATCTGACAGAAACAGAAACAAATCCCTCAAGGCT 461
QY 81 G1UG1LEU1GLYVALLEUPROG1YGLYASPTHTYRMECH1SGUG1YPHEGLUARG 100
| | | | |
DB 462 GAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATGATGAAAGATTGAAAG 521
QY 101 ALASERGLU1GLY1ETRYRGLU1A1RGMESERPH1E1VALPHE 120
| | | | |
DB 522 GCCAGTGAAGAGATTATTAATGAAACAGCAAGGTAACAGACAGCCAGCTCATCAT 581
QY 121 ALALEUTHRASPGLYGLUEUHIH1A1RGMESERPH1E1VALPHE 140
| | | | |
DB 582 GCTTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTCAAGAGAGAGGCTAAT 641
QY 141 ARGSEAR1A1RGMESERGLY1A1LEVALTYR1CYVAL1GLYVALY1A1RGMESER 160
| | | | |
DB 642 AGGTCTGAGATCTTGCTGCAATGTTACTGTTGCTGTAAGATTCATGAGACA 701
QY 161 G1U1LEU1A1RGMESERGLY1A1RGMESERPH1E1VALPHE 180
| | | | |
DB 702 CACTGAGCCCGAGATGCGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTCA 761
QY 181 ALALEU1GLY1LE1H1SER1LEU1A1RGMESERPH1E1VALPHE 200
| | | | |
DB 762 GCTCTGAGAGCATCATCTCAATTTTGAAGAGCTTCGATCGAAATTCCTHAGCACT 821
QY 201 G1UPROSER1H1E1CYVAL1AG1YGLY1SERPHE1GLY1A1RGMESER 220
| | | | |
DB 822 GAACCATCCACATATGTGACAGAGAGTCAATTCATGTCGTAAGAGAAACGGCTTC 881
QY 221 ARGH1A1A1RGMESERVALPHE1A1RGMESERPH1E1VALPHE 240
| | | | |
DB 882 CGACATGCCCGCAACGTGACAGGCTCTCTGACGCTTCAAGATCAATGACCTGGTCA 941
QY 241 LEU1A1RGMESERVALPHE1A1RGMESERPH1E1VALPHE 260
| | | | |
DB 942 CTCAATGAGAAAGCCCTTTCTGTCGAGAGATCTTATTATCTGTCTCCAGGCTTAT 1001
QY 261 LYSGL1VAL1GLY1E1H1SER1LEU1A1RGMESERPH1E1VALPHE 280
| | | | |
DB 1002 AAAGAAAGTGGCATGAAAGCTGCACCTCAGGTGACATGAAAGATGAGCTCTTAT 1061
QY 281 SERSEAR1A1RGMESERVALPHE1A1RGMESERPH1E1VALPHE 295
| | | | |
DB 1062 TCCAGTTCTGTCAATCATCACCAACACTGTTCTGACGGTTC 1106
RESULT 8
US-10-474-794-231
; Sequence 231, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
```

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; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-231
Alignment Scores:
Pred. No.: 2,876-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-09-970-076-2_copy_27_321 (1-295) x US-10-474-794-231 (1-5540)
QY 1 G1YGLNG1YGYARARGLUAPRG1YGLYPRALCYETRYG1YGLYPHEAPLEUTYR 20
| | | | |
DB 222 GGGCAAGGGGAGCGAGGAGATGGGGCTCCAGCTCGTACCGGGATTGACCTGTAC 281
QY 21 PHE1LEUAPLYSERGLYSERVALLEUHIH1ETPAANG1U1ETRYTPHEVAL 40
| | | | |
DB 282 TTCATTTTGGCAAAATCAGAGAGTGCTGCACCACTGGAATGAAATCTATTACTTTG 341
QY 41 G1UG1LEU1A1H1S1YSPHE1LESERPROG1LEU1A1RGMESERPH1E1VALPHE 60
| | | | |
DB 342 GAACAGTTGGCTCAAAATTCATCAGCCACAGTGAAGATGCTTTATTTGTTCTCC 401
QY 61 THRARG1YTHRTHREUMETLYLEU1A1RGMESERPH1E1VALPHE 80
| | | | |
DB 402 ACCCGAGGAACCACTTAATGAAACTGACAGAAACAGAAACAAATCCCTCAAGGCT 461
QY 81 G1UG1LEU1GLYVALLEUPROG1YGLYASPTHTYRMECH1SGUG1YPHEGLUARG 100
| | | | |
DB 462 GAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATGATGAAAGATTGAAAG 521
QY 101 ALASERGLU1GLY1ETRYRGLU1A1RGMESERPH1E1VALPHE 120
| | | | |
DB 522 GCCAGTGAAGAGATTATTAATGAAACAGCAAGGTAACAGACAGCCAGCTCATCAT 581
QY 121 ALALEUTHRASPGLYGLUEUHIH1A1RGMESERPH1E1VALPHE 140
| | | | |
DB 582 GCTTTGACTGATGAGAACTCCATGAAAGATCTTTTCTATTCAAGAGGAGGCTAAT 641
QY 141 ARGSEAR1A1RGMESERGLY1A1LEVALTYR1CYVAL1GLYVALY1A1RGMESER 160
| | | | |
DB 642 AGGTCTGAGATCTTGCTGCAATGTTACTGTGTTGTTGTAAGATTCATGAGACA 701
QY 161 G1U1LEU1A1RGMESERGLY1A1RGMESERPH1E1VALPHE 180
| | | | |
DB 702 CACTGAGCCCGAGATTCGGAAGTAAGATCATGTGTTCCGCTGATGACGGCTTCA 761
QY 181 ALALEU1GLY1LE1H1SER1LEU1A1RGMESERPH1E1VALPHE 200
| | | | |
DB 762 GCTCTGAGAGCATCATCTCAATTTTGAAGAGATCTCTGATCGAAATTCCTHAGCACT 821
QY 201 G1UPROSER1H1E1CYVAL1AG1YGLY1SERPHE1GLY1A1RGMESER 220
| | | | |
DB 822 GAACCATCCACATATGTGACAGAGAGTCAATTCATGTCGTAAGAGAAACGGCTTC 881
QY 221 ARGH1A1A1RGMESERVALPHE1A1RGMESERPH1E1VALPHE 240
| | | | |
DB 882 CGACATGCCCGCAACGTGACAGGCTCTCTGACGCTTCAAGATCAATGACCTGGTCA 941
QY 241 LEU1A1RGMESERVALPHE1A1RGMESERPH1E1VALPHE 260
| | | | |
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| | | | |
|--|------|---|------|
| Db | 942 | CTCAATGAGAAAGCCCTTTTCTGTGGAAAGTACTTATTACTGTGTCCAGCGCTATCTTA | 1001 |
| Qy | 261 | LYEGTUVAlGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIle | 280 |
| Db | 1002 | AAAGAACTGGGATGATAAAGCTGCACCTCCAGGCGACAGAAAGAGGCGCTCTTTTATTC | 1061 |
| Qy | 281 | SerSerSerValIleIleThrThrThrHisCysSerAspGlySer | 295 |
| Db | 1062 | TCCAGTCTGTGATCATCATCACCAACCACTGTTCTGAAGGTTCC | 1106 |
| RESULT 9 | | | |
| US-10-979-159-176 | | | |
| Sequence 176, Application US/1079159 | | | |
| Publication No. US20050142138A1 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Brad St. Croix | | | |
| APPLICANT: Bert Vogelstein | | | |
| APPLICANT: Kenneth Kinzler | | | |
| TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS | | | |
| FILE REFERENCE: 1107.00134 | | | |
| CURRENT APPLICATION NUMBER: US/10/979,159 | | | |
| PRIOR FILING DATE: 2004-11-03 | | | |
| PRIOR APPLICATION NUMBER: US/09/918,715 | | | |
| PRIOR FILING DATE: 2001-08-01 | | | |
| PRIOR APPLICATION NUMBER: 60/222,599 | | | |
| PRIOR FILING DATE: 2000-08-02 | | | |
| PRIOR APPLICATION NUMBER: 60/224,360 | | | |
| PRIOR FILING DATE: 2000-08-11 | | | |
| PRIOR APPLICATION NUMBER: 60/282,850 | | | |
| PRIOR FILING DATE: 2000-04-11 | | | |
| NUMBER OF SEQ ID NOS: 358 | | | |
| SOFTWARE: FASTSEQ for Windows Version 3.0 | | | |
| SEQ ID NO 176 | | | |
| LENGTH: 5540 | | | |
| TYPE: DNA | | | |
| ORGANISM: Homo sapiens | | | |
| US-10-979-159-176 | | | |
| Alignment Scores: | | | |
| Pred. No.: 2,87e-185 | | | |
| Score: 1536.00 | | | |
| Percent Similarity: 100.00% | | | |
| Best local Similarity: 100.00% | | | |
| Query Match: 9 | | | |
| Gaps: 0 | | | |
| US-09-970-076-2_COPY_27_321 (1-295) x US-10-979-159-176 (1-5540) | | | |
| Qy | 1 | GlyGlnGlyValArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyr | 20 |
| Db | 222 | GGCGAAGGGGAGCGCAGGAGGATGGGGGTCCAGCCTCTACGGCGGATTGGACTGTAC | 281 |
| Qy | 21 | PheIleLeuAspLysSerGlySerValLeuHisIleTPAemGluIleTyrPheVal | 40 |
| Db | 282 | TTCAATTTGGACAAATCAGGAAGTGTGTGCGACCACTGAAATGAATCTATTACTTTGTG | 341 |
| Qy | 41 | GluGlnLeuAlaHisLysPheIleSerProGlnLeuAlaGMetSerPheIleValPheSer | 60 |
| Db | 342 | GAAACAGTTGGCTCCAAATTCATCATCGCCACAGTTGAAGAAGTCTCTTATTTGTTTCCTC | 401 |
| Qy | 61 | ThrArgLysThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeu | 80 |
| Db | 402 | ACCGAGGAACAACCTTAAATGAATGACAGAAAGCAAGACAAATCCGTCAGGCTTA | 461 |
| Qy | 81 | GluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArg | 100 |
| Db | 462 | GAAAGAACTCCAGAAAGTTCTGCGCAGGAGAGACACTTACATGCAATGAAGATTGAAAGG | 521 |
| Qy | 101 | AlaSerGlnGlnIleTyrTyrGlnAsnArgGlnGlyTyrArgThrAlaSerValIleIle | 120 |
| Db | 522 | GCCAGTGGCAAGATTATTATGAAGAACAGCAAGGGTACAGAGACGCCAGCGTCACTCACTT | 581 |

| | | | |
|----|------|--|------|
| OY | 121 | laLeuThrAPRgIyGluLeuH;GIuAspPhePhePhetYrSeSglAArgGlAlaAsn | 140 |
| Dd | 582 | GCTTtAGTCATGGAGAATCCCAAGACATCTTTTCTATTCAGAGGGAAGCGCTTAT | 641 |
| OY | 141 | ArGeSerARgAsPLeuGIyAlaIleValTyrcysValGIyAllylAspPheaSngluThr | 160 |
| Dd | 642 | AGGTCTGAGATCTTGtGGCAATTGTtACTGTGTGTGTGAAAGATTTCATGAGACA | 701 |
| OY | 161 | GIuLeuAlaArgIIeAlaAspSerLyAspHisValPheProValaAsnAspGIyPheGln | 180 |
| Dd | 702 | CAGCTGGCCCCGAGATTGCAGACAGTAAGGATCATGTGTTCGCCGAAATGACGGCTTTCAG | 761 |
| OY | 181 | AlaLeuGInGlyIIelIleHisSerIleLeuLysLysSerCysIIegluIleLeuAlaIala | 200 |
| Dd | 762 | GCTCTGCAGAGCATCATCTCACATAATTGGAAGATCTTCATCGAAATTCCTGACACT | 821 |
| OY | 201 | GIuProSerThrIIecysAlaGIyGluSerPheGlnValValaArgGIyAsnGIyPhe | 220 |
| Dd | 822 | GAAcCATTCACCAATATGTGCAGAGAGATCATTTCAAGTTGTCTGTAGAGGAACGGCTTC | 881 |
| OY | 221 | ArgHIsalaaArgAsnValaAspArgValIleucCysSerPheLysIIeAsnAspSerValThr | 240 |
| Dd | 882 | CGAcATGCCCCCAACGTGAGACAGGCTCTCTGCAGCTTCAGAGTCANTGATCTCGGTACA | 941 |
| OY | 241 | LeuAngluIyProPheSerValGIuAspThrTyrlEuLeuCySProlaIleu | 260 |
| Dd | 942 | CTCATATGAGAACGCTTTTCTGTGGAAGATCACTTATTTACTGTGTCCAGCGCTATCTTA | 1001 |
| OY | 261 | LysGluValGIyMetLysAlaIalaLeuGlnValSerMetAsnAspGIyLeuSerPheIle | 280 |
| Dd | 1002 | AAAAGAGTGGCAAGAAAGCTGACCTCCAGGTCCAGCATGAACGATGGCGCTCTCTTTTATC | |
| OY | 281 | SerSerSerValIIelIethrThrThHisCysSerAspGIySer | 295 |
| Dd | 1062 | TTCAGTTCTGCATCATCACACACACACTGTTCTTGACGGTTC | 1106 |

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RESULT 10
US-10-979-159-231
; Sequence 231, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-979-159-231

Alignment Scores:
Pred. No.:          2,87e-185
Score:              1536.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:        100.00%
                    9
Gaps:               0

Length:            5540
Matches:           295
Conservative:      0
Mismatch:          0
Indels:            0

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QY      1  GLYGLNGLYG1YARGRG1UAAPG1YGLYPROALCYETRYG1YGLYPHEAPLEUYR 20
      222  GGGCAAGGGGAGCGCAGGAGATGGGGGTCGAGCCGTCGACGGCGATTGACCTGTAC 281
QY      21  PHE1LEUAPLYSERG1YSERVALLEUHIHISTRPANGLU1LETYTRYRPHVAL 40
      282  TTCATTTTGGACAAATCAGAGAGTGTGCTGCACCATGGAATGAAATCTATTACTTTG 341
QY      41  GLUG1LEUAIH1ETYSRPH1ESERPROG1LEUARGMERSERPHE1LEVALPHESER 60
      342  GAACAGTGGCTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTATTGTTTCTCC 401
QY      61  THRARG1YTHRTRLEUWELYSLEUTHRG1UAAPRG1UG1N1LEARG1NG1YLEU 80
      402  ACCCGAGAACCACTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTTA 461
QY      81  GLUG1LEUGL1NLYVALLEUPROG1YGLYASPTHTYRMECH1SG1UG1YPHEGLUARG 100
      462  GAAGAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATGCATGAAAGATTGAAAG 521
QY     101  ALASERGLUG1N1LETYTRYRG1UAAPARG1NG1YTRYRGRH1ASERVAL1LE1LE 120
      522  GCCAGTGAGCAGATTATATGAAAAACAGCAAGGGTACAGACAGCCAGCTCATCTATT 581
QY     121  ALALEUTHRASPGLYGLUEUH1SG1UASPLEUPHEPHE1YRSERG1UAARG1UALAASN 140
      582  GCTTTGACTGATGAGAACTCCATGAAAGACTCTTTTTCATTTCAGAGAGAGGCTTAAT 641
QY     141  ARGSEARARGAPLEUG1YAL1LEVALTRYCYEVALG1YVAL1YSAAPRHEANG1UTHR 160
      642  AGCTTCGAGATCTGTGGTCAATTGTACTGTGTGTTGTAAGATTCCAATGAGACA 701
QY     161  GL1LEUAIARGL1LE1ASPSERYASPH1EVALPHEPROVALAANAPRG1YPHEGLN 180
      702  CAGCTGGCCCGAGTCCGAGCAGTAAAGATCATGTGTTCCCGTAATGACGGCTTCAG 761
QY     181  ALALEUG1NG1Y1LE1LEH1SER1LELEUY1SEYSECY11LEGLU1LEUAI1ALA 200
      762  GCTCTCGAAGCATCATCCACTCAATTTTGAAGAAGCTCGCATGAAATTCATGACAGCT 821
QY     201  GIUPROSERTHR1LECYBALAG1YGLUSERPHENGL1VAL1VALARG1YANG1YPHE 220
      822  GAACATCCACCATATGTGACAGAGAGTCAATTTCAATGTCGTGAGAGAAACGGCTTC 881
QY     221  ARGH1E1ALARGANVALAAPARGVALLEUCYSESERPHE1YSL1EANAAPSERVAL1THR 240
      882  CGACATGCCCGCAACGTGACAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTCA 941
QY     241  LEUANG1ULYSPROPHESERVAL1GLUASPTHTYRLEU1LEUCYSPROAL1PRO1LEU 260
      942  CTCAATGAGAAAGCCCTTTTCTGTGAGAGATCTTATTACTGTCTCCAGCGCTATCTTA 1001
QY     261  LYEGL1VALG1YMETLYSAL1A1ALEUG1NVAL1SERMECHANAPRG1YLEUSERPHE1 280
      1002  AAAGAAGTTGACATGAAGCTGCATCCAGTCAAGTGAAGATGAGCTCTTTATTC 1061
QY     281  SERSESERVAL1LE1ETHTHTHTH1E1CYSESERAPG1YSESR 295
      1062  TCCAGTTCGTGCATCATCACCAACACACACTGTTCTGACGGTTCC 1106
      DB
      RESULT 11
      US-11-047-278-5
      ; Sequence 5, Application US/11047278
      ; Publication No. US20050196407A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Young, John A.T.
      ; APPLICANT: Bradley, Kenneth A.
      ; APPLICANT: Collier, Robert J.
      ; APPLICANT: Mogridge, Jeremy S.
      ; TITLE OF INVENTION: Anthrax Toxin Receptor
      ; FILE REFERENCE: 960296.97745
      ; CURRENT APPLICATION NUMBER: US/11/047,278
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      ; CURRENT FILING DATE: 2005-01-31
      ; PRIOR APPLICATION NUMBER: US/09/970,076
      ; PRIOR FILING DATE: 2001-10-03
      ; PRIOR APPLICATION NUMBER: 60/251,481
      ; PRIOR FILING DATE: 2000-12-05
      ; NUMBER OF SEQ ID NOS: 10
      ; SOFTWARE: PatentIn Ver. 2.1
      ; SEQ ID NO 5
      ; LENGTH: 5540
      ; TYPE: DNA
      ; ORGANISM: Homo sapiens
      ; FEATURE:
      ; NAME/KEY: CDS
      ; LOCATION: (144)..(1835)
      ; US-11-047-278-5

      Alignment Scores:
      Pred. No.: 2,876-185 Length: 5540
      Score: 1536.00 Matches: 295
      Percent Similarity: 100.00% Conservative: 0
      Best Local Similarity: 100.00% Mismatches: 0
      Query Match: 100.00% Indels: 0
      DB: Gaps: 0

      US-09-970-076-2_COPY_27_321 (1-295) x US-11-047-278-5 (1-5540)

      QY      1  GLYGLNGLYG1YARGRG1UAAPG1YGLYPROALCYETRYG1YGLYPHEAPLEUYR 20
      222  GGGCAAGGGGAGCGCAGGAGATGGGGGTCGAGCCGTCGACGGCGATTGACCTGTAC 281
QY      21  PHE1LEUAPLYSERG1YSERVALLEUHIHISTRPANGLU1LETYTRYRPHVAL 40
      282  TTCATTTTGGACAAATCAGAGAGTGTGCTGCACCATGGAATGAAATCTATTACTTTG 341
QY      41  GLUG1LEUAIH1ETYSRPH1ESERPROG1LEUARGMERSERPHE1LEVALPHESER 60
      342  GAACAGTGGCTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTATTGTTTCTCC 401
QY      61  THRARG1YTHRTRLEUWELYSLEUTHRG1UAAPRG1UG1N1LEARG1NG1YLEU 80
      402  ACCCGAGAACCACTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTTA 461
QY      81  GLUG1LEUGL1NLYVALLEUPROG1YGLYASPTHTYRMECH1SG1UG1YPHEGLUARG 100
      462  GAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATGCATGAAAGATTGAAAG 521
QY      101  ALASERGLUG1N1LETYTRYRG1UAAPARG1NG1YTRYRGRH1ASERVAL1LE1LE 120
      522  GCCAGTGAGCAGATTATATGAAAAACAGCAAGGGTACAGACAGCCAGCTCATCTATT 581
QY      121  ALALEUTHRASPGLYGLUEUH1SG1UASPLEUPHEPHE1YRSERG1UAARG1UALAASN 140
      582  GCTTTGACTGATGAGAACTCCATGAAAGACTCTTTTTCATTTCAGAGAGAGGCTTAAT 641
QY      141  ARGSEARARGAPLEUG1YAL1LEVALTRYCYEVALG1YVAL1YSAAPRHEANG1UTHR 160
      642  AGCTTCGAGATCTGTGGTCAATTGTACTGTGTGTTGTAAGATTCCAATGAGACA 701
QY      161  GL1LEUAIARGL1LE1ASPSERYASPH1EVALPHEPROVALAANAPRG1YPHEGLN 180
      702  CAGCTGGCCCGAGTTCGAGCAGTAAAGATCATGTGTTCCCGTAATGACGGCTTCAG 761
QY      181  ALALEUG1NG1Y1LE1LEH1SER1LELEUY1SEYSECY11LEGLU1LEUAI1ALA 200
      762  GCTCTCGAAGCATCATCCACTCAATTTTGAAGAAGCTCGCATGAAATTCATGACAGCT 821
QY      201  GIUPROSERTHR1LECYBALAG1YGLUSERPHENGL1VAL1VALARG1YANG1YPHE 220
      822  GAACATCCACCATATGTGACAGAGAGTCAATTTCAAGTGTCTGTGAGAGAAACGGCTTC 881
QY      221  ARGH1E1ALARGANVALAAPARGVALLEUCYSESERPHE1YSL1EANAAPSERVAL1THR 240
      882  CGACATGCCCGCAACGTGACAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTCA 941
      DB
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QY 241 LeuAaNGluYpPProPheSerValGluAAspThrTyrlleuLeuCySProlAaProlleLeu 260
DB 942 CTCATATGAGAAAGCCCTTTTCTGTGAGAAATCTTATTACTGTCTCAGGCGCTATCTTA 1001
QY 261 LysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPhe1le 280
DB 1002 AAAGAAAGTGGCATGAAGCTGCACTCCAGGTGAGTGAACATGAGTGGCTCTTTTATC 1061
QY 281 SerSerSerValIleIleThrThrThiHisCySerSerAspGlySer 295
DB 1062 TCAGATTCTGTCATCATCACCAACACACACTGTTCTGACGGTTCC 1106

RESULT 12
US-10-038-307-17
; Sequence 17, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANYNK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ. ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-17

Alignment Scores:
Pred. No.: 1,396-185 Length: 1674
Score: 1532.00 Matches: 294
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.74% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-10-038-307-17 (1-1674)
QY 1 G1YG1NG1YGLYARGAGG1UAAPG1YGLYPR0ALCYSTYRGLYGLYPheAAspLeuTYR 20
DB 91 GGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCCGTGACGCGGATTTGACCTGTAC 150
QY 21 Phe1leuAAspLysSerGlySerValleuH1SH1STrAsnGlu1leTYRtyrPheVal 40
DB 151 TTCATTTTGGACAAATAGAGAGTGTCTGACCACTGGAAATCTTATTCTTTGTG 210
QY 41 GluGlnLeuAlaH1slyPhe1leSerProGlnLeuArgMetSerPhe1leValPheSer 60
DB 211 GAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCCCTTATTGTTCTCC 270
QY 61 ThrArgGlyThrThrleuMetLysleuThrGluAAspArgGluGlnleatGng1yLeu 80
DB 271 ACCCGAGAACCAACTTAAATGAAACTGACAGAAACAGAAACAAATCCGTCAAGGCTTA 330
QY 81 GluGluLeuGlnLysValleuProGlyGlyAAspThrTyrlleuH1slyGluGlyPheGluArg 100
DB 331 GAAGAACTCCAGAAAGTCTTCCAGAGAGAGACACTTACATGATGAAGATTTGAAGG 390
QY 101 AlSerGluGln1leTYRtyrGluAAsnArgGng1yTYRArgThrAlaSerVal1le1le 120
DB 391 GCCAGTGAAGCAGATTTATTAAGAAAACAGCAAGGGTACAGACAGCCAGCTCATCAT 450
QY 121 AlaLeuThrArgGlyGluLeuH1slyGluAAspLeuPheHeryrSerGluArgGluAlaAsn 140
DB 451 GCTTTGACTGATGAGAACTCCATGAAGATCTTTTTCATTCAGAGAGGGGAGCTTAAT 510
QY 141 ArgSerArgAspLeuGlyAla1leVal1yrcyvalGlyValLysAAspPheAsnGluThr 160
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DB 511 AGGCTGAGATCTTGTGCAATTTGTTATCTGATGGTGTGAAGATTTCAATGAGACA 570
QY 161 GlnLeuAlaArgG1leAlaAspSerLysAspH1sValPheProValAsnAspGlyPheGln 180
DB 571 CAGCTGGCCCGGATGGAGTGGAGCAGTAAGATCATGTGTTCCTGTGATGACGGCTTTCAG 630
QY 181 AlaLeuGng1y1le1leH1sSer1leLeuLysSerCyS1leGlu1leuAlaAla 200
DB 631 GCTTGCAGGCAATCATCTCAATTTTGAAGATCTTGCATCGAAATTTCTAGCAGCT 690
QY 201 GluProSerThr1leCySAlaGlyGlySerPheGlnValValArgGlyAsnGlyPhe 220
DB 691 GAACATCCACCATATGTGACAGAGATCATTTCAAGTTCTCGTAGAGAGAAAAGGCTTC 750
QY 221 ArgH1sAlaArgAsnValAspArgValleuCySerPheLys1leAsnAspSerValThr 240
DB 751 CGACATGCCCGCAACGGGACAGGGTCTCTGACAGTTCAAGATCATGACTCGGTCCACA 810
QY 241 LeuAaNGluYpPProPheSerValGluAAspThrTyrlleuLeuCySProlAaProlleLeu 260
DB 811 CTCATATGAGAAAGCCCTTTTCTGTGAAAGATCTTATTACTGTGTCCAGCGCTATCTTA 870
QY 261 LysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPhe1le 280
DB 871 AAAGAAAGTGGCATGAAGCTGCACTCCAGGTGAGTGAACATGAGATGGCTCTTTTATC 930
QY 281 SerSerSerValIleIleThrThrThiHisCySerSerAspGly 294
DB 931 TCAGATTCTGTCATCATCACCAACACACTGTTCTGACCGT 972

RESULT 13
US-10-201-292-17
; Sequence 17, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANYNK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ. ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-17

Alignment Scores:
Pred. No.: 1,396-185 Length: 1674
Score: 1532.00 Matches: 294
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.74% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-10-201-292-17 (1-1674)
QY 1 G1YG1NG1YGLYARGAGG1UAAPG1YGLYPR0ALCYSTYRGLYGLYPheAAspLeuTYR 20
DB 91 GGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCCGTGACGCGGATTTGACCTGTAC 150
QY 21 Phe1leuAAspLysSerGlySerValleuH1SH1STrAsnGlu1leTYRtyrPheVal 40
DB 151 TTCATTTTGGACAAATAGAGAGTGTCTGACCACTGGAAATCTTATTCTTTGTG 210
QY 41 GluGlnLeuAlaH1slyPhe1leSerProGlnLeuArgMetSerPhe1leValPheSer 60
DB 211 GAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCCCTTATTGTTCTCC 270
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 238.049 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536
Sequence: 1 GCGGRREDGPGACGCGFDLY.....GLSFSSSVITTTTSCSDS 295

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-TRANS=human40.csl -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076@cgn_1_1_675@runat_14122005_111853_21065
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-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Published Applications NA New:*

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2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
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8: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1536 | 100.0 | 5540 | 7 | US-11-186-284-198 |
| 2 | 145.5 | 9.5 | 4740 | 7 | US-11-080-026-3 |
| 3 | 131 | 8.5 | 11447 | 7 | US-11-186-284-25 |
| 4 | 122 | 7.9 | 2834 | 6 | US-10-750-185-39040 |
| 5 | 113.5 | 7.4 | 1325 | 6 | US-10-750-185-56394 |
| 6 | 113.5 | 7.4 | 2501 | 6 | US-10-821-234-182 |
| 7 | 113.5 | 7.4 | 3449 | 6 | US-10-131-826A-293 |
| 8 | 111 | 7.2 | 3564 | 6 | US-10-601-368-20 |

| | | | | | | |
|----|-------|-----|-------|---|---------------------|--------------------|
| 9 | 111 | 7.2 | 4858 | 6 | US-10-601-368-19 | Sequence 19, Appl |
| 10 | 107.5 | 7.0 | 3175 | 6 | US-10-995-561-464 | Sequence 464, App |
| 11 | 107.5 | 7.0 | 3464 | 6 | US-10-995-561-465 | Sequence 465, App |
| 12 | 107.5 | 7.0 | 3468 | 6 | US-10-995-561-466 | Sequence 466, App |
| 13 | 107 | 7.0 | 3564 | 6 | US-10-601-368-2 | Sequence 2, Appl1 |
| 14 | 107 | 7.0 | 3967 | 7 | US-11-000-463-574 | Sequence 574, App |
| 15 | 107 | 7.0 | 3969 | 7 | US-11-000-463-102 | Sequence 102, App |
| 16 | 107 | 7.0 | 5042 | 6 | US-10-601-368-1 | Sequence 1, Appl1 |
| 17 | 105.5 | 6.9 | 3868 | 6 | US-10-995-561-404 | Sequence 404, App |
| 18 | 103.5 | 6.7 | 2755 | 6 | US-10-750-185-25275 | Sequence 25275, A |
| 19 | 101.5 | 6.6 | 47572 | 6 | US-10-995-561-13356 | Sequence 13356, A |
| 20 | 100 | 6.5 | 2773 | 7 | US-11-102-240-33 | Sequence 33, Appl1 |
| 21 | 96 | 6.2 | 3884 | 6 | US-10-601-368-17 | Sequence 17, Appl |
| 22 | 94 | 6.1 | 1062 | 7 | US-11-137-465-11 | Sequence 11, Appl1 |
| 23 | 94 | 6.1 | 1347 | 7 | US-11-137-465-12 | Sequence 12, Appl |
| 24 | 91.5 | 6.0 | 1881 | 6 | US-10-467-657-5431 | Sequence 5431, Ap |
| 25 | 84.5 | 5.5 | 2715 | 6 | US-10-507-275-4 | Sequence 4, Appl1 |
| 26 | 82 | 5.3 | 3189 | 7 | US-11-137-465-10 | Sequence 10, Appl |
| 27 | 81.5 | 5.3 | 1688 | 6 | US-10-510-386-157 | Sequence 157, App |
| 28 | 81 | 5.3 | 11115 | 6 | US-10-513-786-6 | Sequence 6, Appl1 |
| 29 | 81 | 5.3 | 11115 | 6 | US-10-513-786-8 | Sequence 8, Appl1 |
| 30 | 79.5 | 5.2 | 2317 | 6 | US-10-793-626-4357 | Sequence 4357, Ap |
| 31 | 79.5 | 5.2 | 2987 | 6 | US-10-793-626-3398 | Sequence 3398, Ap |
| 32 | 79.5 | 5.2 | 3366 | 6 | US-10-467-657-6111 | Sequence 6111, Ap |
| 33 | 78.5 | 5.1 | 1895 | 6 | US-10-750-185-42451 | Sequence 42451, A |
| 34 | 78 | 5.1 | 1329 | 6 | US-10-467-657-3293 | Sequence 3293, Ap |
| 35 | 78 | 5.1 | 1443 | 6 | US-10-467-657-3291 | Sequence 3291, Ap |
| 36 | 77.5 | 5.0 | 960 | 6 | US-10-793-626-1039 | Sequence 1039, Ap |
| 37 | 77.5 | 5.0 | 1311 | 6 | US-10-763-612A-118 | Sequence 178, Appl |
| 38 | 77.5 | 5.0 | 20600 | 6 | US-10-829-826B-91 | Sequence 91, Appl |
| 39 | 77.5 | 5.0 | 28586 | 6 | US-10-829-826B-89 | Sequence 89, Appl |
| 40 | 77.5 | 5.0 | 28586 | 6 | US-10-829-826B-90 | Sequence 90, Appl |
| 41 | 76.5 | 5.0 | 1548 | 6 | US-10-467-657-7037 | Sequence 7037, Ap |
| 42 | 76 | 4.9 | 1407 | 6 | US-10-467-657-4369 | Sequence 4369, Ap |
| 43 | 75.5 | 4.9 | 8157 | 6 | US-10-523-912-1 | Sequence 1, Appl1 |
| 44 | 75 | 4.9 | 3435 | 6 | US-10-793-626-3648 | Sequence 3648, Ap |
| 45 | 74.5 | 4.9 | 2361 | 6 | US-10-467-962B-102 | Sequence 102, App |

ALIGNMENTS

RESULT 1
US-11-186-284-198
: Sequence 198, Application US/11186284
: Publication No. US20050266493A1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Berger, Allison
: APPLICANT: Guillemette, Tracy L.
: APPLICANT: Kamackar, Shubhangi
: APPLICANT: Schlegel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Thibodeau, Stephen N.
: APPLICANT: Burgart, Lawrence J.
: TITLE OR INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: TITLE OR INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: THERAPY OF COLON CANCER
: FILE REFERENCE: MP01-029P2RNM
: CURRENT APPLICATION NUMBER: US/11/186,284
: CURRENT FILING DATE: 2005-07-21
: PRIOR APPLICATION NUMBER: US/10/301,822
: PRIOR FILING DATE: 2002-11-21
: PRIOR APPLICATION NUMBER: US 60/339,971
: PRIOR FILING DATE: 2001-12-10
: PRIOR APPLICATION NUMBER: US 60/361,978
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/381,988
: PRIOR FILING DATE: 2002-05-20
: NUMBER OF SEQ ID NOS: 228
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 198
: LENGTH: 5540
: TYPE: DNA

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; ORGANISM: Homo Sapiens
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (144) ... (1838)
US-11-186-284-198

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Alignment Scores:

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| Pred. No.: | 3,42e+180 | Length: | 5540 |
| Score: | 1536.00 | Matches: | 295 |
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| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |

US-09-970-076-2_COPY_27_321 (1-295) x US-11-186-284-198 (1-5540)

| | | | |
|----|------|---|------|
| Oy | 1 | 1lylYngInglYglYARGARGlUaAspG1YglYProAlaCysTrpYnglYglYpHaAspLeuThr | 20 |
| Db | 222 | GGGCAAGGGGGAGCGAGGGAGAGATGGGGGGCTCCAGCTGTCTACGGGGGATTTGACCTTGAC | 281 |
| Oy | 21 | PheIleLeuAAspLYSerSerGlySerValLeuHIsHISTPAAsngluIleTYrTYrPheVal | 40 |
| Db | 282 | TTTCATTTTGGACAATTCAGGAAGTGTGTGCACCACTGGAAATGAATCTATTACTTTGTG | 341 |
| Oy | 41 | GlUglInLeuAlaHIsLYsPheHIsSerProGlnLeuArgMetSerPheIleValPheSer | 60 |
| Db | 342 | GAACAGTGGGTCCAAATTCATCATCGCCCAAGTGGAAATAGTCCCTTATTTGTTTCTCC | 401 |
| Oy | 61 | ThrArgGlyThrThrLeuMetLYsLeuThrGluAAspGluGlnIleAAsGlnGlyLeu | 80 |
| Db | 402 | ACCGGAGAACACTTATATGAACTGACAGAAACAGAAACAAATCCGTCAAGGCTTA | 461 |
| Oy | 81 | GluGluLeuGlnLYsValLeuProGlyGlyAspThrTYrMetHIsGluGlyPheGluArg | 100 |
| Db | 462 | GAAGAACTCCCAAAAGTTCTCGCCAGAGAGACACTTTCATGCACTGAAGGATTTGAAGG | 521 |
| Oy | 101 | AlaSerGluGlnIleTYrTYrGluAsnArgGlnGlyTYrArgThrAlaSerValIleIle | 120 |
| Db | 522 | GCCAGTGACAGATTATTATGAAACAGACAGGGTACAGACAGCCAGGCTCATCTT | 581 |
| Oy | 121 | AlaLeuThrAAspGlyGlnLeuHIsGluAspLeuPhePheTYrSerGluArgGluAlaAsn | 140 |
| Db | 582 | GCTTTGACTGATGAGAACTCCATGAACATCTCTTTTCTATTGACAGAGGAGGCTAT | 641 |
| Oy | 141 | ArgSerArgAspLeuGlyAlaIleValTYrCysValGlyValLYsAspPheAsnGluThr | 160 |
| Db | 642 | AGGTCCTCAGATCTTGGTGCAATTGTTTACTGTGTGTGGTGAAGAATTTCAATGAGACA | 701 |
| Oy | 161 | GlnLeuAlaArgIleAlaAspSerLYsAspHIsValPheProValAsnAspGlyPheGln | 180 |
| Db | 702 | CAGCTGGCCCGGATTTGCCGACAGTAAAGATCATGTGTTTCCCGTGAATGACGGCTTTGAG | 761 |
| Oy | 181 | AlaLeuGlnGlyIleIleHIsSerIleLeuLYsLYsSerCysIleGluIleLeuAlaAla | 200 |
| Db | 762 | GCTCGCAAGGCATCATCCACTCAATTTTGAAGAGCTCGTCATGGAATTTCTAGACAGCT | 821 |
| Oy | 201 | GluProSerThrIleCysAlaGlyGluSerPheGlnValValValArgGlyAsnGlyPhe | 220 |
| Db | 822 | GAACCATCCACCAATATGTGCAGAGAAAGTCATTTCAGTTGTGTGAGAGGAAACGGCTTC | 881 |
| Oy | 221 | ArgHIsAlaArgAsnValAspArgValLeuCysSerPheLYsIleAsnAspSerValThr | 240 |
| Db | 882 | CGACATGCCCGCAAGCTGACAGGGTCTCTGCACACTTCAGATCAATGATCATCGGTACA | 941 |
| Oy | 241 | LeuAsnGluLYsProPheSerValGluAspThrTYrLeuLeuCysProAlaProIleLeu | 260 |
| Db | 942 | CTCAATGAGAAAGCCCTTTTCTGTGGAAATCTTATTACTGTGTCCAGCGCTATCTTA | 1001 |
| Oy | 261 | LYsGluValGlyMetLYsAlaAlaLeuGlnValAspMetAsnAspGlyLeuSerPheIle | 280 |
| Db | 1002 | AAAGAAAGTTGGCATAAAGCTGACACTCCAGGTCACACATGAAGAGAGGCTCTCTTTATTC | 1061 |
| Oy | 281 | SerSerSerValIleIleThrThrThrHIsCysSerAspGlySer | 295 |

Db 1062 TCCAGTCTGTCAATCACCACACACTGTTCTGACGGTCC 1106

RESULT 2

US-11-080-026-3

; Sequence 3, Application US/11080026
; Publication No. US20050260192A1

APPLICANT: Springer, Timothy A.

APPLICANT: Lu, Chafen

TITLE OF INVENTION: DESIRED CO

CURRENT APPLICATION NUMBER: US/11/080,026

; PRIOR APPLICATION NUMBER: 09

PRIOR APPLICATION NUMBER: US 60/229,700

; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 3

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; TYPE: DNA

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US-11-080-026-3

Alignment Scores:

Score:

Best Local Site

DB:

US-09-970-076-2_COPY_27_32

18 2y

[illegible]

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Oy 175 ValLenAapGjLyPhcGAlaIenCingLyIleIleH;assertIleuLyLySerGys 194
Oy |||||-----|||||:::|||||:::|||||
Db GTGAATTAAC---TTTGAGGCTCTGAAACCAATTCAGAACCAAGCTTCGGGAAG----- 10655
Oy 195 IlegIuIleuAlaIaIaGluPProSerThrIleCysAlaGlyIuSerPheGluValVal 214
Oy ||||| ||||| ||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 1066 -----ATCTTTGGCAGTCGAGGGTACTCAGACAGGAGTAGACAGCTCCTTTGAGCAGTAG 1119
Oy 215 ValArgGlyAengLyPheArgH;eAla 223
Oy ::| ||||| |||||
Db 1120 ATGTCTCAGGAAGGCTTCAGCGCTGCC 1146

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RESULT 3
US-11-186-284-25
; Sequence 25, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
; US-11-186-284-25

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| Score: | 131.00 | Matches: | 59 |
| Percent Similarity: | 48.99% | Conservative: | 38 |
| Best Local Similarity: | 25.80% | Mismatches: | 75 |
| Query Match: | 8.53% | Indels: | 26 |
| DB: | 7 | Gaps: | 13 |

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|----|------|---|------|
| Oy | 18 | AspLeuTyrPheIleLeuAspLysSerCysVal---LeuH1AsnIleArgGlnIle | 36 |
| | | | |
| Db | 1318 | GATATGTGCTTTTGGTGTGAGCGCTCCATAGCATGTGGAGATGCAGAACTTTGTTAAAGTT | 1377 |
| Oy | 37 | TyrTyrPheValGlnGlnLeuAlaIleValPhe---IleSerPro---GlnLeuArgMet | 54 |
| Db | 1378 | AGAGCCTTTTGGAGAGTCTTGTAAAGTTTGAAATTTACCAAAATGGGGTCCAGATT | 1437 |
| Oy | 55 | SerPheIleValPheSerThr-----ArgGlnThrIleMetLysLeuThrGln | 71 |
| | | | |
| Db | 1438 | AGTTGTGTGCATATCAGCCGGATCTCATCTAGATGCATCTTTGAGAAAAAATTCACCAA | 1497 |

Oy 72 AsprhngluginlIearxgInglYleuclnIgluleuInlYsValIeuprO-----gIy 89
 Db 1498 GTTGAGATATAATT-----GAGCAATAAACACCTTCCCTTACAGAGGA 1542
 Oy 90 GlYAspThrTyrmecHlsglulYpHeclulArgAlaserIugInlIeTyTyrcIulAsn 109
 Db 1543 GGATCTACAAATACTGGCAAAAGCAATAGACTTATGTCAAGAGAAATATTGTGTGCATGC 1602
 Oy 110 ArgInglYTyraGthr-----AlaserValIeIleAlaIeuthAspGlycluleu 127
 Db 1603 AAG---GGATCAAAAGCAATAGTCCAAAGGTCAATGATTCTTATCACGAGTGGAGAA-- 1658
 Oy 128 HlsglulAspleuPhePheTysercIulArgIulAlasnArgserArGAspleuclYAla 147
 Db 1657 TCATCAAGTGGCTTTC-----AGAGATCCTCGATTAACAGGAAATTCAGATGTT 1707
 Oy 148 IlleValTyrcysValglYValIyAspPheasnIulthrIcInleuAlaArgIleAlaAsp 167
 Db 1708 GAATCTTTCGACGTTGGTGTGAAGATGCCCTTGGCTCAGAAATTGGAAAGCATATGGCTCT 1766
 Oy 168 -----SerIyAspHlIeValIePheProValAsnAspGlyPheGlnAlaIeugInglYIle 185
 Db 1768 CCTCCTCGACAGACCCATGTCTTCAACAGTGAAGAT--TTTGATGCTTTTCAAGAGATA 1824
 Oy 186 IlleHlsSerIleleuYslyserCyAlleGlnIle-----leuAlaAla 200
 Db 1825 TCTTTTGAACACACAGCTTATCTGCCTTGAATTGAGCAAGAAATGGACGCT 1878

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? RESULT 4
? US-10-750-185-39040/c
? Sequence 39040, Application US/10750185
? Publication No. US20050260603A1
? GENERAL INFORMATION:
? APPLICANT: MMI GENOMICS, INC.
? APPLICANT: DENISE, Sue K.
? APPLICANT: KERR, Richard
? APPLICANT: ROSENFELD, David
? APPLICANT: HOLM, Tom
? APPLICANT: BATES, Stephen
? APPLICANT: FANTIN, Dennis
? TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
? FILE REFERENCE: MM11100-2
? CURRENT APPLICATION NUMBER: US/10/750,185
? CURRENT FILING DATE: 2003-12-31
? PRIOR APPLICATION NUMBER: US 60/437,482
? PRIOR FILING DATE: 2002-12-31
? NUMBER OF SEQ ID NOS: 64922
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 39040
? LENGTH: 2834

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ORGANISM: Bovine 19866880867914
US-10-750-185-39040

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| Score: | 123.00 |
| Percent Similarity: | 50.00% |
| Best Local Similarity: | 29.03% |
| Query Match: | 7.94% |
| DB: | 6 |
| Length: | 2834 |
| Matches: | 54 |
| Conservative: | 39 |
| Mismatches: | 71 |
| Indels: | 24 |
| Gaps: | 10 |

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US-09-970-076-2_COPY_27_321 (1-295) x US-10-750-185-39040 (1-2834)

Oy 18 AspleuYrPhelIeuaaplySeSGlySeValIeuhIshstRpaGlu----- 35
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Db 2115 GACATTACTTCCTTATTGACGGGTCTGCAGTACC-----CACCAAGACAGATTTC 2062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 36 ---IleYrTyrPheValGluGlnIeuaIahIeLyPhe---IleSerProGlnIeuaArg 53
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2061 GCGATGAAGGCTGTTTCATGATGACGTATTAAGATGTTTCCACGTTGACCGGAC--AGA 2005
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 54 MetSerPheIleVal-PheSerThrArgGlyThrThrLeuMetLybLeuThrGluAspar 73
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Best Local Similarity: 19.58% Mismatches: 109
Query Match: 7.39% Indels: 99
DB: 6 Gaps: 17

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Qy 2 GlnGlyGlyArgArgGlySerGly---GlyProAla----- 12
Db 1631 GAAGAGTGTGATGTGAGATGGGACGGGACAAACAGAGGAGATGTC 1572
Qy 13 -----CyGlyGlyGlyPheAspLeuThrPheIleuAspGlySerVal--- 29
Db 1571 CTGAGCCCTTCAGGCTCATTAACATCTACCTGCTAGATGATGACAGCATGGG 1512
Qy 30 -----LeuHleHleTPAEngIuLeuIleuIleuIleuIleuIleu 45
Db 1511 GCCAGCAATTCACAGAGCCAAAGTGTCTATCAATTAATGAGAGGTGCAAGT 1452
Qy 46 LysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThr 65
Db 1451 TATGCTGTGAAGCA-----AGATATGCTGTATGATACATATGCCACATCCCAAAATT 1398
Qy 66 LeuMetLysLeuThrGlu-----AspArgGluGlnIleArgGlnGlyLeuGlu 81
Db 1397 TGGGTCAAGTGTGTGAAGCAGACAGCATGATACAGATGGGTACAGAGCATCAAT 1338
Qy 82 GluLeu-----GlnLysValLeuProGlyGlyAspThrThrMetHleGluGly 97
Db 1337 GAATTCATTAATGAGACCAACAGTTGAGTACAGGAGCTAACACC----- 1293
Qy 98 PheGluAlaSerGluGlnIleIleThrGluLysArg----- 110
Db 1292 ----AAGAAGCCCTCCAGCAGGTATACAGCATGTAGTGGCCAGATGACGTCCCTCT 1236
Qy 111 GlnGlyThr---ArgThrAlaSerValIleIleIleAspLeuThrAspGly----- 125
Db 1235 GAAGGCTGAACCCGACCCGCGCATGATCATCTCTCACTGATGATGATGACAAACATG 1176
Qy 126 -----GluLeuHleGluAspLeuPhePheThrSerGlu 136
Db 1175 GCGCGGAGCCCAATTACTGTATGATGATGATGATGATGATGATGATGATGATGAT 1116
Qy 137 ArgGluAlaAspArgSerArgAspLeuGlyValAlaIleValThrCysValGly-----Val 154
Db 1115 CGCAAAACCCAGAGGAGATATATCTGATGTCTATGTGTTGGGCTCGGCGCTTGGTG 1056
Qy 155 LysAspPheAspGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 174
Db 1055 AACCAAGTGAACATCATGCTTGGCTTCCAAAGAAAGACATGACAAATGTGTTCAAA 996
Qy 175 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleIleSerIleLeuLysSerCys 194
Db 995 GTCAGAGAT--ATGAAACCTGGAAGATGTTTTCACAAAGATCGATGAAGC--- 942
Qy 195 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 214
Db 941 -----CAGTCTCTAGTCTCTGT----- 924
Qy 215 ValArgGlyAspGlyPheArgHisAlaArgAspValAlaAspArgValLeuCysSerPheLys 234
Db 923 -----GCGATGCTTGGGAACACAGAGAGGTACCAT----- 891
Qy 235 IleAspAspSerValThrLeuAspGlnLysPheProPheSerValGluAspThrThrLeuLeu 254
Db 890 -----TACCACACAGCAACCAAGCAGAGCCAGCAATCTCAGTC----- 855
Qy 255 CysProAlaProIleLeuLysGluValGlyMetLysValAlaAlaLeuGlnValSerMetAsn 274
Db 854 -----ATTGCCCTTCAAAGGACACAGAGAGCTGTATGGG----- 819
Qy 275 AspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrHisCys 291
Db 818 -----GCTGAGTGTCTGAGTACTTGTCTGCTGACAGACAGACATTTG 777

```

```

RESULT 7
US-10-131-826A-293
? Sequence 293, Application US/10131826A
? Publication No. US20050245730A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Maureen
? APPLICANT: Deforge, Laura
? APPLICANT: Denoyere, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerltsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P330R1C128
? CURRENT APPLICATION NUMBER: US/10/131,826A
? CURRENT FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 293
? LENGTH: 3449
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-131-826A-293

Alignment Scores:
Pred. No.: 0.0074 Length: 3449
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 7.39% Indels: 35
DB: 6 Gaps: 13

US-09-970-076-2_COPY_27_321 (1-295) x US-10-131-826A-293 (1-3449)

Qy 18 AspLeuThrPheIleuAspLysSerGlySerVal---LeuHleHleTPAEngIuLeu 36
Db 372 GACCTGCTTTCATCTACATGACCTTCGACAGTGTCAACCCCATGACTATGCAAGATC 431
Qy 37 TyrThrPhe---ValGluGlnLeuAlaHisLysAspPheIleSerProGlnLeu---ArgMet 54
Db 432 AAGAGTTCATCTGTGACATCTTGCATATCTTGTGACATTTGCTCTGATGTACCCGAGTG 491

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| | | | |
|---|------|---|------|
| Qy | 55 | SerHeIleValPheSerThrArgGlyThrThrLeu-----MetLeu | 69 |
| Db | 492 | GGCTGCTCCAAAT-----GGCAGCACTGTCAAGAAATGAGTTCCCTCAAGAC | 542 |
| Qy | 70 | ThrGluAparGrgJugInIleArgGInglyLeuGluGluGluValLeuProGly | 89 |
| Db | 543 | TTCAAGAGGAAGTCCGAGGTGAGAGGTCTCTCAAGAGAAAGAGCGGCACTGTCCACGGGG | 602 |
| Qy | 90 | GlyAserThrTrpMetHisGluGlyPheGluArgAlaSerGluGluIleTyrTyrGluAsn | 109 |
| Db | 603 | ACCATGACTGGAGCTGGCCATCCAGTAT-----GCCCTGAACATCGCATTTTCAGAA | 653 |
| Qy | 110 | ArgGInglyTyrArg-----ThrAlaSerValIleIleAlaLeuThrAsp | 124 |
| Db | 654 | GCAAGAGGGGGCCCGCCCTTAGGAGAAATGTCCACGGGTCAATATGATGTGTACAGAT | 713 |
| Qy | 125 | GlyGluLeuHisGluAparLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp | 144 |
| Db | 714 | GGGAGACCTCAGAGACTCCGTG-----GCCGAGTGGCTGCTAAGCACGGGAC | 761 |
| Qy | 145 | LeuGlyAlaIleValTyrCysValGlyVal-----LysAapPheAsnGluThrGInLeu | 162 |
| Db | 762 | ACGGGCACTCCAAATCTTTGGCATTTGTGGGCCAGGTAGCACTTCAACACCTTGAAGTCC | 821 |
| Qy | 163 | AlaArgIleAlaAparSerTyrAspHisValPheProValaAsnArgGlyPheGluAlaLeu | 182 |
| Db | 822 | ATTGGAGATGAGCCCAATGAGAGACCATGTCTTCTCTGTGGCCAAAT---TTGACGCAAGATT | 878 |
| Qy | 183 | GInglyIleIleHisSerIleLeuValysSerCysIleGluIleLeuAlaIleGluPro | 202 |
| Db | 879 | GAGACGCTGACCTCCGTCTTCCAGAAAGATTTGTGCAGCGGCCCAATGTGCAGCACCTGTG | 938 |
| Qy | 203 | SerThrIleCysAlaGlyGluSerPheGluValValaArgGlyAsnGlyPheArgHis | 222 |
| Db | 939 | GAGCATTAATCTGTGCC-----CACTTGTGCATCAACATCTCTGTGCTATACGTTCGACG | 992 |
| Qy | 223 | AlaArg-----AsnValAparArgValLeuCysSerPheValaAsnApar | 237 |
| Db | 993 | TGCAAAACAAGGCTCATCTCTCAACTCGGATCGACGCAATTGC-----AGAACTCAGAGAT | 1046 |
| Qy | 238 | SerValThrLeuAenglu | 243 |
| Db | 1047 | CTGTGTGCCATGAGAGAC | 1064 |
| RESULT 8 | | | |
| US-10-601-368-20 | | | |
| ; Sequence 20, Application US/10601368 | | | |
| ; Publication No. US20050260702A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Pan, Yang | | | |
| ; APPLICANT: Lotz, Jose M. | | | |
| ; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF | | | |
| ; FILE REFERENCE: 0734-275001 | | | |
| ; CURRENT APPLICATION NUMBER: US/10/601.368 | | | |
| ; CURRENT FILING DATE: 2003-06-23 | | | |
| ; PRIOR APPLICATION NUMBER: US/09/561.263A | | | |
| ; PRIOR FILING DATE: 2000-04-27 | | | |
| ; PRIOR APPLICATION NUMBER: US 09/322.790 | | | |
| ; NUMBER OF SEQ ID NOS: 40 | | | |
| ; SOFTWARE: FastSeq for Windows Version 3.0 | | | |
| ; SEQ ID NO 20 | | | |
| ; LENGTH: 3564 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Mus musculus | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: CDS | | | |
| ; LOCATION: (1)....(3564) | | | |
| US-10-601-368-20 | | | |
| Alignment Scores: | | | |
| Pred. No.: 0.016 Length: 3564 | | | |

| | | | |
|------------------------|--------|---------------|----|
| Score: | 111.00 | Matches: | 49 |
| Percent Similarity: | 37.93% | Conservative: | 28 |
| Best Local Similarity: | 24.14% | Mismatches: | 88 |
| Query Matchn: | 7.23% | Indels: | 38 |
| Dbl: | 6 | Gaps: | 9 |

US-09-9710-076-2_COPY_27_321 (1-295) x US-10-601-368-20 (1-3564)

```

QY      13 CyarTgTglGlyPheAapRLeuTYrPhelIleuAapRySberGtSberValIeuhIEHie 32
Dl      475 TGCCAGACTTAACATGACATCGATCGTCATTGTCTTAATGGCTCCAAACAGATC--TACC 531
QY      33 TrrApEnluileTYrTYrPheValGlulIeuAlahIsryPhe---IleSerPro--- 50
Dl      532 TGGGTGAAGGTCACACCTTCCTCATCAATATCTCTCAAAAAGTTCTACATTTAGGCCCGGC 591
QY      51 GlndueArGMeSerPheIleValPheSerThzArgLyThrThrIeumetyLyuThr 70
Dl      592 CAGATTCACAGTCGGAATATGTCACAGTATGAGAAGATGCCGTCATGATTCACATCTT--- 648
QY      71 GludApRArgGlunIlleArgGlInGleuglGluLeuglInlyuValIeuProGlyGly 90
Dl      649 AATAGCTACAGAGTCTGTAAAAAGATGTGTGGAGACCCGCCAGCCACATGTGACAGAGGA 708
QY      91 AsprhTrYmeThIesgluGlyPheGlu-----ArgAlaserGlunIlleTyTrtyr 107
Dl      709 GGGACAGAGACCCGCCACGGCATTTGGCATTTGAATTGSCAGCGCTCGAGGCTTTCACAGAG 768
QY      108 GludApRArgGlInGlyTYrArgThrAlaserValIleleAlaIeuthraPrgLyGluIeu 127
Dl      769 GTGTGAAGAAAGGGGCCAAG-----AAAGTAGATATTGTTCATCACAGAGCGGAATTC 822
QY      128 HisgluApR-----HisgluApR----- 130
Dl      823 CACGACAGCCCGACACTGAGAGAGTGATCCGGCAGAGCGAGAGACAACAGTGCACAGA 882
QY      131 -----IeuPheRhTySerGluArgGluAlaAspArgSerArgApRleu 145
Dl      883 TAGCGTGTGGCGGTTTTGGGGCTCTACACACCGCAGGGAGATCAATCCAGAGACTTTTCTA 942
QY      146 GlyAlaIleValIeTYrCYrValIGlyValIyeApR-----PheAsngluThrcIn 161
Dl      943 AATGAATCAATATCAATTCGCCAGGAGCCGTGACACAAAGCACTTCTTCAACGTCAAGAT 1002
QY      162 LeuAlaArgIleAlaApRSerLYeApRHleValPheProValaAspRGlyPheGlAla 181
Dl      1003 GAGCGCGGCCCTG-----AAGACATTGTGTATGCCCTTGGGACAGAGATCTTGACG 1053
QY      182 LeuIngIngly 184
Dl      1054 TTGGAAAGGC 1062

```

RESULT 9
US-10-601-368-19

```

; Sequence 19, Application US/10601368
; Publication No. US20050260702X1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 0734-275001
; CURRENT APPLICATION NUMBER: US/10/601.368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561.263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322.790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4856
; TYPE: DNA
; ORGANISM: Mus musculus

```

```
FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.0257 Length: 4858
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.23% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-601-368-19 (1-4858)

QY 13 CyetylglutylpheleapleuTyrrheleleuaplysSerGlySerValleuHleuHis 32
DB 502 TGCCAGACTTACATGACATGCTGATGCTTATGATGCTTCACACAGCATC---TACCCC 558
QY 33 TrpAengluileTyrrheleleuValleuHleuHisPhe---IleSerPro--- 50
DB 559 TGGGTGAGGTCCACACCTTCTCATCATATCTCTCAAAAGTCTTACATTGGCCCCGCC 618
QY 51 GluLeuArgMetSerPheleleuValPheSerThrArgGlyThrThrleuMetIysleuThr 70
DB 619 CAGATCCAGGTGGAGAAATAGTCCAGTATGAGAGATGCGCTCATGATTCACCTT--- 675
QY 71 GluAparArgGluGlnIleArgGlnIleuGlnIleuGlnIleuValleuProGlyGly 90
DB 676 AATGACTACAGGTGTGAAAGATGTGTGAGCCGCCACGCCCATTTGACAGAGAGA 735
QY 91 AspThrTyrrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrr 107
DB 736 GGGACAGAGACCCCGACGCGCATTTGGCATTAATTTGACCGCTTGAGGCTTTCCAGAG 795
QY 108 GluAparArgGlnIleTyrrArgThrAlaSerValIleIleAlaIleuThrAspGlyGlu 127
DB 796 GGTGAGAAAGAGGGCGCAG---AAAGTATGATTTGATCATCAGAGCGGGAATCC 849
QY 128 HisGluApar----- 130
DB 850 CACGACAGCCCGACACTGAGAGAGTATCCGCGACGAGAGAGACAACTGATCCAGA 909
QY 131 -----LeuphePheTyrrSerGluArgGluAlaAparSerArgAspLeu 145
DB 910 TACGCTGTGCGCTTTGGGCTACTACACCGCGGGGATCAATCCAGACATTTTCTA 969
QY 146 GlyAlaIleValIleTyrrCyValIleValIleAsp-----PheAengluThrGln 161
DB 970 AATGAATCAATATCATCGCAGCGACCCCTGACAGACACTTCTTCAACGTACAGAT 1029
QY 162 LeuAlaArgIleAlaAparSerIysAparHisValPheProValAparGlyPheGlnAla 181
DB 1030 GAGCGCGCCCTG-----AAGACATTTGATGCTTGGGAGACAGATCTTACG 1080
QY 182 LeuGlnIle 184
DB 1081 TTGGAAGGC 1089

RESULT 10
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
```

```
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.0366 Length: 3175
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.00% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-995-561-464 (1-3175)

QY 19 LeuTyrrheleleuAparIysSerGlySerVal----- 29
DB 243 GTGTAATTCGTGCTGACACCTCGAGAGAGTCCACATGACAGTCCCGACGACATCTG 302
QY 30 LeuHisIleThrAenglu---IleTyrrPheValGluGlnIleuAlaHisIysPheIle 48
DB 303 CTCTTCCACATGAAGCAGTTCGTCGCGAGTTCATCGCAGAGAGAGAGTTCAC 362
QY 49 SerProGluLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 64
DB 363 CTGACACAGGTGGCGCTGACCTGCGCTATAGCGCGCTGACATTTCTGACAGAGTGAG 422
QY 65 ThrleuMetIysleuThrGluAparArgGluGlnIleArgGlnIleuGlnIleuGln 84
DB 423 GTGTTACGCCACCGGCGACGACCGGGGCTCTTCATCAAGAACTGACAGGCGATCAGC 482
QY 85 IysValleuProGlyIleAparThrTyrrMetHisGluGlyPheGluAlaSerGluGln 104
DB 483 TCCTTCGCGCGCGC-----ACCTTCACGAGTCCGCGCTGCGCAATGACAGAGCAG 536
QY 105 IleTyrrGluAparArgGlnIleTyrrArgThrAlaSerValIleIleAlaIleuThrAsp 124
DB 537 ATCCGAGAGACCGGACGAGAGG-----ACGTCACATTCGCCGCTGATCACCGAC 590
QY 125 GlyIleuHisIleGluAparIysPheTyrrSerGluArgGluAlaAparSerArgAsp 144
DB 591 GGCACGTGACCGGACGCGCCCTGCGGGGATCATGAGTGAAGCGCGCGCGAG 650
QY 145 LeuGlyAlaIleValIleTyrrCyVal-----GlyValIys 155
DB 651 GAGGCGATCCGCGCTTCGCGCGCGCCCGACCAAGCTGAAGAGAGAGCGGCTTCGG 710
QY 156 AspPheAengluThr-----GlnleuAlaArgIleAlaAparSerIysAparHisValPhe 173
DB 711 GACATCGCCGACACGCGCGACGAGCTTACCGC-----AACGACTACGCCACC 758
QY 174 ProValAparArgIlePheGlnAlaLeuGlnIleIleHisSerIleu----- 190
DB 759 ATGCTGCCATTCACCGAGATCACCAGACCACTCAACGCAATCATCAAGATCATGATG 818
QY 191 -----LysIysSerGlyIleGluIle 197
DB 819 AACACAGAGCTTACGAGAGAGTCTACAAAGTGAAGTGCCTGGAATTC 866

RESULT 11
US-10-995-561-465
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 465
/ LENGTH: 3464
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-465

Alignment Scores:
Pred. No.: 0.0418 Length: 3464
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.00% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-995-561-465 (1-3464)

QY 19 LeuTYRPhelLeuLysSerGlySerVal----- 29
DB 243 GTGTACTTGTGCTGTGGACACCTCGAGAGCGTCAAGTCCATGCCCCAAGCAATCTTG 302
QY 30 LeuHISITPrAsnGlu---lLeTYRTrPheValGluGlnLeuAlaHisLysPheIle 48
DB 303 CTCTTCCACATGAAGCATGTCGTGCGGCACTTCATCAAGCCAGCTGAGAACAGATTCTAC 362
QY 49 SerProGlnLeuArgMetSerPhe-----lLeValPheSerThrArgGlyThr 64
DB 363 CTGGACCAAGTGGCGCTGAGCTGGCGCTAAGCGGCGCTGACCTTCTTACCAAGTGGAG 422
QY 65 ThrLeuMetLysLeuThrGluAparArgGluGlnlLeArgGlnLysLeuGln 84
DB 423 GTGTTCAGCCCAACGGGAGAGACCGGCGCTCTTCATCAAGAACCTGACAGGCGCATCAGC 482
QY 85 LysValLeuProGlyGlyAparThrTyMetHISgluGlyPheGluArgAlaSerGluGln 104
DB 483 TCCTTCGCGCGCGGAC-----ACCTTCAACCACTGCGCGCTGCGCCCAATGACGAGAGAG 536
QY 105 lLeTYRTrGluAparArgGlnGlyTyArgThrAlaSerVallleIleAlaLeuThrAsp 124
DB 537 ATCCGGACAGAGACCGGACAGAGGCG-----ACGTCACACTTCCCGCGTGCATCACCGAC 590
QY 125 GlyGluLeuHISgluAparLeuPhePheTySerGlnArgGluAlaAparSerArgAsp 144
DB 591 GGCACAGTCACCGGACAGCCCTGCGGGGCGATCAAGCTGACAGCGGCGGCGCGGAG 650
QY 145 LeuGlyAlaIleValTyArgVal-----GlyValLys 155
DB 651 GAGGGCATCCGGCTCTTCCGCGTGGCCCCCAACCAAGAACTGAAGAGACAGGCGCTGGG 710
QY 156 AspPheAparGluThr-----GlnLeuAlaArglleAlaAparSerLysAparHisValPhe 173
DB 711 GACATGCCAGACAGCGCGGACAGAGCTTACCG-----AACGACTAGCGCAC 758
QY 174 ProValAparArgLysPheGlnAlaLeuGlnGlyllelHisSerlleu----- 190
DB 759 ATGCTGCYCATCTCCACCGAGATCRAACAGACACCATCAACCGCATCAAGATCATG 818
QY 191 -----LysLysSerCysIleGluIle 197
DB 819 AAACACGAAGCTTACGAGAGTGTCTACAAAGTGAAGTGGCTGGAAATC 866

RESULT 12
US-10-995-561-466
/ Sequence 466, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: C1001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
```

```
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 466
/ LENGTH: 3468
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-466

Alignment Scores:
Pred. No.: 0.0419 Length: 3468
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.00% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-995-561-466 (1-3468)

QY 19 LeuTYRPhelLeuLysSerGlySerVal----- 29
DB 243 GTGTACTTGTGCTGTGGACACCTCGAGAGCGTCAAGTCCATGCCCCAAGCAATCTTG 302
QY 30 LeuHISITPrAsnGlu---lLeTYRTrPheValGluGlnLeuAlaHisLysPheIle 48
DB 303 CTCTTCCACATGAAGCATGTCGTGCGGCACTTCATCAAGCCAGCTGAGAACAGATTCTAC 362
QY 49 SerProGlnLeuArgMetSerPhe-----lLeValPheSerThrArgGlyThr 64
DB 363 CTGGACCAAGTGGCGCTGAGCTGGCGCTAAGCGGCGCTGACCTTCTTACCAAGTGGAG 422
QY 65 ThrLeuMetLysLeuThrGluAparArgGluGlnlLeArgGlnLysLeuGln 84
DB 423 GTGTTCAGCCCAACGGGAGAGACCGGCGCTCTTCATCAAGAACCTGACAGGCGCATCAGC 482
QY 85 LysValLeuProGlyGlyAparThrTyMetHISgluGlyPheGluArgAlaSerGluGln 104
DB 483 TCCTTCGCGCGCGGAC-----ACCTTCAACCACTGCGCGCTGCGCCCAATGACGAGAGAG 536
QY 105 lLeTYRTrGluAparArgGlnGlyTyArgThrAlaSerVallleIleAlaLeuThrAsp 124
DB 537 ATCCGGACAGAGACCGGACAGAGGCG-----ACGTCACACTTCCCGCGTGCATCACCGAC 590
QY 125 GlyGluLeuHISgluAparLeuPhePheTySerGlnArgGluAlaAparSerArgAsp 144
DB 591 GGCACAGTCACCGGACAGCCCTGCGGGGCGATCAAGCTGACAGCGGCGGCGCGGAG 650
QY 145 LeuGlyAlaIleValTyArgVal-----GlyValLys 155
DB 651 GAGGGCATCCGGCTCTTCCGCGTGGCCCCCAACCAAGAACTGAAGAGACAGGCGCTGGG 710
QY 156 AspPheAparGluThr-----GlnLeuAlaArglleAlaAparSerLysAparHisValPhe 173
DB 711 GACATGCCAGACAGCGCGGACAGAGCTTACCG-----AACGACTAGCGCAC 758
QY 174 ProValAparArgLysPheGlnAlaLeuGlnGlyllelHisSerlleu----- 190
DB 759 ATGCTGCYCATCTCCACCGAGATCRAACAGACACCATCAACCGCATCAAGATCATG 818
QY 191 -----LysLysSerCysIleGluIle 197
DB 819 AAACACGAAGCTTACGAGAGTGTCTACAAAGTGAAGTGGCTGGAAATC 866

RESULT 13
US-10-601-368-2
/ Sequence 2, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
```

```
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2

Alignment Scores:
Pred. No.: 0.0504 Length: 3564
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 6.97% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-601-368-2 (1-3564)
QY 13 CyeTyrGlyGlyPheAerPLeuTyrPheIleuAerLysSerGlySerValLeuHleHis 32
DB 475 TGCCAGACCTACATGACATCGTCATTCCTGATGCTCCACACAGCATC---TACCCC 531
QY 33 TrpAenGluIleTyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 50
DB 532 TGGGTGAGGTTGACGACTTCCTCATCAACATCTCTGAAAAGTTTACATTGGCCCGG 591
QY 51 GlnLeuAerGMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 70
DB 592 CAGATCCAGGTTGAGATTGTGCAGTATGCGAAGATGTGTCATGATTCACCTC--- 648
QY 71 GluAerArgGlnGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGly 90
DB 649 AACGACTACACAGCTGTAAAGATGTGTGAGAGCTGCCAGCCACATGACAGAGAGA 708
QY 91 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyr 107
DB 709 GGAACAGAGACCCGAGAGCATTTGGCATTTGAATTTCAGAGCTTCAGAGCTTCAGAG 768
QY 108 GluAerArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAerGlyGluLeu 127
DB 769 GGTGAAAGGAAAGAGGACCAAG-----AAGGTGATGATTGTCAACAGATGGGAGATCC 822
QY 128 HisGluAerPhe----- 130
DB 823 CACGACAGCCCGACAGCTCGAAGAGTGATCCAGCAAGAGCAAGCAAGCAAGCAAG 882
QY 131 -----LeuPhePheTyrSerGlyArgGlnAlaAerArgSerArgAerPhe 145
DB 883 TATCGCGTGGCCGCTCGGCTACTACACCGCAGGGGGATCAATCCAGAAATTTTCTTA 942
QY 146 GlnAlaIleValIleTyrCysValGlyValLysAerPhe-----PheAenGluThrGln 161
DB 943 AATGAATCAATATACATCGCCAGTACCTGATGACAAAGCACTTCTTCAATGTCATGAT 1002
QY 162 LeuAlaArgIleAlaAerSerLysAerPheIleValPheProValAenAerGlyPheGlnAla 181
DB 1003 GAGGCTGCTCTG-----AAGGACATTTGTCATGCTCGGGGAGACAGAAATCTTCAGC 1053
QY 182 LeuGlnGly 184
DB 1054 CTGGAAGGC 1062

RESULT 14
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aenudi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Jie
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 574
; LENGTH: 3967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-574

Alignment Scores:
Pred. No.: 0.0595 Length: 3967
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 6.97% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-11-000-463-574 (1-3967)
QY 13 CyeTyrGlyGlyPheAerPLeuTyrPheIleuAerLysSerGlySerValLeuHleHis 32
DB 524 TGCCAGACCTACATGACATCGTCATTCCTGATGCTCCACACAGCATC---TACCCC 580
QY 33 TrpAenGluIleTyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 50
DB 581 TGGGTGAGGTTGACGACTTCCTCATCAACATCTCTGAAAAGTTTACATTGGCCCGG 640
QY 51 GlnLeuAerGMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 70
DB 641 CAGATCCAGGTTGAGATTGTGCAGTATGCGAAGATGTGTCATGATTCACCTC--- 697
QY 71 GluAerArgGlnGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGly 90
DB 698 AACGACTACACAGCTGTAAAGATGTGTGAGAGCTGCCAGCCACATGACAGAGAGA 757
QY 91 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyr 107
DB 758 GGAACAGAGACCCGAGAGCATTTGGCATTTGAATTTCAGAGCTTCAGAGAGAG 817
QY 108 GluAerArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAerGlyGluLeu 127
DB 818 GGTGAAAGGAAAGAGGACCAAG-----AAGGTGATGATTGTCAACAGATGGGAGATCC 871
QY 128 HisGluAerPhe----- 130
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Db      872 CACGACAGCCAGACCTGGAGAGGTGATCCAGCAAGGAAAGACAACTAACAGA 931
      |||:::
Qy      131 -----LeuPhePheTyTserGluArgGluAlaAsnArgSerArgAspLeu 145
      |||:::
Db      932 TATGCGTGCCGCTCTGGGCTACTACACCGGAGGGATCATCCAGAACTTTTCTA 991
      |||:::
Qy      146 GYAlAlleValTyTserCysValGlyValIysAsp-----PheAsnGluThrGln 161
      |||:::
Db      992 AATGAATCAATACATACCGCAGTACCCGTGATGACAGACATCTTCAATGTCACTGAT 1051
      |||:::
Qy      162 LeuAlaArgIleAlaAspSerIysAspHisValPheProValAsnAspGlyPheGlnAla 181
      |||:::
Db      1052 GAGGCTGCCTTG-----AAGACATGTGATGATGCTGGGGGACAGAACTTTCAGC 1102
      |||:::
Qy      182 LeuGlnGly 184
      |||:::
Db      1103 CTGGAAGGC 1111

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RESULT 15
US-11-000-463-102
/ Sequence 102, Application US/11000463
/ Publication No. US20050266423A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Qian, Xiaohong B.
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhou, Ping
/ APPLICANT: Cao, Yi-Cheng
/ APPLICANT: Dmanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
/ FILE REFERENCE: 785CIP4CN
/ CURRENT APPLICATION NUMBER: US/11/000,463
/ CURRENT FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: 10/291,265
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/922,279
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 09/617,746
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/631,451
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 09/633,870
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 3969
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3618)
US-11-000-463-102

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Alignment Scores:
Pred. No.:      0.0595      Length:      3969
Score:          107.00      Matches:      49
Percent Similarity: 37.93%      Conservative: 28
Best Local Similarity: 24.14%      Mismatches:  88
Query Match:      6.97%      Indels:      38
DB:              7          Gaps:      9

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US-09-970-076-2_COPY_27_321 (1-295) * US-11-000-463-102 (1-3969)

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Qy      13 CysTyTgIyGlyPheAspLeuTyTyrPheIleLeuAspIysSerGlySerValIeuHis 32
      |||:::
Db      526 TCCCAAGCCTACATGAGACATGCTCATTTGCTCGATGGCTCCAAAGCATC---TACCC 582
      |||:::
Qy      33 TTPAnGluIleTyTyrPheValGluGlnLeuAlaHisIysPhe---IleSerPro--- 50
      |||:::
Db      583 TGGTGAGGTCACACATCTCTCATCAACATCCGMAAAAGTTTACATTGGCCCAAGG 642
      |||:::
Qy      51 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThreuMetIysLeuThr 70
      |||:::
Db      643 CAGATTCAGGTGGAGTTGCGATTGCGATGCGCAAGATGTGTCATGACTTCACTC--- 699
      |||:::
Qy      71 GluAspArgGluGlnIleArgGlnIyLeuGluGluIysValLeuProGlyGly 90
      |||:::
Db      700 AACGACTACAGGTCTGTAAAGATGCGTGAAGCTCCAGGCACATTCAGCAGAGAGA 759
      |||:::
Qy      91 AspThrTyTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyTyr 107
      |||:::
Db      760 GGAACAGAGACCCCGACGCGCATTTGCGATTGAATTGCAAGCTCAGAGGCTTTCAGAA 819
      |||:::
Qy      108 GluAsnArgGlnGlyTyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGlu 127
      |||:::
Db      820 GGTGAGGAGAAAGAGCCAG-----AAGTGATGATTGTCTATCACATGGGAGTCC 873
      |||:::
Qy      128 HisGluAsp----- 130
      |||:::
Db      874 CACGACAGCCAGACCTGGAGAGGTGATCCAGCAAGGAAAGACAACTAACAGA 933
      |||:::
Qy      131 -----LeuPhePheTyTserGluArgGluAlaAsnArgSerArgAspLeu 145
      |||:::
Db      934 TATGCGTGCCGCTCTGGGCTACTACACCGGAGGGATCATCCAGAACTTTTCTA 993
      |||:::
Qy      146 GYAlAlleValTyTserCysValGlyValIysAsp-----PheAsnGluThrGln 161
      |||:::
Db      994 AATGAATCAATACATCCCGCAGTACCCGTGATGACAGACATCTTCAATGTCACTGAT 1053
      |||:::
Qy      162 LeuAlaArgIleAlaAspSerIysAspHisValPheProValAsnAspGlyPheGlnAla 181
      |||:::
Db      1054 GAGGCTGCCTTG-----AAGACATGTGATGATGCTGGGGGACAGAACTTTCAGC 1104
      |||:::
Qy      182 LeuGlnGly 184
      |||:::
Db      1105 CTGGAAGGC 1113

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Search completed: December 19, 2005, 02:29:47
 Job time : 260.049 secs

APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-46

Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFI SPOLRMSFIYFSTRGTTLMK 67
DB 144 PECPGEMDI AFILDSGSI DSGDFQMKDFVAKMGQLASTSTSFSLQYSNLIKTHFT 203
QY 68 LTEDR-----EQIRQGLEIELQKVLPGSDTYMHGFEFASQIYYENRGYRTA-SVIAL 121
DB 204 FTFKSLSPQSLVDIVQLQ-----GLTYTASGIQVKELFPHSKNGARKSAKILIVI 258
QY 122 TDEGLHEDLFFYSE--REANRSDLAIVYCVGVKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDQQRDPDPLEYHVIPEAKA---GIRYAIGVDAFREPTALQELNTIGSAPSDHVF 315

QY 173 PVNDGFQALOGIHSILKSCIEILAAPEPTICAGSEFQVYVANGNGFRHARNVD 226
DB 316 KVGN-FVALRSIQROIQEK-----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 3
US-08-485-618-46
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago

STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-46

Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFI SPOLRMSFIYFSTRGTTLMK 67
DB 144 PECPGEMDI AFILDSGSI DSGDFQMKDFVAKMGQLASTSTSFSLQYSNLIKTHFT 203
QY 68 LTEDR-----EQIRQGLEIELQKVLPGSDTYMHGFEFASQIYYENRGYRTA-SVIAL 121
DB 204 FTFKSLSPQSLVDIVQLQ-----GLTYTASGIQVKELFPHSKNGARKSAKILIVI 258
QY 122 TDEGLHEDLFFYSE--REANRSDLAIVYCVGVKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDQQRDPDPLEYHVIPEAKA---GIRYAIGVDAFREPTALQELNTIGSAPSDHVF 315

QY 173 PVNDGFQALOGIHSILKSCIEILAAPEPTICAGSEFQVYVANGNGFRHARNVD 226
DB 316 KVGN-FVALRSIQROIQEK-----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 4
US-08-362-652-46
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States


```
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-46
```

```
Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
```

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QY 10 PACYG-GFDLYFILDKSGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVSTRGTTLMK 67
DB 144 PECGQEMDIAPFLDGGSGSIDQSPFTQKDFVAKLMGQLASTSTSFELMOSNLKTHFT 203
QY 68 LTEDR-----EQIRGLSEIQKVLPGDPTMHGSEFASQIYYENRGRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLVTASGIQKVVLELPHSKNGAKSAKILIVI 258
QY 122 TDGELHEDLFFYSE--REARSRDLGAIYVCVKVD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGQKRPDPLEYRHVIRPEAKA---GIRIYAIVGDAFREPTALQELINTGSAPOHVF 315
QY 173 PVNDGFOALOGIHSILKSKCIEILAEPTICAGESFOYVVRGNGFRHARNVD 226
DB 316 KVGN-FVALMSIQRIQIEK---IFALIGTESRSSSFQHEMGOEGFSALSMD 364
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RESULT 5
US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46
```

```
Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
```

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QY 10 PACYG-GFDLYFILDKSGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVSTRGTTLMK 67
DB 144 PECGQEMDIAPFLDGGSGSIDQSPFTQKDFVAKLMGQLASTSTSFELMOSNLKTHFT 203
QY 68 LTEDR-----EQIRGLSEIQKVLPGDPTMHGSEFASQIYYENRGRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLVTASGIQKVVLELPHSKNGAKSAKILIVI 258
QY 122 TDGELHEDLFFYSE--REARSRDLGAIYVCVKVD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGQKRPDPLEYRHVIRPEAKA---GIRIYAIVGDAFREPTALQELINTGSAPOHVF 315
QY 173 PVNDGFOALOGIHSILKSKCIEILAEPTICAGESFOYVVRGNGFRHARNVD 226
DB 316 KVGN-FVALMSIQRIQIEK---IFALIGTESRSSSFQHEMGOEGFSALSMD 364
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RESULT 6
US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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```
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
APPLICATION NUMBER: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46
```

```
Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
```

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QY 10 PACYG-GFDLYFLDKSGV-LHHNRIYFVEQLAKFTSPQLRMSFIVSTRGTTLMK 67
DB 144 PECPCGEMDIAFLIDSGSIDSDFTQMKDFVQALMGQLASTSTSLMYSNILKTHFT 203
QY 68 LTEDR-----EQIRGLLELOKVLPGSDTYMHGFEFASQIYYENRGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQVVKELPHSKNGAKSAKKILIVI 258
QY 122 TDELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TQLARI-----ADSKDHVF 172
DB 259 TDGQKRDPLEHYRHVHVAPEAKA---GIRYALGVDAFREPVLQELNTIGSAPSDHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEIILAEPSSTICAGSFQVYVRNGNGFRHARND 226
DB 316 KVGN-FVALRSIORQIOEK-----IFAIEGTESRSSSSSFQHEMGEQFSLSLMD 364
```

```
RESULT 7
US-08-943-363-46
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
```

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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-46
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Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
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QY 10 PACYG-GFDLYFLDKSGV-LHHNRIYFVEQLAKFTSPQLRMSFIVSTRGTTLMK 67
DB 144 PECPCGEMDIAFLIDSGSIDSDFTQMKDFVQALMGQLASTSTSLMYSNILKTHFT 203
QY 68 LTEDR-----EQIRGLLELOKVLPGSDTYMHGFEFASQIYYENRGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQVVKELPHSKNGAKSAKKILIVI 258
QY 122 TDELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TQLARI-----ADSKDHVF 172
DB 259 TDGQKRDPLEHYRHVHVAPEAKA---GIRYALGVDAFREPVLQELNTIGSAPSDHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEIILAEPSSTICAGSFQVYVRNGNGFRHARND 226
DB 316 KVGN-FVALRSIORQIOEK-----IFAIEGTESRSSSSSFQHEMGEQFSLSLMD 364
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RESULT 8
US-09-193-043-46
Sequence 46, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46
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Query Match      10.9%: Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%: Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRTGLMK 67
DB 144 PECPCGQMDIAFLIDGSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMQYSNLTKHT 203
QY 68 LTER-----EQIRQGLEBLQKVLPGDDTYMHGFEFASBQIYYENQGRTA-SVIAL 121
DB 204 FTEFKSSLSPOSILDAIVOLQ-----GLTYTASGIQKVLELPHSKGARKSARKKILIVI 258
QY 122 TDGELHEDLFFYSE--REANRSRLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGCKFRDPLEYRNVIPBAEKA---GIIRYAIYGVDAREPTLQELANTIGSAPSQDHF 315
QY 173 PVNDGFOALOGIHSILKSKCIEILAEPTICAGESFOVVVRNGFRHARNVD 226
DB 316 KVGK-FVALRSIQIOIEK----IFAIEGTSSRSSSFQHEMSQEGFSALSMD 364

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RESULT 9
US-09-688-307A-46
; Sequence 46, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46

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Query Match      10.9%: Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%: Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRTGLMK 67
DB 144 PECPCGQMDIAFLIDGSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMQYSNLTKHT 203
QY 68 LTER-----EQIRQGLEBLQKVLPGDDTYMHGFEFASBQIYYENQGRTA-SVIAL 121
DB 204 FTEFKSSLSPOSILDAIVOLQ-----GLTYTASGIQKVLELPHSKGARKSARKKILIVI 258
QY 122 TDGELHEDLFFYSE--REANRSRLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGCKFRDPLEYRNVIPBAEKA---GIIRYAIYGVDAREPTLQELANTIGSAPSQDHF 315
QY 173 PVNDGFOALOGIHSILKSKCIEILAEPTICAGESFOVVVRNGFRHARNVD 226
DB 316 KVGK-FVALRSIQIOIEK----IFAIEGTSSRSSSFQHEMSQEGFSALSMD 364

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RESULT 10
US-09-350-259-46
; Sequence 46, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-259-46

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Query Match      10.9%: Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%: Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRTGLMK 67
DB 144 PECPCGQMDIAFLIDGSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMQYSNLTKHT 203
QY 68 LTER-----EQIRQGLEBLQKVLPGDDTYMHGFEFASBQIYYENQGRTA-SVIAL 121
DB 204 FTEFKSSLSPOSILDAIVOLQ-----GLTYTASGIQKVLELPHSKGARKSARKKILIVI 258
QY 122 TDGELHEDLFFYSE--REANRSRLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGCKFRDPLEYRNVIPBAEKA---GIIRYAIYGVDAREPTLQELANTIGSAPSQDHF 315
QY 173 PVNDGFOALOGIHSILKSKCIEILAEPTICAGESFOVVVRNGFRHARNVD 226
DB 316 KVGK-FVALRSIQIOIEK----IFAIEGTSSRSSSFQHEMSQEGFSALSMD 364

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RESULT 11
US-08-485-618-53
; Sequence 53, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-53

Query Match 10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6,5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYV-GPDLVFLDKSGSV-LHHMNEYFVFEQLAHKFI SPQLRMSPFVSTRTGLTK 67
DB 144 PEPGQEMDIAFLIDSGSIDSDFTQMDPVKALMGQLASTSTSLMYSLTKHTFT 203
QY 68 LTEDR-----EQIRGLLELOKVLPGGDTYMHGFERASEQIYYENRGYRTA-SVYIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYASGIQKVVELPHSKNGAKSAKILLIYI 258
QY 122 TDGELHEDLFFYSE--REANRSDLCALYYCVGKQ-FNE-TQLARI-----ADSKDHVF 172
DB 259 TDQKFRDPLREYRHVLEAEKA---GIIRYAIGVDAFREPTALQELINTIGSAPSDHVF 315

QY 173 PVNDGFQALQGIHSLIKKSCIEILAAPSTICAGSFQVYVNGFRHARND 226
DB 316 KVGN-FVALKSTORQIOEK---IFALGTERSSSSSFQHEMSQEGFSSLSMD 364

RESULT 12

US-08-362-652-53
Sequence 53, Application US/08362652
Patent No. 576850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 576850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-53

Query Match 10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6,5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYV-GPDLVFLDKSGSV-LHHMNEYFVFEQLAHKFI SPQLRMSPFVSTRTGLTK 67
DB 144 PEPGQEMDIAFLIDSGSIDSDFTQMDPVKALMGQLASTSTSLMYSLTKHTFT 203
QY 68 LTEDR-----EQIRGLLELOKVLPGGDTYMHGFERASEQIYYENRGYRTA-SVYIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYASGIQKVVELPHSKNGAKSAKILLIYI 258
QY 122 TDGELHEDLFFYSE--REANRSDLCALYYCVGKQ-FNE-TQLARI-----ADSKDHVF 172
DB 259 TDQKFRDPLREYRHVLEAEKA---GIIRYAIGVDAFREPTALQELINTIGSAPSDHVF 315

QY 173 PVNDGFQALQGIHSLIKKSCIEILAAPSTICAGSFQVYVNGFRHARND 226
DB 316 KVGN-FVALKSTORQIOEK---IFALGTERSSSSSFQHEMSQEGFSSLSMD 364

RESULT 13

US-08-605-672-53
Sequence 53, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-53

Query Match 10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIVSTRGTLMK 67
DB 144 PECPGEMDIAFLIDSGSIDQSDFTQMDKDFVAKLMQGLASTSTSFSLMYSNLKTHFT 203
QY 68 LTEDR-----EQIRQGLEBLQKVLPGDITYMHGFEFASQIYENRQGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDIAIVQ-----GLTYTAGSIQVVELFHSKNGAKSAKILIVI 258
QY 122 TDGELHEDLFFYSE--REANRSRDGAIVYCVGKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDQKFRDPLEYHNVPEAKA--GIIRYAIGVDLFRPTALQELNLTIGSAPSQDHF 315
QY 173 PVNDGFQALQGIHSLIKSCIEILAEPTICAGESFQVVGNGFRHARNVD 226
DB 316 KVGN-FVALRSIQROIEK----IFALEGTSRSSSFQHEMGEGSSALSMD 364

RESULT 14
US-08-482-293A-53
Sequence 53, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-53

Query Match 10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIVSTRGTLMK 67
DB 144 PECPGEMDIAFLIDSGSIDQSDFTQMDKDFVAKLMQGLASTSTSFSLMYSNLKTHFT 203
QY 68 LTEDR-----EQIRQGLEBLQKVLPGDITYMHGFEFASQIYENRQGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDIAIVQ-----GLTYTAGSIQVVELFHSKNGAKSAKILIVI 258
QY 122 TDGELHEDLFFYSE--REANRSRDGAIVYCVGKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDQKFRDPLEYHNVPEAKA--GIIRYAIGVDLFRPTALQELNLTIGSAPSQDHF 315
QY 173 PVNDGFQALQGIHSLIKSCIEILAEPTICAGESFQVVGNGFRHARNVD 226
DB 316 KVGN-FVALRSIQROIEK----IFALEGTSRSSSFQHEMGEGSSALSMD 364

RESULT 15
US-08-943-363-53
Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Query Match 10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

| | | | |
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| QY | 10 | PACYG-GFDLYPTLDKSGV-LHANEIYFVEQLAHKFTSPQLRMSPIVSTRGTTLMK | 67 |
| DB | 144 | PECPGQEMDIAFLIDSGSIDSDFTQMKDFVXALMGQLASTSTSPSLMQYSNLTHTFT | 203 |
| QY | 68 | LTEDR-----EOIRQGLEIELQKVLPGADTYMHEGFERASBOIYYENRQGYRTA-SVIAL | 121 |
| DB | 204 | FTFEKSSLSPQSLVDALIVQLQ-----GLYTTASGIQKVVKELPHSKGAKSKAKILIVI | 258 |
| QY | 122 | TGSELHEDLFFYSE--REANRSRLGAIYVCVVKD-FNE-TQLARI-----ADSKDHYF | 172 |
| DB | 259 | TGQKFRDPLEYHVIPEAEKA---GIIRYALGVDAFREPTALQELNTIGSAPQDHVF | 315 |
| QY | 173 | PVNDGFQALQGIHSLTKKSCIEILAEPESTICAGSFQYVVRGNGFRHARNVD | 226 |
| DB | 316 | KVGN-FVALRSIQRIQIEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD | 364 |

Search completed: December 14, 2005, 11:21:06
Job time : 27.4228 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:07 / Search time 88.2719 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526

Sequence: 1 QGRRREDGACGACGFDLYF.....DGLSFSSSVITTTTCSDG 293

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1 | 1526 | 100.0 | 368 | 6 US-11-047-278-2 | Sequence 2, Appli |
| 2 | 1526 | 100.0 | 403 | 3 US-09-833-245-621 | Sequence 621, App |
| 3 | 1526 | 100.0 | 551 | 4 US-10-038-307-18 | Sequence 18, Appl |
| 4 | 1526 | 100.0 | 551 | 4 US-10-201-292-18 | Sequence 18, Appl |
| 5 | 1526 | 100.0 | 564 | 3 US-09-918-715-187 | Sequence 187, App |
| 6 | 1526 | 100.0 | 564 | 3 US-10-301-822-193 | Sequence 232, App |
| 7 | 1526 | 100.0 | 564 | 4 US-10-408-765A-1823 | Sequence 193, App |
| 8 | 1526 | 100.0 | 564 | 4 US-10-474-794-187 | Sequence 187, App |
| 9 | 1526 | 100.0 | 564 | 4 US-10-474-794-232 | Sequence 232, App |
| 10 | 1526 | 100.0 | 564 | 5 US-10-979-159-187 | Sequence 187, App |
| 11 | 1526 | 100.0 | 564 | 5 US-10-979-159-232 | Sequence 232, App |
| 12 | 1526 | 100.0 | 564 | 6 US-11-047-278-6 | Sequence 6, Appli |
| 13 | 1515 | 99.3 | 403 | 3 US-09-833-245-620 | Sequence 620, App |
| 14 | 1515 | 99.3 | 403 | 3 US-09-796-753-12 | Sequence 12, Appl |
| 15 | 1514 | 99.2 | 333 | 4 US-10-038-307-2 | Sequence 2, Appli |
| 16 | 1514 | 99.2 | 333 | 4 US-10-201-292-2 | Sequence 2, Appli |
| 17 | 1514 | 99.2 | 333 | 4 US-10-201-292-8 | Sequence 8, Appli |
| 18 | 1514 | 99.2 | 333 | 4 US-10-038-307-24 | Sequence 24, Appl |
| 19 | 1514 | 99.2 | 345 | 4 US-10-201-292-24 | Sequence 24, Appl |
| 20 | 1514 | 99.2 | 345 | 4 US-10-038-307-20 | Sequence 20, Appl |
| 21 | 1514 | 99.2 | 345 | 4 US-10-201-292-20 | Sequence 20, Appl |
| 22 | 1509 | 98.9 | 562 | 3 US-09-918-715-194 | Sequence 194, App |
| 23 | 1509 | 98.9 | 562 | 3 US-09-918-715-301 | Sequence 301, App |
| 24 | 1509 | 98.9 | 562 | 3 US-10-474-794-194 | Sequence 194, App |
| 25 | 1509 | 98.9 | 562 | 4 US-10-474-794-301 | Sequence 301, App |
| 26 | 1509 | 98.9 | 562 | 5 US-10-979-159-194 | Sequence 194, App |
| 27 | 1509 | 98.9 | 562 | 5 US-10-979-159-194 | Sequence 194, App |

| | | | | | |
|----|--------|------|-----|---------------------|-------------------|
| 28 | 1509 | 98.9 | 562 | 5 US-10-979-159-301 | Sequence 301, App |
| 29 | 1501 | 98.4 | 328 | 4 US-10-038-307-26 | Sequence 26, Appl |
| 30 | 1501 | 98.4 | 328 | 4 US-10-201-292-26 | Sequence 26, Appl |
| 31 | 1499.5 | 98.3 | 342 | 4 US-10-038-307-22 | Sequence 22, Appl |
| 32 | 1499.5 | 98.3 | 342 | 4 US-10-201-292-22 | Sequence 22, Appl |
| 33 | 1493 | 97.8 | 543 | 4 US-10-038-307-14 | Sequence 14, Appl |
| 34 | 1493 | 97.8 | 543 | 4 US-10-038-307-16 | Sequence 16, Appl |
| 35 | 1493 | 97.8 | 543 | 4 US-10-201-292-16 | Sequence 16, Appl |
| 36 | 1493 | 97.8 | 543 | 4 US-10-201-292-16 | Sequence 16, Appl |
| 37 | 1483 | 97.2 | 543 | 4 US-10-038-307-10 | Sequence 10, Appl |
| 38 | 1483 | 97.2 | 543 | 4 US-10-201-292-10 | Sequence 10, Appl |
| 39 | 1478 | 96.9 | 534 | 4 US-10-038-307-12 | Sequence 12, Appl |
| 40 | 1478 | 96.9 | 534 | 4 US-10-201-292-12 | Sequence 12, Appl |
| 41 | 1413 | 92.6 | 529 | 4 US-10-201-292-34 | Sequence 34, Appl |
| 42 | 1299.5 | 85.2 | 504 | 4 US-10-201-292-34 | Sequence 34, Appl |
| 43 | 1172 | 76.8 | 479 | 4 US-10-201-292-32 | Sequence 32, Appl |
| 44 | 1058 | 69.3 | 460 | 4 US-10-201-292-28 | Sequence 28, Appl |
| 45 | 1048 | 68.7 | 460 | 4 US-10-201-292-30 | Sequence 30, Appl |

ALIGNMENTS

```
RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Query Match          100.0%; Score 1526; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.1e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGRRREDGACGACGFDLYFILDKSGSVLHNMNEIYFVQLAHKFISPOLRMSFIVFST 60
DB 28 QGRRREDGACGACGFDLYFILDKSGSVLHNMNEIYFVQLAHKFISPOLRMSFIVFST 87
QY 61 RGTTLMLKLTDRQIROGLSELOKVLPGCTTVHSGFERASQOYYENRGGYRTASTYIA 120
DB 88 RGTTLMLKLTDRQIROGLSELOKVLPGCTTVHSGFERASQOYYENRGGYRTASTYIA 147
QY 121 LTGGLHEDEDFPFSBRANRSDLGAIIVCVGKDFNETOLAIASKDHVFPVNDGFOA 180
DB 148 LTGGLHEDEDFPFSBRANRSDLGAIIVCVGKDFNETOLAIASKDHVFPVNDGFOA 207
QY 181 LOGIHSILKSCIEILAAEPSTICAGSEQVAVVNGGFRHARVNDVRLCSFKINDSVTL 240
DB 208 LOGIHSILKSCIEILAAEPSTICAGSEQVAVVNGGFRHARVNDVRLCSFKINDSVTL 267
QY 241 NEKPFVSEDTYLLCPAFLKEVGKALQVSNNDGJSFSSSVIITTTTCSDG 293
DB 268 NEKPFVSEDTYLLCPAFLKEVGKALQVSNNDGJSFSSSVIITTTTCSDG 320
```

```
RESULT 2
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albulin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Query Match          100.0%; Score 1526; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  OGGRRDGGPACGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLRMSFIVFST 60
      |||
      28  OGGRRDGGPACGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLRMSFIVFST 87
      |||
QY      61  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTVMHGEFERASEQIYYENRQGYRTASVITA 120
      |||
      88  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTVMHGEFERASEQIYYENRQGYRTASVITA 147
      |||
QY      121 LTDGELHEDLFFYSEREANRSRDLAGIIVCVGKDNENETOLARIADSKDHVPVNDGFOA 180
      |||
      148 LTDGELHEDLFFYSEREANRSRDLAGIIVCVGKDNENETOLARIADSKDHVPVNDGFOA 207
      |||
QY      181 LOGIHSILKSCIEILAEPSITCAGESFOVVRNGRHRANVRVLCSPKINDSVTL 240
      |||
      208 LOGIHSILKSCIEILAEPSITCAGESFOVVRNGRHRANVRVLCSPKINDSVTL 267
      |||
QY      241 NEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFISSVIITTHCSDG 293
      |||
      268 NEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFISSVIITTHCSDG 320
      |||
Db

RESULT 3
US-10-038-307-18
; Sequence 18, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18

Query Match          100.0%; Score 1526; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  OGGRRDGGPACGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLRMSFIVFST 60
      |||
      28  OGGRRDGGPACGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLRMSFIVFST 87
      |||
QY      61  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTVMHGEFERASEQIYYENRQGYRTASVITA 120
      |||
      88  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTVMHGEFERASEQIYYENRQGYRTASVITA 147
      |||
QY      121 LTDGELHEDLFFYSEREANRSRDLAGIIVCVGKDNENETOLARIADSKDHVPVNDGFOA 180
      |||
      148 LTDGELHEDLFFYSEREANRSRDLAGIIVCVGKDNENETOLARIADSKDHVPVNDGFOA 207
      |||
QY      181 LOGIHSILKSCIEILAEPSITCAGESFOVVRNGRHRANVRVLCSPKINDSVTL 240
      |||
      208 LOGIHSILKSCIEILAEPSITCAGESFOVVRNGRHRANVRVLCSPKINDSVTL 267
      |||
QY      241 NEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFISSVIITTHCSDG 293
      |||
      268 NEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFISSVIITTHCSDG 320
      |||
Db

RESULT 4
US-10-201-292-18
; Sequence 18, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-18

Query Match          100.0%; Score 1526; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  OGGRRDGGPACGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLRMSFIVFST 60
      |||
      28  OGGRRDGGPACGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLRMSFIVFST 87
      |||
QY      61  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTVMHGEFERASEQIYYENRQGYRTASVITA 120
      |||
      88  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTVMHGEFERASEQIYYENRQGYRTASVITA 147
      |||
QY      121 LTDGELHEDLFFYSEREANRSRDLAGIIVCVGKDNENETOLARIADSKDHVPVNDGFOA 180
      |||
      148 LTDGELHEDLFFYSEREANRSRDLAGIIVCVGKDNENETOLARIADSKDHVPVNDGFOA 207
      |||
QY      181 LOGIHSILKSCIEILAEPSITCAGESFOVVRNGRHRANVRVLCSPKINDSVTL 240
      |||
      208 LOGIHSILKSCIEILAEPSITCAGESFOVVRNGRHRANVRVLCSPKINDSVTL 267
      |||
QY      241 NEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFISSVIITTHCSDG 293
      |||
      268 NEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFISSVIITTHCSDG 320
      |||
Db

RESULT 5
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
```


APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 187
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-187

Query Match 100.0%; Score 1526; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGGRRDGGPACGCGFPLYLFDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFST 60
Db 28 OGGRRDGGPACGCGFPLYLFDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFST 87
Qy 61 RGTLMKLTEDREOIRQGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 120
Db 88 RGTLMKLTEDREOIRQGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 147
Qy 121 LTGDELHEDLFFYSERANSRDGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 180
Db 148 LTGDELHEDLFFYSERANSRDGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 207
Qy 181 LOGIHSILKKSCEIIIAEPSTICAGEFQVVRNGGFRHARVNDVLCGFKINDSVTL 240
Db 208 LOGIHSILKKSCEIIIAEPSTICAGEFQVVRNGGFRHARVNDVLCGFKINDSVTL 267
Qy 241 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSG 293
Db 268 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSG 320

RESULT 6

US-09-918-715-232
Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-232
Query Match 100.0%; Score 1526; DB 3; Length 564;

Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGGRRDGGPACGCGFPLYLFDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFST 60
Db 28 OGGRRDGGPACGCGFPLYLFDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFST 87
Qy 61 RGTLMKLTEDREOIRQGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 120
Db 88 RGTLMKLTEDREOIRQGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 147
Qy 121 LTGDELHEDLFFYSERANSRDGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 180
Db 148 LTGDELHEDLFFYSERANSRDGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 207
Qy 181 LOGIHSILKKSCEIIIAEPSTICAGEFQVVRNGGFRHARVNDVLCGFKINDSVTL 240
Db 208 LOGIHSILKKSCEIIIAEPSTICAGEFQVVRNGGFRHARVNDVLCGFKINDSVTL 267
Qy 241 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSG 293
Db 268 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSG 320

RESULT 7

US-10-301-822-199
Sequence 199, Application US/10301822
Publication No. US20030146410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301.822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-10-301-822-199

Query Match 100.0%; Score 1526; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGGRRDGGPACGCGFPLYLFDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFST 60
Db 28 OGGRRDGGPACGCGFPLYLFDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFST 87
Qy 61 RGTLMKLTEDREOIRQGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 120
Db 88 RGTLMKLTEDREOIRQGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 147
Qy 121 LTGDELHEDLFFYSERANSRDGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 180
Db 148 LTGDELHEDLFFYSERANSRDGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 207

| | | | |
|-----------|-----|--|-----|
| Qy | 18 | LGGIHSILKKSCTEIIAAEPSTICAGESFQVAVGNGRPHRANDRLCGFKINDSVTL | 240 |
| Db | 208 | LGGIHSILKKSCTEIIAAEPSTICAGESFQVAVGNGRPHRANDRLCGFKINDSVTL | 267 |
| Qy | 241 | NEKPSVEDYTYLLCPAPILKEVGMKALOVSNMDSIFSSVSITTHHCSDG | 293 |
| Db | 268 | NEKPSVEDYTYLLCPAPILKEVGMKALOVSNMDSIFSSVSITTHHCSDG | 320 |

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RESULT 8
US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumltra S.
; APPLICANT: Fahy, Boi D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088, 465
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

```

| Query Match | 100.0% | Score 1526 | DB 4 | Length 564 |
|-----------------------|--------|---|------|---------------------------------|
| Best Local Similarity | 100.0% | Pred. No. 2e-147 | | |
| Matches | 293 | Conservative | 0 | Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 | QGGRRDDGPAACGYGFDLYFIIDKSGSVLHMNNIYYVEQLAKFISPOLMSTIVST | 60 | |
| Db | 28 | QGGRRDDGPAACGYGFDLYFIIDKSGSVLHMNNIYYVEQLAKFISPOLMSTIVST | 87 | |
| Qy | 61 | RGTTLMKLTDEBQJROGLEBLQKYLPGDRTMHGFEFASQIYYENRQGRATASVIA | 120 | |
| Db | 88 | RGTTLMKLTDEBQJROGLEBLQKYLPGDRTMHGFEFASQIYYENRQGRATASVIA | 147 | |
| Qy | 121 | LTDGELHEDLPFYSSREANRSRDGLAIYYCVGKQFNETQLARINDSKDHPPVNDGFOA | 180 | |
| Db | 148 | LTDGELHEDLPFYSSREANRSRDGLAIYYCVGKQFNETQLARINDSKDHPPVNDGFOA | 207 | |
| Qy | 161 | LOGIHSILTKSCIEILAAEPSTICAGESFQVVVGVNGGPHRARNDRVLCSEKINDSVTL | 240 | |
| Db | 208 | LOGIHSILTKSCIEILAAEPSTICAGESFQVVVGVNGGPHRARNDRVLCSEKINDSVTL | 267 | |
| Qy | 241 | NEKPSVSDVTYLLCAPILIKVGMKALQVSNNDGSLFSSSVITTTTHCSNG | 293 | |
| Db | 268 | NEKPSVSDVTYLLCAPILIKVGMKALQVSNNDGSLFSSSVITTTTHCSNG | 320 | |

```

1 RESULT 9
2 US-10-474-794-187
3 / Sequence 187, Application US/10474794
4 / Publication No. US20040213793A1
5 /
6 / GENERAL INFORMATION:
7 /
8 / APPLICANT: Carson-Walter, Eleanor
9 /
10 / APPLICANT: St. Croix, Brad
11 /
12 / APPLICANT: Vogelstein, Bert
13 /
14 / APPLICANT: Kinler, Kenneth
15 /
16 / TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
17 /
18 / FILE REFERENCE: 1107 00179
19 /
20 / CURRENT APPLICATION NUMBER: US/10/474,794
21 /
22 / CURRENT FILING DATE: 2003-10-14
23 /
24 / PRIOR APPLICATION NUMBER: 60/282,850
25 /

```

```

? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: 60/308,829
? PRIOR FILING DATE: 2001-08-01
? NUMBER OF SEQ ID NOS: 359
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 187
? LENGTH: 564
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-474-794-187

```

| | | | | | |
|----|-----------------------|---|-------------------|-----------|-------------|
| | Query Match | 100.0%; | Score 1526; | DB 4; | Length 564; |
| | Best Local Similarity | 100.0%; | Pred. No. 2e-147; | | |
| | Matches 293; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Oy | 1 | QGGRRDDGDPACVGGFDLYITLDSGVSVAHHNMEIYYFVFOQLAHKFSIPQLRMSFIYFST | 60 | | |
| Db | 28 | QGGRRDDGACVGGFDLYITLDSGVSVAHHNMEIYYFVFOQLAHKFSIPQLRMSFIYFST | 87 | | |
| Oy | 61 | RGTLMLTLTDREQIRQGLEELQVLEGGDTVMHGEGERASEQIYYENRGYRTASVIAA | 120 | | |
| Db | 88 | RGTLMLTLTDREIRQGLEELQVLEGGDTVMHGEGERASEQIYYENRGYRTASVIAA | 147 | | |
| Oy | 121 | LTDGELHEDLFFYSERANRSRDIGAIYVCYGVKDFNETOLARIADSKHVFPPNDGFOA | 180 | | |
| Db | 148 | LTDGELHEDLFFYSERANRSRDIGAIYVCGVDFNETOLARIADSKHVFPPNDGFOA | 207 | | |
| Oy | 181 | LOGIHSILKKSCEIIAAEPSTICAGESFOVWVNGGPFHARNVDVLCSFKINDSVTL | 240 | | |
| Db | 208 | LOGIHSILKKSCEIIAAEPSTICAGESFOVWVNGGPFHARNVDVLCSFKINDSVTL | 267 | | |
| Oy | 241 | NEKPSVEDTYLLCPAPILKEVGKALQVSNMDGLSFISSVITTTTHSGDG | 293 | | |
| Db | 268 | NEKPSVEDTYLLCPAPILKEVGKALQVSNMDGLSFISSVITTTTHSGDG | 320 | | |

```

RESULT 10 US-10-474-794-232
; Sequence 232, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-232

Query Match      100.0%; Score 1526; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  QGGRREDGPAACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFST 60
DB      28  QGGRREDGPAACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFST 87

QY      61  RGTTLMKTEREQLRQLELEQVLRGGDTYMHGEPFRAEQLIYENRQGRVRTASVILA 120
DB      88  RGTTLMKTEREQLRQLELEQVLRGGDTYMHGEPFRAEQLIYENRQGRVRTASVILA 147

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RESULT 12
US-10-979-159-232
; Sequence 232, Application US/10979159
; Publication No. US2005042128A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein

| | | | | |
|-----------------------|---------|-------------------|-------|-------------|
| Query Match | 100.0%; | Score 1526; | DB 6; | Length 564; |
| Best Local Similarity | 100.0%; | Pred. No. 2e-147; | | |

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Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QGGRREDGPGACGCGFDLYFILDKSGSVLHHMNEIYFVQQLAHKFIISPOLRMSFIYFST 60
Db 28 QGGRREDGPGACGCGFDLYFILDKSGSVLHHMNEIYFVQQLAHKFIISPOLRMSFIYFST 87
QY 61 RGTTLMLKLTEDREQIRQGLELOKVLPGSDTYMHGEPERASEQIYYENRGYRTASVITA 120
Db 88 RGTTLMLKLTEDREQIRQGLELOKVLPGSDTYMHGEPERASEQIYYENRGYRTASVITA 147
QY 121 LTGGELEHDLFFYSERANRSRDGAIVYCVGVKDFNETQLARIADSKDHVPVNDGFOA 180
Db 148 LTGGELEHDLFFYSERANRSRDGAIVYCVGVKDFNETQLARIADSKDHVPVNDGFOA 207
QY 181 LOGIHSILKSCIEILAAEPSTICAGESFOVVVNGNGFRHARNRVLCSPKINDSVTL 240
Db 208 LOGIHSILKSCIEILAAEPSTICAGESFOVVVNGNGFRHARNRVLCSPKINDSVTL 267
QY 241 NEKPSVEDTYLLCPAPILKEVGKMAALQVSNMDGSLFISSVITTTTCSDG 293
Db 268 NEKPSVEDTYLLCPAPILKEVGKMAALQVSNMDGSLFISSVITTTTCSDG 320

RESULT 14
US-09-833-245-620
; Sequence 620, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (331)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (368)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Query Match 99.3%; Score 1515; DB 3; Length 403;
Best Local Similarity 99.7%; Pred. No. 1,7e-146;
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QGGRREDGPGACGCGFDLYFILDKSGSVLHHMNEIYFVQQLAHKFIISPOLRMSFIYFST 60
Db 28 QGGRREDGPGACGCGFDLYFILDKSGSVLHHMNEIYFVQQLAHKFIISPOLRMSFIYFST 87
QY 61 RGTTLMLKLTEDREQIRQGLELOKVLPGSDTYMHGEPERASEQIYYENRGYRTASVITA 120
Db 88 RGTTLMLKLTEDREQIRQGLELOKVLPGSDTYMHGEPERASEQIYYENRGYRTASVITA 147
QY 121 LTGGELEHDLFFYSERANRSRDGAIVYCVGVKDFNETQLARIADSKDHVPVNDGFOA 180
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Db 148 LTGGELEHDLFFYSERANRSRDGAIVYCVGVKDFNETQLARIADSKDHVPVNDGFOA 207
QY 181 LOGIHSILKSCIEILAAEPSTICAGESFOVVVNGNGFRHARNRVLCSPKINDSVTL 240
Db 208 LOGIHSILKSCIEILAAEPSTICAGESFOVVVNGNGFRHARNRVLCSPKINDSVTL 267
QY 241 NEKPSVEDTYLLCPAPILKEVGKMAALQVSNMDGSLFISSVITTTTCSDG 292
Db 268 NEKPSVEDTYLLCPAPILKEVGKMAALQVSNMDGSLFISSVITTTTCSDG 319

RESULT 15
US-09-796-753-12
; Sequence 12, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
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; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12

Query Match 99.2%; Score 1514; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.6e-146;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QGSRREDGGPACGPGDLYFIIDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVFST 60
   |||
Db 28 QGSRREDGGPACGPGDLYFIIDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVFST 87
   |||

QY 61 RGTTLMKLTEDREQIROGLEELQKVLPGDVTYMHGFERASEQIYYENRQGYRTASVIA 120
   |||
Db 88 RGTTLMKLTEDREQIROGLEELQKVLPGDVTYMHGFERASEQIYYENRQGYRTASVIA 147
   |||

QY 121 LTDELHEDLFFYSEERANRSRDLAGIYVCVGVKDFNETQLARIADSKDHFPPVNDGFOA 180
   |||
Db 148 LTDELHEDLFFYSEERANRSRDLAGIYVCVGVKDFNETQLARIADSKDHFPPVNDGFOA 207
   |||

QY 181 LOGIHSILKSCIEILAAEPSTICAGSFQVVRGNGFRHARVNDRLCSFKINDSVTL 240
   |||
Db 208 LOGIHSILKSCIEILAAEPSTICAGSFQVVRGNGFRHARVNDRLCSFKINDSVTL 267
   |||

QY 241 NEKPFVSDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCS 291
   |||
Db 268 NEKPFVSDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCS 318
   |||
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Search completed: December 14, 2005, 11:59:00
Job time : 89.4385 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 4.30595 Seconds

(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526
Sequence: 1 QGGRREDGACGACGFDLYF.....DGLSFSSVITTHCSDG 293

Scoring table:

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Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/p/codata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/p/codata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/p/codata/1/pubpaa/US07_NEW_PUB.pep:*
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6: /cgn2_6/p/codata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1 | 1526 | 100.0 | 564 | US-11-186-284-199 | Sequence 199, App |
| 2 | 145.5 | 9.5 | 1152 | US-11-080-026-4 | Sequence 4, Appl |
| 3 | 131 | 8.6 | 3063 | US-11-186-284-26 | Sequence 26, Appl |
| 4 | 113.5 | 7.4 | 739 | US-11-057-047-2 | Sequence 2, Appl |
| 5 | 113.5 | 7.4 | 764 | US-11-057-047-1 | Sequence 1, Appl |
| 6 | 113.5 | 7.4 | 798 | US-10-821-234-1034 | Sequence 1034, App |
| 7 | 113.5 | 7.4 | 915 | US-10-131-826A-294 | Sequence 294, App |
| 8 | 113.5 | 7.4 | 956 | US-11-113-424-39 | Sequence 39, Appl |
| 9 | 111 | 7.3 | 1141 | US-10-601-368-24 | Sequence 24, Appl |
| 10 | 111 | 7.3 | 1166 | US-10-601-368-22 | Sequence 22, Appl |
| 11 | 111 | 7.3 | 1188 | US-10-601-368-21 | Sequence 21, Appl |
| 12 | 110.5 | 7.2 | 761 | US-11-057-047-6 | Sequence 6, Appl |
| 13 | 107 | 7.0 | 1141 | US-10-601-368-6 | Sequence 6, Appl |
| 14 | 107 | 7.0 | 1166 | US-10-601-368-4 | Sequence 4, Appl |
| 15 | 107 | 7.0 | 1188 | US-10-601-368-3 | Sequence 3, Appl |
| 16 | 107 | 7.0 | 1188 | US-11-000-463-338 | Sequence 338, App |
| 17 | 107 | 7.0 | 1188 | US-11-000-463-810 | Sequence 810, App |
| 18 | 104.5 | 6.8 | 828 | US-10-995-561-983 | Sequence 983, App |
| 19 | 104.5 | 6.8 | 918 | US-10-995-561-981 | Sequence 981, App |
| 20 | 104.5 | 6.8 | 1019 | US-10-995-561-982 | Sequence 982, App |
| 21 | 103.5 | 6.8 | 182 | US-10-601-368-25 | Sequence 25, Appl |
| 22 | 100 | 6.6 | 678 | US-11-102-240-34 | Sequence 34, Appl |
| 23 | 99.5 | 6.5 | 182 | US-10-601-368-7 | Sequence 7, Appl |
| 24 | 95.5 | 6.3 | 1179 | US-11-097-125-1 | Sequence 1, Appl |
| 25 | 95.5 | 6.3 | 1196 | US-10-995-561-921 | Sequence 921, App |

| | | | | | |
|----|------|-----|------|--------------------|--------------------|
| 26 | 95 | 6.2 | 1167 | US-11-097-125-2 | Sequence 2, Appl |
| 27 | 94 | 6.2 | 353 | US-11-137-465-44 | Sequence 44, Appl |
| 28 | 94 | 6.2 | 448 | US-11-137-465-45 | Sequence 45, Appl |
| 29 | 91.5 | 6.0 | 627 | US-10-467-657-5432 | Sequence 5432, App |
| 30 | 91 | 6.0 | 1167 | US-10-601-368-18 | Sequence 18, Appl |
| 31 | 82 | 5.4 | 1062 | US-11-137-465-43 | Sequence 43, Appl |
| 32 | 81 | 5.3 | 1804 | US-10-513-786-2 | Sequence 2, Appl |
| 33 | 81 | 5.3 | 3704 | US-10-513-786-1 | Sequence 1, Appl |
| 34 | 79.5 | 5.2 | 904 | US-10-507-275-5 | Sequence 5, Appl |
| 35 | 77.5 | 5.1 | 319 | US-10-793-626-1040 | Sequence 1040, App |
| 36 | 77.5 | 5.1 | 415 | US-10-763-712A-25 | Sequence 25, Appl |
| 37 | 77.5 | 5.1 | 426 | US-10-763-712A-5 | Sequence 5, Appl |
| 38 | 76 | 5.0 | 469 | US-10-467-657-4370 | Sequence 4370, App |
| 39 | 75.5 | 4.9 | 1933 | US-10-523-912-2 | Sequence 2, Appl |
| 40 | 74 | 4.8 | 384 | US-10-510-386-158 | Sequence 158, App |
| 41 | 74 | 4.8 | 509 | US-10-793-626-2880 | Sequence 2880, App |
| 42 | 74 | 4.8 | 619 | US-10-999-886-3 | Sequence 3, Appl |
| 43 | 74 | 4.8 | 640 | US-10-999-886-4 | Sequence 4, Appl |
| 44 | 73.5 | 4.8 | 5935 | US-10-595-561-776 | Sequence 776, App |
| 45 | 73 | 4.8 | 264 | US-10-793-626-388 | Sequence 388, App |

ALIGNMENTS

RESULT 1
US-11-186-284-199
; Sequence 199, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangt
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Tibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-199

Query Match 100.0%; Score 1526; DB 7; Length 564;
Best Local Similarity 100.0%; Pred. No. 6.8e-135;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGGRREDGACGACGFDLYFILDKSGSVLHNMNIYFVQLAHKTISPQLRMSFVFSF 60
DB 28 QGGRREDGACGACGFDLYFILDKSGSVLHNMNIYFVQLAHKTISPQLRMSFVFSF 87
QY 61 RGTTLMLKLTDRQIQIGLELOKVPFGGTTYHBSGFERASQIYYENRGYTTASVITA 120
DB 88 RGTTLMLKLTDRQIQIGLELOKVPFGGTTYHBSGFERASQIYYENRGYTTASVITA 147
QY 121 LTGGLHEDLFPYSREARNRDLGAIYVCVGVKDFNETQTLARIADSKDHVPVNDGFOA 180


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Oy 1 QGGRRED-GR-----CYGFDLYPILKXSSV-----LHMNELYYVEQIAH 44
Db 218 EGVADBDHGHPQEQQKRIVLDPSSGMNIVLVLDSDSDIGASNFTGAKKCVNLLIKVAS 277
Oy 45 KFI$POLM$PFI$FSTRGSTIMKLT-----DREQIRQLEJL-----QKVLPGGDTYMHG 96
Db 278 YGVKP--RYGLVTVATYPIKWKXSEADSSNADWYTKQLEININEDHKLXSGTNT----- 330
Oy 97 FERASEQIYENR-----OQY-RTASVIALTDG-----ELHEDLFFYSE 135
Db 331 -KKLLQAYSNMMSWEPDVPPEGMNRTRVITLMTDGLNMGGDPITVIDELRDLLYIGXD 389
Oy 136 REAN$RDLGAIYCVG--VKDPNETQIARIAD$KDHVPYNDGFQALQGIHSILKSC 193
Db 390 RKNPREDYLDVYFVGVLNVQVNNALASKKQDNQHFVKYD--MENLEDVYQIMDES- 447
Oy 194 IEILAE$STICAGESFQVYVRGNGFRLARVRDPLCSFKINDSVTLN$K$P$VEDTYLL 253
Db 448 -----QSL$LC-----GMWEIRKGTD-----YHKOPWAKISV- 476
Oy 254 CPAPILKEVGMKAALQV$MNDGL$FIS$SVIITTHC 290
Db 477 ----IRPSKGH$SCMG-----AV$SEYFVLLTAHC 502

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RESULT 5
US-11-057-047-1
Sequence 1, Application US/11057047
Publication No. US20050260198A1
GENERAL INFORMATION:
APPLICANT: Holters, Vernon
APPLICANT: Thutman, Joshua
APPLICANT: Taube, Christian
APPLICANT: Gelfand, Erwin
APPLICANT: Gilkeson, Gary
TITLE OF INVENTION: Identification of Factor B, The Alternative Complement Pathway and
FILE REFERENCE: 2848-66
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: US/11/057, 047
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/543, 594
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/636, 239
PRIOR FILING DATE: 2004-12-14
PRIOR APPLICATION NUMBER: US04/015040
PRIOR FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 764
TYPE: PRT
ORGANISM: Homo sapiens
US-11-057-047-1

Query Match          7 4% Score 113.5; DB 7; Length 764;
Beet Local Similarity 19.6%; Pred. No. 0.0061;
Matches    66; Conservative      63; Mismatches 109; Indels   99; Gaps   17;

QY       1 QGGRREDS-GPA-----CYGGFDLYFLDKSGSV-----LHNNELIYYVEQLAH 44
           ||| |         :||| |        :||| |
DB     243 EGVDAEDDHGEHQEQQRKIVLDPSGSNMIIYLVDSSDSDIGASNFTGAKKCLVNIIEKYAS 302
           ::::            ::::
QY       45 KPIISQILMSRIFVSFTRGTTLMLKTE---DRBQIRGLLELI---QVLPGSOTRYMHEG 96
           :||| |        :||| |        :||| |
DB     303 YGVVK--HYGLATYATYPRKIWKYSSEADSNADWWTLKOLNEINVEDHKLSKGTYT---- 355
           :||| |        :||| |        :||| |
QY       97 FERASEOIQYEVR-----OGY-RTAGVIIALTDG-----ELHEDIIFYXE 135
           :||| |        :||| |        :||| |
DB     356 -KKALQAAYSMNSMEDDVPEEGMNKTFRVIIIMLTDLGNMGGDPTITVIDEIRDLLYIXKD 414
           :||| |        :||| |        :||| |
QY     136 REANSRLDGAIYCVG---VDFNETQLARLAIDSODHVFPVNDEGFQALQGIIHSILLKSCC 193
           :||| |        :||| |        :||| |

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Db      415  RKNPREDYDVVYFGVGLPVGNIINALASKDNGHQHFVKYD--MENNEDVFQYMDIS- 4722
Qy      194  IELLAEPTSCIGSEFQVYVANGNGFRHABANDRILCSFKINDSVTLINKEPFSVEDPYLL 2533
Db      473  -----QSLSLC-----GMVWERKRGTD-----YHKQPMQAKISV-- 501
Qy      254  CPAPILKEVGMKALQVSNMDGLSTISSVIIITTHC 290
Db      502  -----IRPSKSHSCMG-----AVSEYFVYLTAAHC 527

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RESULT 6
US-10-821-234-1034
; Sequence 1034, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Yom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 66/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL_SEQ_genes Version 1.0
; SEQ ID NO 1034
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1034

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Query March          7.4%; Score 113.5; DB 6; Length 798;
Best Local Similarity 19.6%; Pred. No. 0.0064;
Matches    66; Conservative   63; Mismatches 109; Indels   99; Gaps   17;

OY      1 OQGRREDG-GPA-----CYGFDLFILDKSGSV-----LHMNEIYYFVEQLAH 44
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     277 EGVADAEHGHEGEQQKRKIIVDPESGNMVIYLVDDGSISAGSNFTGAKKCVMLIEKVAS 336
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY      45 KFIIPQLMSFIVSTGTTLMKLTE---DREQIRGLEEL---OKVLPGDTVMHGG 96
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     337 YGVNP--RYGLVATYATPKIWMKVSEADSSNADVLTQNLNEINEDHKLSGTNT----- 389
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY      97 FERASEQIYYENR-----OGY-RTASVIIALTDG-----ELHEDIFFYSE 135
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     390 -KKALOAYTSMSPWDVPPEGMKRIHVIIIMLTDDGHNNGGDEITYIDEIRDLTYIGKD 448
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY     136 REARSRDLGAIVYCVG--VKDFEETOLARIADSKDHVPFNVDGFQALGIHSILKSC 193
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     449 RKNREDYLDVYVGCEPLVNQVINIMLASKDNEGHFVKD-MENLEDEVFYGMIDES 506
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY     194 IEIIAABPTICAGESFOVVVRNGFGFHARNVDRVLCSFKINDSVITNEKPFVSIEDLYLL 253
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     507 -----QSLSLC-----GWVWEHRKGTD-----YHKOPWQAKISV-- 535
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY     254 CPAPILKEVMKALQVSNNDGLSFISSVIITTHC 290
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     536 ---IRPSKGHSCMG-----AVSEYFLTAHC 561
           ||| ||| | :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 7
US-10-131-826A-294
; Sequence 294, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

```

APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIORITY APPLICATION NUMBER: 60/049911
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059184
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059263
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/059352
PRIORITY FILING DATE: 1997-09-19
PRIORITY APPLICATION NUMBER: 60/059588
PRIORITY FILING DATE: 1997-09-19
Remaining Priority Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 294
LENGTH: 915
TYPE: PRT
ORGANISM: Homo Sapien
OS-10-131-826A-294

```

[illegible]

```

1 Publication No. US20050260713A1
2 GENERAL INFORMATION:
3 APPLICANT: Ganggoli et al.
4 TITLE OF INVENTION: polyamides and Nucleic Acids Encoding Same
5 FILE REFERENCE: 21402-225
6 CURRENT APPLICATION NUMBER: US/11/113,424
7 PRIOR FILING DATE: 2005-04-21
8 PRIOR APPLICATION NUMBER: 60/256,704
9 PRIOR FILING DATE: 2000-12-19
10 PRIOR APPLICATION NUMBER: 60/311,550
11 PRIOR FILING DATE: 2001-08-10
12 PRIOR APPLICATION NUMBER: 60/257,314
13 PRIOR FILING DATE: 2000-12-20
14 PRIOR APPLICATION NUMBER: 60/311,613
15 PRIOR FILING DATE: 2001-08-10
16 PRIOR APPLICATION NUMBER: 60/315,617
17 PRIOR FILING DATE: 2001-08-29
18 PRIOR APPLICATION NUMBER: 60/307,506
19 PRIOR FILING DATE: 2001-07-24
20 PRIOR APPLICATION NUMBER: 60/322,358
21 PRIOR FILING DATE: 2001-09-14
22 PRIOR APPLICATION NUMBER: 60/294,075
23 PRIOR FILING DATE: 2001-05-29
24 PRIOR APPLICATION NUMBER: 60/288,153
25 PRIOR FILING DATE: 2001-05-02
26 NUMBER OF SEQ ID NOS: 190
27 SOFTWARE: PatentIn Ver. 2.1
28 SEQ ID NO 39
29 LENGTH: 956
30 TYPE: prt
31 ORGANISM: Homo sapiens
32 US-11-113-424-39

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```

Query Match      7.4%; Score 113.5; DB 7; Length 956;
Best Local Similarity 22.4%; Pred No. 0.0083;
Matches 55; Conservative 53; Mismatches 103; Indels 35; Gaps 13.

OY      17 DLVEILDKSGSV-LHHNNEIYF-VEOLAHKFIPOU-RMSFVSTGRTL-----MKL 68
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      57 DLVEIISSRSVNTHDPAKVEFIVDLQFLDIDPDVTRVGLLQY---GSIVKNEFLKT 113
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY      69 TEDREQIRQGLEELQKVLPGSDIYMHGFEERASEQIYYENRQYR----TASVIATLD 123
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      114 FKRSVEPAKVRMRHRLSTGTMGTALQY---ALNIAFSEAGARPLRENVPRVIMVITD 170
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY      124 GELHEDLFPSERERANSPDGLAVYCVG--KQENRQLARIDSKDHVFPVNDGPAAL 181
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      171 GRPDQSV---AEVAAKARDTGIIIFAIIGVQGVFNTLKSIGSEPHEDHVLVAN-FSQI 225
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY      182 QGIHSILKKSCIEILAEPTICAGSFQVAVVGNRPFRRHAR-----NVDERVLCSPKIND 236
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      226 ETLISVQKLCCTAHMCSLEHNC--HFCINIFGSYVCRCKQGIYILNSDQTT--RIQD 281
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY      237 SVTLNE 242
      :::|
Db      282 LCAMED 287

RESULT 9
US-10-601-368-24
; Sequence 24, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601.368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28

```



```

; ORGANISM: Mus musculus
US-11-057-047-6

Query Match
Best Local Similarity 20.5%; Pred. No. 0.011;
Matches 71; Conservative 59; Mismatches 99; Indels 117; Gaps 20;

QY 1 OGGRRRDG-----GPACYGGFDTLTKSGSV-----LHNNNEY 36
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 240 EGDADBDGSPGQQRKIVLDS--GSNNIYVLDSBSIGSNFTGAKCLTN----- 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 37 YFVEOLAHKFISSDQMSPIVSTRTGTLTKLTEDR-----EQIRGLEELQKVLPG 88
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 293 -LIEKVAAYGVBP--RYGLLTVAIVPKVLAVSDERSDDAWYTEKLNQISYEDHKLKSG 349
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 89 GDTYMEGPERASEQIYY-----ENRQCY--RTASVIALTNGELH-----EDL 130
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 350 TNT-----KRALQAVYSMMWSMAGDAPPEGMNRTIRHIIIMTDG--LHNGNPNVTYIODI 402
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 131 FFYSE--REANRGRD--LGAIVYCVG--VKDFNETOLARIADSKDHVPVNDGFOALOGI 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 403 RALDDGRDPKRNREDYLDVYVGVGPVLDVSVINIALASKDNEHIVFKYD--MEDLENV 461
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 185 IHSILKSCIEILAAEBSITCAGESPQVYVNGGFRHARNVDVLSFKINDSVTLNEXP 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 462 FYQMIDET-----KSLSLC-----GMVWEHKKGNDYHKQPWQAKISVT---RP 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 FSVEDTYLCPAPILKEVGMKALQVSMNDGLSFSSVITTTTC 290
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 502 LKGHET---CMGAV-----VSEYFVLTAAHC 524
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-601-368-6
; Sequence 6, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 1141
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) ... (122)
US-10-601-368-6

Query Match
Best Local Similarity 7.0%; Score 107; DB 6; Length 1141;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 12 CYGSPDLYFTLDSGSLVHNNIYFVEQLAHKF--SP--OLNMSPIVSTRTGTLTKLT 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 159 CQYMDVIVLDGNSI--YFWVEVQHFLINILKKFYIGQIQGVGVQYEDVVEHFL-- 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 EDREQLRQGLEELQKVLPGQDTYMEHGF--RASEQIYYENRQGYRTASVIALTDGEL 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 NDYRSVQDVVEASHIQRGRTETRTAFGIEFARSAEAFQGGKRKAK--KVMIVTDGES 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 HED-----LFFYSERANRSDILGAIYVCVYKD---FNEIQ 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 275 HDSPLDEKVIQOSERNVTRVAVAVLGYNRRGINPETFINEIKYIASDDDKHFFNVTD 334
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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QY 161 LARIADSKDHVPVNDGFOALQG 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 335 EAAI---KDIYDALGDRIFSLG 354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-601-368-4
; Sequence 4, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 1166
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-368-4

Query Match
Best Local Similarity 7.0%; Score 107; DB 6; Length 1166;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 12 CYGSPDLYFTLDSGSLVHNNIYFVEQLAHKF--ISP--OLNMSPIVSTRTGTLTKLT 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 137 CQYMDVIVLDGNSI--YFWVEVQHFLINILKKFYIGQIQGVGVQYEDVVEHFL-- 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 EDREQLRQGLEELQKVLPGQDTYMEHGF--RASEQIYYENRQGYRTASVIALTDGEL 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 195 NDYRSVQDVVEASHIQRGRTETRTAFGIEFARSAEAFQGGKRKAK--KVMIVTDGES 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 HED-----LFFYSERANRSDILGAIYVCVYKD---FNEIQ 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 253 HDSPLDEKVIQOSERNVTRVAVAVLGYNRRGINPETFINEIKYIASDDDKHFFNVTD 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 161 LARIADSKDHVPVNDGFOALQG 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 313 EAAI---KDIYDALGDRIFSLG 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-10-601-368-3
; Sequence 3, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 1188
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
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LOCATION: (1)...(22)
US-10-601-368-3

Query Match 7.0%; Score 107; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.045;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

| | | | |
|----|-----|--|-----|
| QY | 12 | CYGGFDLYFTIDKSGSVLHMHNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLT | 69 |
| DB | 159 | CQYMDIVIVLDGNSI-YPMVEVQHFLINILKKFYIGPGQIQGVVQYGEDVVEHFL- | 216 |
| QY | 70 | EDREQIRQGLEBELQKVLPGSDTYMHGFE--RASEQIYYENROGYRTASVIALTDGEL | 126 |
| DB | 217 | NDYRSVQDVVEAASHIEQRGSTETRTAFGIEPARSEAFQKGRKAK--KMIIVITDGS | 274 |
| QY | 127 | HED-----LFFYSERANRSDLGAIYVCVKD---FNETQ | 160 |
| DB | 275 | HDSPDLKVIQOSERDNTRYAVAVLGYYNRGINPETFLNEIKYIASDPDDKHFFVTTD | 334 |
| QY | 161 | LARIADSKDHYFPVNDGFOALQG | 183 |
| DB | 335 | EAAL--KDIYDALGDRIFSLEG | 354 |

Search completed: December 14, 2005, 11:59:28
Job time : 5.30595 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_pgm model

Run on: December 18, 2005, 07:01:37 ; Search time 205.707 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526
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Scoring table: BLOSUM62

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| Xgapop 10.0 , Xgapext 0.5 |
| Xgapop 6.0 , Xgapext 7.0 |
| Delop 6.0 , Delext 7.0 |

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pc -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*

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| 2: /cgn2_6/ptodata/1/ina/5.COMB.seq.* |
| 3: /cgn2_6/ptodata/1/ina/68.COMB.seq.* |
| 4: /cgn2_6/ptodata/1/ina/68.COMB.seq.* |
| 5: /cgn2_6/ptodata/1/ina/H.COMB.seq.* |
| 6: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.* |
| 7: /cgn2_6/ptodata/1/ina/PP.COMB.seq.* |
| 8: /cgn2_6/ptodata/1/ina/RE.COMB.seq.* |
| 9: /cgn2_6/ptodata/1/ina/backfile1.seq.* |

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------------|
| 1 | 1257 | 82.4 | 1609 | 3 | US-09-620-312D-8 |
| 2 | 786 | 51.5 | 2234 | 3 | US-10-104-047-669 |
| 3 | 709 | 46.5 | 1492 | 3 | US-09-774-528-297 |
| 4 | 709 | 46.5 | 1492 | 3 | US-10-130-988-297 |
| 5 | 658 | 43.1 | 3981 | 3 | US-09-789-451-250 |
| 6 | 166 | 10.9 | 3519 | 2 | US-08-286-889-45 |
| 7 | 166 | 10.9 | 3519 | 2 | US-08-485-618-45 |
| 8 | 166 | 10.9 | 3519 | 2 | US-08-362-652-45 |
| 9 | 166 | 10.9 | 3519 | 2 | US-08-605-672-45 |

| | | | | | | |
|----|-------|------|------|---|-------------------|-------------------|
| 10 | 166 | 10.9 | 3519 | 2 | US-08-482-293A-45 | Sequence 45, Appl |
| 11 | 166 | 10.9 | 3519 | 2 | US-08-943-363-45 | Sequence 45, Appl |
| 12 | 166 | 10.9 | 3519 | 3 | US-09-193-043-45 | Sequence 45, Appl |
| 13 | 166 | 10.9 | 3519 | 3 | US-09-688-307A-45 | Sequence 45, Appl |
| 14 | 166 | 10.9 | 3519 | 3 | US-09-350-259-45 | Sequence 45, Appl |
| 15 | 166 | 10.9 | 3803 | 2 | US-08-485-618-52 | Sequence 52, Appl |
| 16 | 166 | 10.9 | 3803 | 2 | US-08-362-652-52 | Sequence 52, Appl |
| 17 | 166 | 10.9 | 3803 | 2 | US-08-605-672-52 | Sequence 52, Appl |
| 18 | 166 | 10.9 | 3803 | 2 | US-08-482-293A-52 | Sequence 52, Appl |
| 19 | 166 | 10.9 | 3803 | 2 | US-08-943-363-52 | Sequence 52, Appl |
| 20 | 166 | 10.9 | 3803 | 3 | US-09-193-043-52 | Sequence 52, Appl |
| 21 | 166 | 10.9 | 3803 | 3 | US-09-688-307A-52 | Sequence 52, Appl |
| 22 | 166 | 10.9 | 3803 | 3 | US-09-350-259-52 | Sequence 52, Appl |
| 23 | 159.5 | 10.5 | 3528 | 2 | US-08-286-889-36 | Sequence 36, Appl |
| 24 | 159.5 | 10.5 | 3528 | 2 | US-08-485-618-36 | Sequence 36, Appl |
| 25 | 159.5 | 10.5 | 3528 | 2 | US-08-362-652-36 | Sequence 36, Appl |
| 26 | 159.5 | 10.5 | 3528 | 2 | US-08-605-672-36 | Sequence 36, Appl |
| 27 | 159.5 | 10.5 | 3528 | 2 | US-08-482-293A-36 | Sequence 36, Appl |
| 28 | 159.5 | 10.5 | 3528 | 2 | US-08-943-363-36 | Sequence 36, Appl |
| 29 | 159.5 | 10.5 | 3528 | 3 | US-09-193-043-36 | Sequence 36, Appl |
| 30 | 159.5 | 10.5 | 3528 | 3 | US-09-688-307A-36 | Sequence 36, Appl |
| 31 | 159.5 | 10.5 | 3528 | 3 | US-09-350-259-36 | Sequence 36, Appl |
| 32 | 159.5 | 10.5 | 3528 | 2 | US-08-485-618-54 | Sequence 54, Appl |
| 33 | 159.5 | 10.5 | 3528 | 2 | US-08-362-652-54 | Sequence 54, Appl |
| 34 | 159.5 | 10.5 | 3528 | 2 | US-08-605-672-54 | Sequence 54, Appl |
| 35 | 159.5 | 10.5 | 3528 | 2 | US-08-482-293A-54 | Sequence 54, Appl |
| 36 | 159.5 | 10.5 | 3528 | 2 | US-08-943-363-54 | Sequence 54, Appl |
| 37 | 159.5 | 10.5 | 3528 | 3 | US-09-193-043-54 | Sequence 54, Appl |
| 38 | 159.5 | 10.5 | 3528 | 3 | US-09-688-307A-54 | Sequence 54, Appl |
| 39 | 159.5 | 10.5 | 3528 | 3 | US-09-350-259-54 | Sequence 54, Appl |
| 40 | 156 | 10.2 | 2499 | 2 | US-08-485-618-96 | Sequence 96, Appl |
| 41 | 156 | 10.2 | 2499 | 2 | US-08-605-672-96 | Sequence 96, Appl |
| 42 | 156 | 10.2 | 2499 | 2 | US-08-482-293A-96 | Sequence 96, Appl |
| 43 | 156 | 10.2 | 2499 | 2 | US-08-943-363-96 | Sequence 96, Appl |
| 44 | 156 | 10.2 | 2499 | 3 | US-09-193-043-96 | Sequence 96, Appl |
| 45 | 156 | 10.2 | 2499 | 3 | US-09-688-307A-96 | Sequence 96, Appl |

ALIGNMENTS

RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aundai, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhilwei
; APPLICANT: John Tillinheast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic acids and
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_Fl_genes Version 1.0

```
/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309) .. (1202)
US-09-620-312D-8
```

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 5.03e-153 | Length: | 1609 |
| Score: | 125.90 | Matches: | 240 |
| Percent Similarity: | 100.00% | Conservative: | 2 |
| Best Local Similarity: | 99.17% | Mismatches: | 0 |
| Query Match: | 82.37% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-09-970-076-2_copy_28_320 (1-293) x US-09-620-312D-8 (1-1609)

```
QY      1  GlnGlyArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyrPhe 20
DB      390  CAAGGGGAGCGGAGGAGATGGGGGCTCCAGCTGCTACGGCGGATTGACCTGACTTC 449
QY      21  IleuAspLysSerGlySerValLeuHisTyrAsnGluIleTyrTyrPheValGlu 40
DB      450  ATTTGGACAATCAGAGAGTGTGCTSCACCACTGGAAATGAAATCTATTCTTTGTGAA 509
QY      41  GlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB      510  CAGTTGGCTCACAATTGATCAGCCCAAGTTGAGAAATGCTTTATTTGTTTCTCCACC 569
QY      61  ArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
DB      570  CGAGGAACAACCTTAATGAATCGACGAGAACAGAGAACAAATCCCTCAAGGCTTAGAA 629
QY      81  GlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAla 100
DB      630  GAACCTCCAGAAAGTTCTGCAGAGGAGACACTTACATGATGAAAGATTGAAAGGGCC 689
QY      101  SerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrTrpTrpThrLysSerValIleIleAla 120
DB      690  AGTGAGAGATTTATTTATTTGAAAACAGCAAGGGTACAGACACGCCAGCTCATTTGCT 749
QY      121  LeuThrAspGlyGlnLeuHisGluAspLeuPheTyrSerGluArgGluAlaAsnArg 140
DB      750  TTGACTGATGAGAACTCCATGAAGATCTTTTTCATTCAAGAGGAGGCGCTAATAGG 809
QY      141  SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAspPheAsnGluThrGln 160
DB      810  TCTGAGATCTTGGTGCATTTGTTTACTGTGTGGTGTGAAAAGATTTCATATGAGACACAG 869
QY      161  LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
DB      870  CTGGCCCGAGATGGGAGCAGTAAGATCATGTGTTCCCTGAATGACGGCTTTCAGGCT 929
QY      181  LeuGlnGlyIleIleHisSerIleLeuLysSerCysIleGluIleLeuAlaAlaGlu 200
DB      930  CTGCAAGGCATCATCTCAATTTTGAAGAAGCTTCGCATCGAAATTTCTAGCAGCTGAA 989
QY      201  ProSerThrIleCysAlaGlyGluSerPheGlnValValAlaArgGlyAsnGlyPheArg 220
DB      990  CCATCCACCATATGTGCAGAGAGTCAATTCAGATTGTCGTGAGAGAGAAACGGCTTCGA 1049
QY      221  HisAlaArgPheAspLysAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
DB      1050  CATGCGCGCAATGTGGAGAGGCTCTCTGACGTTCAAGATCAATGACTCGGTCAACATC 1109
QY      241  AsnGlu 242
DB      1110  AGTAA 1118
```

RESULT 2
US-10-104-047-669

```
/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: NO. 6943241el full length cdna
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669
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Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 1.61e-91 | Length: | 2234 |
| Score: | 786.00 | Matches: | 153 |
| Percent Similarity: | 72.89% | Conservative: | 54 |
| Best Local Similarity: | 53.87% | Mismatches: | 75 |
| Query Match: | 51.51% | Indels: | 2 |
| DB: | 3 | Gaps: | 1 |

US-09-970-076-2_copy_28_320 (1-293) x US-10-104-047-669 (1-2234)

```
QY      10  ProAlaCysTyrGlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeu 29
DB      637  CCTCTCGAGAAAGACCTTTGATCTCTACTGCTGCTGACAAAGCTGGAGCTGTGGCA 696
QY      30  HisHisTyrAsnGluIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerPro 49
DB      697  AATTAAGTGAATTAATTAATTTATTTCTGACAGCAACTTCGGAGAGATTTGAGACCTC 756
QY      50  GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 69
DB      757  GAAATGAGATTATCTTTCATGTTGTTTCTCTCAAGCAACTATATTGTCATTAACCT 816
QY      70  GluAspArgGlnGlnIleArgGlnGlyLeuGlnGlnLysValLeuProGlyGly 89
DB      817  GGAGACAGAGGCAAAATCAGTAAGGCTTGAGGATTTAAACGTGTAGTCCAGTAGGA 876
QY      90  AspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArg 109
DB      877  GAGACATATATCTATGAAGACTAAAGCTAGCGCAAGCAAAATTT-----CAGAAAGCA 930
QY      110  GlnGlyTyrArgThrLysSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAsp 129
DB      931  GAGGCTTGAAACCTCCAGTATCATTAATTGCTCTGACAGATGGCAAGTTGACGGCTTG 990
QY      130  LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlnIleAlaIleValTyr 149
DB      991  GTGCCATCATATGCAAGAGAAAGGCAAGATATCCAGGTCACTTGAGGCTAGCTGTTAT 1050
QY      150  CysValGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAsp 169
DB      1051  TGTGTGTGTCTCTTAATTTTGAACAAGCAGACCTTGAAGAAATTCGATTTCCAAAGAG 1110
QY      170  HisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 189
DB      1111  CAAGTTTTTCCCTGTCAAAGGTGATTTCAAGGCTCTTAAGGAATTAATTAATCTATATCTA 1170
QY      190  LysLysSerCysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSer 209
DB      1171  GCTCAGTCAATGTACTAATAATCCTAAGATTCAGACCCCTCAAGTGTCTGTGTGGGGAGAA 1230
QY      210  PheGlnValValAlaArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeu 229
DB      1231  TTTCAGATTGCTTTAAGTAGAGAGATTCATGCTGGCAGCTGGAATGCAAGTGTCTTC 1290
QY      230  CysSerPheLysIleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAsp 249
```



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Db      1291 TGCACCTTACACTGTAATGAACAATATKCAACAGACTGTAAACCAGTAAGTGTCAGCTT   1350
Qy      250 ThrTYrLeuLeuCysProAlaProIleLeuYbgIValGlyMetLysAlaAlaLeuGI n    269
          ::::::::::::::::::::
Db      1351 AATTCTAAGCTTTGGTCCCGCACACTTACCTGAAATAAACGTGGAGAAACCTTGAGTGTCCA   1410
Qy      270 ValSerMetAsnAspArgLYLeuSerPheIleSerSerValIleIleThrThriHis     289
          1411 GTGACCTTTAATGGAGAAATCTGTCAITTCAGGATCATTAAATGTGCACGCCACAGAA   1470
Qy      290 CysSerAspGly 293
          |||:::||||
Db      1471 TGTTCTAACGGG 1482

RESULT 3
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyun
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehtman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunruo
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pl_FL_genes Version 2.0
; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-09-774-528-297

Alignment Scores:
Pred. No.:      8,776-82           Length:      1492
Score:         709.00            Matches:     139
Percent Similarity: 72.35%       Conservative: 52
Best Local Similarity: 52.65%     Mismatches:  71
Query Match:    46.46%           Indels:      2
DB:             3                Gaps:         1

US-09-970-076-2_COPY_28_320 (1-293) x US-09-774-528-297 (1-1492)

Qy      30 HisHietPRaengGiUlieTyTyRvheValGIuInLeuAlaHisLysPheIleSerPro 49
          ::::::::::::::::::::
Db      16 AATACTGGATGGAAATTATATATTTCTGTAACAGCAACTTGGCGGADAGATTTGTGAGCCCT 75
Qy      50 GluLeuAspMetSerPheIleValPheSerThrAdgGlyThrThiLeuMetLysValenThr 69
          ::::::::::::::::::::
Db      76 GAATAGAGATTAATCTTCACTGTGTGTTTTCTTCAAGCAACATATTATTTGGCATTAAC 135
Qy      70 GluAPRAcGUGlInIleaRGlInGlyLeuGIuLeuGIuLeuGIuLeuValIleuProGIyGly 89
          |||:::||||
Db      136 GGAGACAGAGCGCAAATACGTAAAGGCTTTGGAGGATTTTAAACSGTTAAGTCSAGTAGAGA 195
Qy      90 AepTrHYrMechHisGIuGIyPheGIuIdrgAlasergGIuInIleTyTyGIuIdrvnAdrg 109

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| | | | |
|---|-----|---|------|
| Db | 196 | GAACATATTTTCATTAAGCACTAAAGCCTTAAGGAGTGAACAAATT-----CAGAAAGCA | 249 |
| QY | 110 | gncgllyttrgrthrnlaserVallellealaleuthraerglyuleuhiegluAsp | 1299 |
| Db | 250 | GGAGGCTTGAAACCTCCAGTATCATTAATTGCTGACAGATGGCAAGTTGACGCTG | 3099 |
| QY | 130 | leupherheyletserlulrgrlulalavnaugserladyarlerlueglYAlAlleValTyr | 1499 |
| Db | 310 | GTGCATCATTAATTCAGAAAGGCAAGATATCCAGTCACTTGGGGCTAAGTGTAT | 3699 |
| QY | 150 | CyeValglYValLysAspPheAengluThrGlnleuAlaIgrlleAlaAspSerLysAsp | 1699 |
| Db | 370 | TGCTTGGGCTCTTAATTTTGAACACAGCAGCTTGAAGATTTGCTGATTCGAAAGAG | 4299 |
| QY | 170 | HisValPheProValAsnAspGlyPheGlnAlaleuGlnGlylleIleHisSerLysleu | 1899 |
| Db | 430 | CAAGTTTTCCTCTCAAGAGTGAGATTTCAGGCTTTAAAGATTAATTAATTCATCTA | 4899 |
| QY | 190 | LysLysSerCysAlleglulleuAlaIagluProSerThrIleCysAlaGlyGluSer | 2099 |
| Db | 490 | GCTCAGCAGTACTGAAATCTTAGAATTGCAGCCCTCAAGTGTGTGTGGGGAGAGAA | 5499 |
| QY | 210 | PheGlnValValAlaIrgLysAnGlyPheArgHisAlaIcArganValAspArgValLeu | 2299 |
| Db | 550 | TTTCAGATTCTCTTAAGTGAAGAGGATTCATGCTGGGCACTGGGAATGCGAGTTCCTC | 6099 |
| QY | 230 | CysSerPheLysIleAsnAspSerValThrLeuAnGlnLysProPheSerValGluAsp | 2499 |
| Db | 610 | TGCACTTACACGTAAATGAACATATCAACAGATGTAACAGTAAACAGTAAAGTACAGCTT | 6699 |
| QY | 250 | ThrTyrleuLeuCysProAlaProIleleuLysGluValGlyMetLysAlaLeuGln | 2699 |
| Db | 670 | AATTCATGCTTTTGCTCCTCAGCTTCTCGATTAAGCTGAGAAACCTTTGATGTTCA | 7299 |
| QY | 270 | ValSerMetAsnAspGlyLeuSerPheIleSerSerValIleIleThrThrHis | 2899 |
| Db | 730 | GTGAGCTTAAATGAGAGAAATCTGTCAATTCAGATCATTAATTGTGCACGCCAGAA | 7899 |
| QY | 290 | CysSerAspGly 293 | |
| Db | 790 | TGTTCTAACGG 801 | |
| RESULT 4 | | | |
| US-10-120-988-297 | | | |
| ; Sequence 297, Application US/10120988 | | | |
| ; Patent No. 6919193 | | | |
| GENERAL INFORMATION: | | | |
| ; APPLICANT: Tang, Y. Tom | | | |
| ; APPLICANT: Goodrich, Ryle | | | |
| ; APPLICANT: Liu, Chenghua | | | |
| ; APPLICANT: Ren, Feiyan | | | |
| ; APPLICANT: Wang, Dunrui | | | |
| ; APPLICANT: Demanac, Radoje T. | | | |
| ; TITLE OF INVENTION: No. 6919193el Nucleic Acids and | | | |
| ; FILE REFERENCE: Polypeptides | | | |
| ; CURRENT APPLICATION NUMBER: US/10/120,988 | | | |
| ; CURRENT FILING DATE: 2002-04-11 | | | |
| ; PRIOR APPLICATION NUMBER: 09/774,528 | | | |
| ; PRIOR FILING DATE: 2001-01-30 | | | |
| ; NUMBER OF SEQ ID NOS: 441 | | | |
| ; SOFTWARE: Pct_Fl_genes Version 2.0 | | | |
| ; SEQ ID NO 297_ | | | |
| ; LENGTH: 1492 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapiens | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: CDS | | | |
| ; LOCATION: (79)..(1434) | | | |
| US-10-120-988-297 | | | |
| Alignment Scores: | | | |

Pred. No.: 8,77e-82 Length: 1492
 Score: 709.00 Matches: 139
 Percent Similarity: 72.35% Conservative: 52
 Best Local Similarity: 52.65% Mismatches: 71
 Query Match: 46.46% Indels: 2
 DB: 3 Gaps: 1

US-09-970-076-2_COPY_28_320 (1-293) x US-10-120-988-297 (1-1492)

```

QY 30 HIAHSTRPANGIUIETRYRYPHEVALGIGLNUENLAHIALYSPHEIISESPRO 49
   |||||
DB 16 AATPACTGGATGTAATTAATTGTAACAGACTTCGAGAGATTGGAGCCCT 75
   |||||
QY 50 GINLEUARGMESERPHIELVALPHESETHARGSLYTHRIEUMETLYSELEUTH 69
   |||||
DB 76 GAATAGGATTAATCTTTCATGTTGTTTCTTCACACCACTATATTGGCATTAAC 135
   |||||
QY 70 GIUAPARGIUGNIIEARGINGLYLEUGLNUENLYVALLEUPROGLYGLY 89
   |||||
DB 136 GGAGACGAGGCAAAATCAGTAAAGCCTTGAGGATTAAACGTGTATGTCAGATGGA 195
   |||||
QY 90 AAPTHTYRMEHISGLUGLYPHEGILUARGALASERGLUNILETRYTRYRGIUASARG 109
   |||||
DB 196 GAGACATATATCCATGAAAGACTPAAGCTAGCCGATGAACAAT-----CAGAAAGCA 249
   |||||
QY 110 GINGLYTRYARGTHRALASERVALLEIALALEUTHRASPGLYUENHISGLUASP 129
   |||||
DB 250 GGAGGCTTGAAACCTCAATATCAATATGCTTCGACATGGCAAGTTGGAGCGCTG 309
   |||||
QY 130 LEUPHEBETHYRSERGILUARGILUALAASARGSERARGASPLEUGILVALLEVALTYR 149
   |||||
DB 310 GTGCCATCATATGACAGAAAGAGCAAAAGATATCCAGTCCACTGGGCGCTAGGTAT 369
   |||||
QY 150 CYVALIGLYVALYASAPRHEANGIUTHRGILNUENLAHIALYSPHEIISESPRO 169
   |||||
DB 370 TGTGTTGGGCTCTTGATTTTGAACACAGCTTAAAGATGCTGATTCACAGGAG 429
   |||||
QY 170 HIEVALPHEPROVALAENASPGLYPHEGILALEUGNILELIEHISERILELEU 189
   |||||
DB 430 CAAGTTTCCCTGTCGAAAGGAGGATTCAGGCTTTAAAGAAATTAATTCATATCTA 489
   |||||
QY 190 LYLAYSERCYBIIIEGILUEUALALEGLUPROSETHRIEYVALIGLYUSER 209
   |||||
DB 490 GCTCAGCTAGTACTGAATCTCTGAATTCAGCCCTCAAGTCTGTGGGGGAGAA 549
   |||||
QY 210 PHEGLNALVALVALARGGLYASNGLYPHEARGHIALARGAENVALAPARGVALLEU 229
   |||||
DB 550 TTTCAAGTGTCTTAAAGTGAAGAGATTCATGCTGGGCACTCGAAATGCGAGTTCTC 609
   |||||
QY 230 CYSESPHEIYBIIIEANASPSERVALTHRIEUNANGIULYSPROPHESERVALIGLUASP 249
   |||||
DB 610 TGCACTTAACACTGAATTAATGAACATATACACAGCTTAACACAGTAAGTGTACAGCT 669
   |||||
QY 250 THRTYRLEUENUCYSPROIALAPROIIIELEULYSGILVALIGLYMETLYSALALAEUGL 269
   |||||
DB 670 AATTCATGCTTGTCTGCACTGCACTGCTGAATTAACCTGAGAACTCTTGATTTCA 729
   |||||
QY 270 VALSERETANASPGLYLEUSERPHEIISESPERVALLEIETHTHRIETHIS 289
   |||||
DB 730 GTGAGCTTTAATGAGGAAATCTGTATTCAGGATCATTAATGTACAGACCCAGAA 789
   |||||
QY 290 CYSESPARGLY 293
   |||||
DB 790 TGTTCCTAACGG 801
   |||||

```

RESULT 5
 US-09-799-451-250
 ; Sequence 250, Application US/09799451
 ; Patent No. 6783969

; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle

```

; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungting
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 250
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(1118)
; US-09-799-451-250

```

Alignment Scores:
 Pred. No.: 1.84e-74 Length: 3981
 Score: 658.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 43.12% Indels: 0
 DB: 3 Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-09-799-451-250 (1-3981)

```

QY 166 AASPSELYAPHSIIVALPHEPROVALAENASPGLYPHEGILALEUGNILELIE 185
   |||||
DB 3 GACAGTAGAGATCATATGTTTCCCGTAATGACGGCTTCAGGCTTCGAAAGCATCATC 62
   |||||
QY 186 HIASERILELEULYBYSERCYBIIIEGILUEUALALEGLUPROSETHRIEY 205
   |||||
DB 63 CACTCAATTTTGAAGAGTCTGCATCGAAATTTGACAGCTGAACCATTCACCATATGT 122
   |||||
QY 206 ALAIGLYUSERPHEGINVALVALARGGLYASNGLYPHEARGHIALARGAENVAL 225
   |||||
DB 123 GCGAGAGATCATTTCAAGTTGCGTGAAGGAAAGGGCTTCGACATGCCGCAACGTG 182
   |||||
QY 226 AASPARGVALLEUCYSESPHEIYBIIIEANASPSERVALTHRIEUNANGIULYSPRO 245
   |||||
DB 183 GACAGGCTCTCTGCACTTCAAGATCAATGACTCGCTCACCTCATATGAGAACTCTT 242
   |||||
QY 246 SERVALIGLUASPHRTYRLEUENUCYSPROIALAPROIIIELEULYSGILVALIGLY 265
   |||||
DB 243 TCTGTGAAGATATCTTATTAATCTGTGCAAGCCCTTATTAAGAAAGTTGGCATGAA 302
   |||||
QY 266 ALAALAEUGINVALSERETANASPGLYLEUSERPHEIISESPERVALLEIETHT 285
   |||||
DB 303 GCTGCACTCAGGCTCAGCATGAAGATGAGCTCTCTTTATATCCAGTTCTGTCAATC 362
   |||||
QY 286 THRTHTHRIEYSESPARGLY 293
   |||||
DB 363 ACCACCAACACATGTTCTGACGGT 386
   |||||

```

RESULT 6
 US-08-286-889-45
 ; Sequence 45, Application US/08286889
 ; Patent No. 5470953

```

: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Mich
: APPLICANT: Van der Vlieten, Monica
: TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive, 6300 Sear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/286,889
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: P38,659
: REFERENCE/DOCKET NUMBER: 27866/32168
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3519 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 52..3519
: US-08-286-889-45

Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-286-889-45 (1-3519)
Qy 10 ProbaLcYerYrYgYl---GlyPheAspLeuYrPheIleuAspLysSerGlySerVal 28
Db 481 CCAAGAGTCCAGGACAGAGATGAGACATTCCTTCCTGATGATGGCTCGGAGACAT 540
Qy 29 ---LeuH1eH1eStrAengluIleTyTyTyPheValgluInleuAlaH1eLysPheIle 47
Db 541 GATCAAGTAGCTTACCCAGATGAGAGACTTGTCAAGCTTTGATGGCGCACTTGGCG 600
Qy 48 SerProgluLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 67
Db 601 AGCACCGACACCTGCTCTCCCTGATGCAATACCAACATCTGAAGACTCATTTTACC 660
Qy 68 LeuThrgluLeuArg---GluInleuArggluInleuArggluInleu 82
Db 661 TTCACGAAATTCAGAGACAGCCTGAGCCCTCAGAGCTGTGGATGCCATGCTCAGCTC 720
Qy 83 GluInleuValleuProgluYAspThrTyTMeCh1eGlulgluPhegluArgAlaSerGlu 102
Db 721 CAA-----GGCCTGACGTACACACCTCGGCGCATTCAGAAAGTGCTGAA 765
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Qy 103 GluIleTyTyrgluAsnArggluInglYTyArgThrAla---SerValIleAlaLeu 121
Db 766 GAGCTATTTCATACCAAGATGGGGCCCGAAAGAGTCCAGAAAGATTAATTGTCATC 825
Qy 122 ThrAspGlygluLeuH1eH1eStrAengluPhePheTySerGlu-----ArgGluAlaAsn 139
Db 826 ACAGATGGGAGAAATTCAGAGACCCCTGGAGATATGACATGTCATCCCTGAAGCAGAG 885
Qy 140 ArgSerArgAspLeuGlyAlaIleValTyTyCysValGlyValLysAsp---PheAsnGlu 158
Db 886 AAAGCT-----GGATCATTCGCTATGATAGGGGTGGAGATGCTTCGCGGAA 936
Qy 159 ---ThrInleuAlaArgIle-----AlaAspSerLysAspH1eValPhe 172
Db 937 CCCATGCTCCCTACAGAGCTGAACACCATTTGGCTCAGCTCCCTCGCAGACACGTGTTC 996
Qy 173 ProValAsnAspGlyPheGluAlaLeuGluInglYIleIleH1eSerIleLeuLysLysSer 192
Db 997 AAGGTGGGCAAT---TTTGATGACATTCGACATTCAGCGGCAATTCAGAGAA--- 1050
Qy 193 CysIleGluIleleuAlaIaIaGluProSerThrIleCysAlaGlyGluSerPheGluVal 212
Db 1051 -----ATCTTGGCATTTGAAGCAACCAATCAAGTCAAGTCAAGTACTTCTTCAGCAC 1101
Qy 213 ValValArgGlyAsnGlyPheArgH1eAlaArgAsnValAsp 226
Db 1102 GAGATGTCAAGAAAGGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 7
US-08-485-618-45
: Sequence 45: Application US/08485618
: Patent No. 5728533
: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Michael
: APPLICANT: Van der Vlieten, Monica
: TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 103
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive, 6300 Sear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,618
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,889
: FILING DATE: 5-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/362,652
: FILING DATE: 21-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32797
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
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/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
US-08-485-618-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-485-618-45 (1-3519)
QY 10 ProAlaCytyrGly---GlyPheApleuTyRPhelIleuAplysSerGlySerVal 28
DB 481 CCAAGATGTCAGAGACAGAGATGACATTCCTTCTGATTAAGCTCCGGCAGCATT 540
QY 29 ---LeuHisHisTrpApsngluIleTyTyR-PheValGluGlnIleuAlaHisLysPheIle 47
DB 541 GATCAAGTACATTACCCAGATGAAGGACTTGTCAAAGCTTTGATGGCCAGTTGGCG 600
QY 48 SerPProGlnIleuAryMetSerPheIleValPheSerThrArgGlyThrThreLysMetLys 67
DB 601 AGCACACGACACCTCGTTCTCCCTGATGCAATACCAAACTCTGAAGACTCATTTTACC 660
QY 68 LeuThGluApsArg-----GluGlnIleArgGlnIleuGluGluIleu 82
DB 661 TTCACGGAATTCAGAGACAGACCTGAGCCCTCAGAGCTGTGATGCCATCGCCAGCTC 720
QY 83 GlnIleValIleuProGlyIleApsThrTyRmetHisGluIlePheGluArgAlaSerGlu 102
DB 721 CAA-----GGCCTGACGTCACAGACCTCGGGCATCCGAAAGTGGTGAA 765
QY 103 GlnIleTyTyRglnIleuApsnglnGlyTyRArgThrAla---SerValIleIleAlaIle 121
DB 766 GAGCTATTTCATGACAGAAATGGGGCCCGAAAGTCCCAAGAAATCAATATTTGTCATC 825
QY 122 ThrApsGlyIleuIleuHisGluApsLeuPhePheTyRserGlu-----ArgGluAlaAsn 139
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATATGACATGTCATCCCTGAAGCAGAG 885
QY 140 ArgSerArgApsLeuGlyAlaIleValTyRCyValGlyValIlyAps---PheAsnGlu 158
DB 886 AAGGCT-----GGGATCATTCGCTATGCTATAGGGGAGAGATGCCCTTCCGGGAA 936
QY 159 ---ThrGlnIleuAlaArgIle-----AlaApsSerLysApsHisValPhe 172
DB 937 CCCACTGCCCCCTACAGAGACCTGAACACCATTTGCTCAGCTCCCTCGCGAGCAACGTGTC 996
QY 173 ProValAsnApsGlyPheGlnAlaIleuGlnIlyIleIleHisSerIleuLysLysSer 192
DB 997 AAGGTGGGCAAT---TTTGTAGCATTGGCAGCATCCAGCGGCAAAATTCAGAGAA--- 1050
QY 193 CyelIleuIleuAlaIleuApsIleuProSerThrIleCyAlaGlyIleuSerPheGlnVal 212
DB 1051 -----ATCTTGGCATTGAAGGAAACCGAATCAAGCTCACTTCTTCAAGCAC 1101
QY 213 ValValArgGlyApsnglyPheApsnglyAlaArgAsnValAps 226
DB 1102 GAGATGTCAAGAAAGGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 8
US-08-362-652-45
/ Sequence 45, Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
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/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ. ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
US-08-362-652-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-362-652-45 (1-3519)
QY 10 ProAlaCytyrGly---GlyPheApleuTyRPhelIleuAplysSerGlySerVal 28
DB 481 CCAAGATGTCAGAGACAGAGATGACATTCCTTCTGATTAAGCTCCGGCAGCATT 540
QY 29 ---LeuHisHisTrpApsngluIleTyTyR-PheValGluGlnIleuAlaHisLysPheIle 47
DB 541 GATCAAGTACATTACCCAGATGAAGGACTTGTCAAAGCTTTGATGGCCAGTTGGCG 600
QY 48 SerPProGlnIleuAryMetSerPheIleValPheSerThrArgGlyThrThreLysMetLys 67
DB 601 AGCACACGACACCTCGTTCTCCCTGATGCAATACCAAACTCTGAAGACTCATTTTACC 660
QY 68 LeuThGluApsArg-----GluGlnIleArgGlnIleuGluGluIleu 82
DB 661 TTCACGGAATTCAGAGACAGACCTGAGCCCTCAGAGCTGTGATGCCATCGCCAGCTC 720
QY 83 GlnIleValIleuProGlyIleApsThrTyRmetHisGluIlePheGluArgAlaSerGlu 102
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Db 721 CAA-----GGCTACCGTACACAGCTCGGGCATCCAGAAAGTGTAA 765
Qy 103 GlnleTyTyrGluAsnArgGlnGlyTyrArgThrAla---SerVallelleAlaLeu 121
Db 766 AGCTATTTCATCCAGAAATGGGCCCCGAAAGAGTCCAGAAAGATCTAATTGTCATC 825
Qy 122 ThrAspGlyGluLeuHsiGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 139
Db 826 ACAGATGGGCAAAATTCAGAGACCCCTGGAGTATAGACATGTCATCCCTGAAAGCAGAG 885
Qy 140 ArgSerArgAspLeuGlyAlaAlaIleValTyrCysValGlyValysAsp---PheAsnGlu 158
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGGTGGAGATGCTTCGGGAA 936
Qy 159 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 172
Db 937 CCCACTGCCCCCTACGAGAGCTGACACCATTTGGCTCAGCTCCCTCGCAGAGACAGTGTTC 996
Qy 173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 192
Db 997 AAGTGGGCAAT---TTTGATGACCTTCGACATCCAGCGGCAAAATTCAGAGAA--- 1050
Qy 193 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
Db 1051 -----ATCTTGGCATTTGAAGAAAGCAACCAATCAAGGTCAAGTACTCTTTACAGCAC 1101
Qy 213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
Db 1102 GAGATGTACAGAAAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 9
US-08-605-672-45
; Sequence 45, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seair Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856

```

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; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..3519
; US-08-605-672-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-605-672-45 (1-3519)

Qy 10 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 28
Db 481 CCAAGAGTGTCCAGAGCAAGAGATGACATTCCTTCTGATGTATGAGCTCGGACAGCATT 540
Qy 29 ---LeuHisIleStrPheGlnGlyIleTyrTyrPheValGlnIleuAlaHisLysPheIle 47
Db 541 GATCAAAAGTACCTTCCCGCATGAAAGAGACCTGTCGCAAACTTGTATGGCGAGTTGGCG 600
Qy 48 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 67
Db 601 AGCACAGACACCTCGTTCTCTCTGATGCAATCTCAACACTCTGAAAGACTCTTTTACC 660
Qy 68 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 82
Db 661 TTCACGGAATTCAGAGACAGACCTGAGCCCTGAGAGCTGTGATGTCAGCTCGACGCTC 720
Qy 83 GlnLysValLeuProGlyGlyAspThrTyrMetHisGlnGlyPheGluAlaSerGlu 102
Db 721 CAA-----GGCTGACGTACACAGCCTCGGCAATCCAGAAAGTGTGTAA 765
Qy 103 GlnIleTyTyrGluAsnArgGlnGlyTyrArgThrAla---SerVallelleAlaLeu 121
Db 766 AGCTATTTCATGCAAGAAATGGGCCCCGAAAGAGTCCAGAAAGATCTAATTGTCATC 825
Qy 122 ThrAspGlyGluLeuHsiGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 139
Db 826 ACAGATGGGCAAAATTCAGAGACCCCTGGAGTATAGACATGTCATCCCTGAAAGCAGAG 885
Qy 140 ArgSerArgAspLeuGlyAlaAlaIleValTyrCysValGlyValysAsp---PheAsnGlu 158
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGGTGGAGATGCTTCGGGAA 936
Qy 159 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 172
Db 937 CCCACTGCCCCCTACAGAGAGCTGAAACACCATTTGCTCAGCTCCCTGCAAGAGAGTTC 996
Qy 173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 192
Db 997 AAGTGGGCAAT---TTTGATGACCTTCGACATCCAGCGGCAAAATTCAGAGAA--- 1050
Qy 193 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
Db 1051 -----ATCTTGGCATTTGAAGAAAGCAACCAATCAAGGTCAAGTACTCTTTACAGCAC 1101
Qy 213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
Db 1102 GAGATGTACAGAAAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 10
US-08-482-293A-45
; Sequence 45, Application US/08482293A

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Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3866
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-482-293A-45
Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 2 Gaps: 12
US-09-970-076-2_copy_28_320 (1-293) x US-08-482-293A-45 (1-3519)
QY 10 ProalaGyetyrGly---GlyPheApPLeuTyRpheLeuApPLeuSerGlySerVal 28
DB 481 CCAAGAGTCCAGGACAAGAGATGACATTCCTTCTCGATTGATGCTCCGCGCAGATT 540
QY 29 ---LeuHishTTPAEngIuileTyTyRpheValGluInleuAlahIstysPheile 47
DB 541 GATGAAGTAGACTTACCCAGATGAAGAGACTTGTCAAGCTTTGATGGCGCAGTGGCG 600
QY 48 SerProGlnleuArgMetSerPheileValPheSerThrArgGlyThrThrleuMetLys 67
DB 601 AGCACGACGACCTGCTTCTCCCTGATGCAATACCAAACTCCTGAAGACTCATTTTACC 660

QY 68 LeuThrgIuAspArg-----GluGlnIleArgGlnGlyLeuGlnIleu 82
DB 661 TTCACGGAATTCAGAGAGCTGAGACCTGAGACCTGGATGGATGCCATCGTCCAGCTC 720
QY 83 GlnIysValleuProGlyGlyAspThrTyRmetHishGlnGlyPheGlnArgIAspSerGlu 102
DB 721 CA-----GGCTGACGTACACAGACCTCGGCGATCCAGAAAGTGTGAA 765
QY 103 GlnIleTyTyRgluAsnArgGlnGlyTyArgThrAla---SerValIleIleAlaLeu 121
DB 766 GAGCTATTTCATAGCAAGAAATGGGCGCCGAAAGATGCCAAGAAATATTATTGTGCATC 825
QY 122 ThrAspGlyGluLeuHishGlnAspLeuPhePheTyRSerGlu-----ArgGluAlaAsn 139
DB 826 ACAGATGGGCGAAGAAATTCAGAGACCCCTGAGATAGACATGTATCCCTGAAGCAGAG 885
QY 140 ArgSerArgAspLeuGlyAlaIleValTyRcySValGlyValIleAsp---PheAsnGlu 158
DB 886 AAGAGCT-----GGATCATTCGCTATGTATAGGGGTGGAGATGCTTCCGGGAA 936
QY 159 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 172
DB 937 CCCACTGCCCTTACAGAGAGCTGAACACATTTGGCTAGCTCCCTCCGAGACCACTGTTC 996
QY 173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHishSerIleLeuLysSer 192
DB 997 AAGTGGCGCAAT---TTGTAGCATTCCGACATCCAGACATCCAGCAAAATTCAGAGAAA--- 1050
QY 193 CysIleGluIleuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
DB 1051 -----ATCTTGCCATTGAAGAACCGAATCAAGGTCAAGTAGTTCCTTCAGCAC 1101
QY 213 ValValArgGlyAsnGlyPheArgHishAlaArgAsnValAsp 226
DB 1102 GAGATTCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAT 1143
RESULT 11
US-08-943-363-45
Sequence 45, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659


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Db      886 AAGCT-----GGATCATTCGCTATGCTATAGGGGTGGAGATCCTTCGGGAA 936
Qy      159 ---ThrgInLeuAlaArgIle-----AlaSPSerLyAspHisValPhe 172
Db      937 CCCACTGCCCTCAGAGAGTGAACACCATTTGGCTGCTCCCTCCGAGACACCGTTC 996
Qy      173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLySer 192
Db      997 AAGGTGGCAAT---TTTGTAGCACTTCGACAGATCCAGCGCAATTCAGAGAA--- 1050
Qy      193 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
Db      1051 -----ATCTTGCCCATTTGAAAGGACCGAATCAAGGTCAAGTAGTCTTTCAGCAC 1101
Qy      213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
Db      1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 13
US-09-688-307A-45
/ Sequence 45, Application US/09688307A
/ Patent No. 6432404
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6432404el Human Beta-2
/ FILE REFERENCE: 27866/36646
/ CURRENT APPLICATION NUMBER: US/09/688,307A
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/605,672
/ PRIOR FILING DATE: 1996-02-22
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 45
/ LENGTH: 3519
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3516)
/ OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-09-688-307A-45 (1-3519)
Qy      10 ProAlaCysPheGly---GlyPheAspLeuTyPheIleLeuAspLySerGlySerVal 28
Db      481 CCAGAGTGTCCAGACAAAGATGACATGCTTTCCTGATGATGAGCTCCGCGCAGCAT 540
Qy      29 ---LeuHisHisThrPheGlnGluIleTyTyPheValGluIleLeuAlaHisLySerPheIle 47
Db      541 GATCAAGTAGTATTACCCAGATGAAGGACTGTCAAAAGCTTTGATGGCCAGTTGGCC 600
Qy      48 SerProGlnLeuAlaArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLy 67
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Db      601 AGCAGCAGACACTCTCTCTCCCTGATGCAMTACTCAAAATCTCTGAAGCTATTTTACC 660
Qy      68 LeuThrgIleAspArg-----GluGlnIleArgGlnGlyLeuGlnLeu 82
Db      661 TTCACGGAATTTCAAGACAGACCTTACGCTTCAGAGCTGTGTGATGCCATCTCCACGTC 720
Qy      83 GlnLyValLeuProGlyIleAspThrTyPheMetHisGlnGlyPheGlnArgAlaSerGln 102
Db      721 CAA-----GGCTGACGTACACAGCTCGGGGATCCAGAAAGGTGGAA 765
Qy      103 GlnIleTyTyTyGlnAsnArgGlnGlyTyArgThrAla---SerValIleIleAlaLeu 121
Db      766 GAGCATATTTCAATAGCAAGAAATGGGCCCCGAAAGGTCCAGAAAGATACTAATTGTCAATC 825
Qy      122 ThrAspGlyLeuLeuHisGluLeuPhePhePheTyPheSerGlu-----ArgGluAlaAsn 139
Db      826 ACAGATGGGCAAAATTCAGAGACCCCTGGAGTATGACATGTCACTCCCTTAAGCAGAG 885
Qy      140 ArgSerArgAspLeuGlyAlaIleValTyTyCysValGlyValLyAsp---PheAsnGln 158
Db      886 AAGCT-----GGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAA 936
Qy      159 ---ThrgInLeuAlaArgIle-----AlaSPSerLyAspHisValPhe 172
Db      937 CCCACTGCCCTCAGAGAGTGAACACCATTTGGCTGCTCCCTCCGAGACACCGTTC 996
Qy      173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLySer 192
Db      997 AAGGTGGCAAT---TTTGTAGCACTTCGACAGATCCAGCGCAATTCAGAGAA--- 1050
Qy      193 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
Db      1051 -----ATCTTGCCCATTTGAAAGGACCGAATCAAGGTCAAGTAGTCTTTCAGCAC 1101
Qy      213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
Db      1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 14
US-09-350-259-45
/ Sequence 45, Application US/09350259
/ Patent No. 6620915
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6620915el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/350,259
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 45
/ LENGTH: 3519
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3516)
/ OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-45
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: December 18, 2005, 07:35:12 ; Search time 938.696 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: Published.Applications.NA.Main.*

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5: /cg2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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7: /cg2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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10: /cg2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1526 | 100.0 | 1414 | US-11-047-278-1 | Sequence 1, Appl1 |
| 2 | 1526 | 100.0 | 1454 | US-10-133-937-58 | Sequence 58, Appl1 |
| 3 | 1526 | 100.0 | 1454 | US-10-159-563-58 | Sequence 58, Appl1 |
| 4 | 1526 | 100.0 | 1674 | US-10-038-307-17 | Sequence 17, Appl1 |
| 5 | 1526 | 100.0 | 1674 | US-10-201-292-17 | Sequence 17, Appl1 |
| 6 | 1526 | 100.0 | 5540 | US-09-918-715-176 | Sequence 176, App |
| 7 | 1526 | 100.0 | 5540 | US-09-918-715-231 | Sequence 231, App |
| 8 | 1526 | 100.0 | 5540 | US-10-301-822-198 | Sequence 198, App |

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| 9 | 1526 | 100.0 | 5540 | US-10-474-794-176 | Sequence 176, App |
| 10 | 1526 | 100.0 | 5540 | US-10-474-794-231 | Sequence 231, App |
| 11 | 1526 | 100.0 | 5540 | US-10-979-159-176 | Sequence 176, App |
| 12 | 1526 | 100.0 | 5540 | US-10-979-159-231 | Sequence 231, App |
| 13 | 1526 | 100.0 | 5540 | US-11-047-278-5 | Sequence 5, Appl1 |
| 14 | 1514 | 99.2 | 1056 | US-10-038-307-23 | Sequence 23, Appl1 |
| 15 | 1514 | 99.2 | 1056 | US-10-201-292-23 | Sequence 23, Appl1 |
| 16 | 1514 | 99.2 | 1650 | US-10-038-307-13 | Sequence 13, Appl1 |
| 17 | 1514 | 99.2 | 1650 | US-10-038-307-15 | Sequence 15, Appl1 |
| 18 | 1514 | 99.2 | 1650 | US-10-201-292-13 | Sequence 13, Appl1 |
| 19 | 1514 | 99.2 | 1650 | US-10-201-292-15 | Sequence 15, Appl1 |
| 20 | 1514 | 99.2 | 1713 | US-10-038-307-19 | Sequence 19, Appl1 |
| 21 | 1514 | 99.2 | 1713 | US-10-201-292-19 | Sequence 19, Appl1 |
| 22 | 1514 | 99.2 | 2112 | US-11-047-278-7 | Sequence 7, Appl1 |
| 23 | 1514 | 99.2 | 2272 | US-09-796-753-11 | Sequence 11, Appl1 |
| 24 | 1514 | 99.2 | 2272 | US-10-038-307-1 | Sequence 1, Appl1 |
| 25 | 1514 | 99.2 | 2272 | US-10-201-292-1 | Sequence 1, Appl1 |
| 26 | 1514 | 99.2 | 2353 | US-10-198-846-9957 | Sequence 9957, App |
| 27 | 1509 | 98.9 | 5220 | US-09-918-715-186 | Sequence 186, App |
| 28 | 1509 | 98.9 | 5220 | US-09-918-715-300 | Sequence 300, App |
| 29 | 1509 | 98.9 | 5220 | US-10-474-794-186 | Sequence 186, App |
| 30 | 1509 | 98.9 | 5220 | US-10-474-794-300 | Sequence 300, App |
| 31 | 1509 | 98.9 | 5220 | US-10-979-159-186 | Sequence 186, App |
| 32 | 1509 | 98.9 | 5220 | US-10-979-159-300 | Sequence 300, App |
| 33 | 1504 | 98.6 | 1650 | US-10-038-307-9 | Sequence 9, Appl1 |
| 34 | 1504 | 98.6 | 1650 | US-10-201-292-9 | Sequence 9, Appl1 |
| 35 | 1501 | 98.4 | 1008 | US-10-038-307-25 | Sequence 25, Appl1 |
| 36 | 1501 | 98.4 | 1008 | US-10-201-292-25 | Sequence 25, Appl1 |
| 37 | 1499.5 | 98.3 | 1047 | US-10-038-307-21 | Sequence 21, Appl1 |
| 38 | 1499.5 | 98.3 | 1047 | US-10-201-292-21 | Sequence 21, Appl1 |
| 39 | 1499 | 98.2 | 1623 | US-10-038-307-11 | Sequence 11, Appl1 |
| 40 | 1499 | 98.2 | 1623 | US-10-201-292-11 | Sequence 11, Appl1 |
| 41 | 1413 | 92.6 | 1608 | US-10-062-674-1757 | Sequence 1757, App |
| 42 | 1385 | 90.8 | 2397 | US-10-201-292-33 | Sequence 33, Appl1 |
| 43 | 1288 | 84.4 | 1436 | US-11-047-278-9 | Sequence 9, Appl1 |
| 44 | 1257 | 82.4 | 1609 | US-10-037-270-8 | Sequence 8, Appl1 |
| 45 | 1257 | 82.4 | 1609 | US-10-037-270-8 | Sequence 8, Appl1 |

ALIGNMENTS

RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Antitoxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Alignment Scores:
Pred. No.: 6.33e-185
Score: 1526.00
Percent Similarity: 100.00%
Length: 1414
Matches: 293
Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-970-076-2_COPY_28_320 (1-293) x US-11-047-278-1 (1-1414)

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DB 185 CAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTACGGCGATTGACCTGACTTC 244
QY 21 ILEUAPLUSERGLYSERVALLEUHSIETPAENGLULETYRYPHEVALGLU 40
DB 245 ATTTTGCAAAATCAGAAAGTGTGCTGCACCTGGAATGAATCTATTACTTTGGGAA 304
QY 41 GINLEUALHIELYAPHEILLESERPROGINTLEUAXMESERPHLEVALPHESETR 60
DB 305 CAGTTGGCTCACAAATTCATCCAGCCACAGTTGAGAAATGCTTTTATTTGTTCTCCACC 364
QY 61 ARGGLYTHRTRLEUMETLYSEUTHRGLUAPARGLUGNILEARGINGLYLEUGLU 80
DB 365 CAGAGAACAACTTATTAAGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTTAGAA 424
QY 81 GIULEUGLNUYVALLEUPROGLYGLYASPTHYRMECHISGLUGLYPHEGLUAGLA 100
DB 425 GAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATGATGAAAGATTGAAAAGGCC 484
QY 101 SERGLUGNILETYRGLUAPARGGLYGLYTYRARGTHRPLASERVALILEI1EALA 120
DB 485 AGTGAACAGATTATTAATGAACAGCAAGGATACAGGACAGCCAGCTCATCATTTGCT 544
QY 121 LEUTHRASPGLYGLIUEUHSI1EGLUAPLEUPHEPHETYRSEGLUARGGLU1A1A1A1 140
DB 545 TTGACATGATGAGAAATCCATGAAGATCTTTTCTATTACAGAGGGAGGCTTAATAGG 604
QY 141 SERARGAPLEUGLYVALILEVALTYRCYVALIGLYVALIYASPPHEAENGU1UTRG1N 160
DB 605 TCTCGAGATCTTGTCGAATTTGTTTACTGTGTGTGTGTAAGATTTCATATGAGACACAG 664
QY 161 LEUALARG1LEAL1A1SPSERLYSAPPHISVALPHEPROVAL1A1A1A1A1A1A1 180
DB 665 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCTGTAATGACGGCTTTACAGCT 724
QY 181 LEUGINGLY1LEI1EHSERILEU1YALYSECYSE1EGULILEU1A1A1AGLU 200
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DB 785 CCATCCACCAATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGGAAACGGCTTCGA 844
QY 221 HISALARGHENV1ASPARGLVLEUCYSESPHELYS1LEA1A1A1A1A1A1A1 240
DB 845 CAGTCCCGGACGTGACAGGGGTCTGTGACGCTTCAAGATCAATGACTGGATCACTC 904
QY 241 AENGLULYBROPHESERVALIGUASPTHYRLEULEUCYSPRO1A1PRO1LEU1Y 260
DB 905 AAGAGAAAGCCCTTTCTGTGAAAGACACTTATTTATGATGCAAGGCTATCTTAATAA 964
QY 261 GLIVALIGLYMETLYSAL1A1ALEUGINVALISERMESAPH1GLYLEUSERPH1LESER 280
DB 965 GAAGTTGGCATGAAGCTGCACCTCCAGTCAAGCATGAAAGTGGCTCTCTTTATCTCC 1024
QY 281 SERSETRVALILETHRTHRH1CYSESPASGLY 293
DB 1025 AGTTCTGTCAATCAACACACACACACTGTTCTGACGGT 1063

RESULT 2
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
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; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133, 937
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 6,61e-185 Length: 1454
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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DB 225 CAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTTACGGCGATTGACCTGACTTC 284
QY 21 ILEUAPLUSERGLYSERVALLEUHSIETPAENGLULETYRYPHEVALGLU 40
DB 285 ATTTTGCAAAATCAGAAAGTGTGCTGCACCACTGGAATGAATCTATTACTTTGGGAA 344
QY 41 GINLEUALHIELYAPHEILLESERPROGINTLEUAXMESERPHLEVALPHESETR 60
DB 345 CAGTTGGCTCACAAATTCATCCAGCCACAGTTGAGAAATGCTTTTATTTGTTCTCCACC 404
QY 61 ARGGLYTHRTRLEUMETLYSEUTHRGLUAPARGLUGNILEARGINGLYLEUGLU 80
DB 405 CAGAGAACAACTTATTAAGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTTAGAA 464
QY 81 GIULEUGLNUYVALLEUPROGLYGLYASPTHYRMECHISGLUGLYPHEGLUAGLA 100
DB 465 GAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATGATGAAAGATTGAAAAGGCC 524
QY 101 SERGLUGNILETYRGLUAPARGGLYGLYTYRARGTHRPLASERVALILEI1EALA 120
DB 525 AGTGAACAGATTATTAATGAACAGCAAGGATACAGGACAGCCAGCTCATCATTTGCT 584
QY 121 LEUTHRASPGLYGLIUEUHSI1EGLUAPLEUPHEPHETYRSEGLUARGGLU1A1A1A1 140
DB 585 TTGACATGATGAGAAATCCATGAAGATCTTTTCTATTACAGAGGGAGGCTTAATAGG 644
QY 141 SERARGAPLEUGLYVALILEVALTYRCYVALIGLYVALIYASPPHEAENGU1UTRG1N 160
DB 645 TCTCGAGATCTTGTCGAATTTGTTTACTGTGTGTGTGTAAGATTTCATATGAGACACAG 704
QY 161 LEUALARG1LEAL1A1SPSERLYSAPPHISVALPHEPROVAL1A1A1A1A1A1A1 180
DB 705 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCTGTAATGACGGCTTTACAGCT 764
QY 181 LEUGINGLY1LEI1EHSERILEU1YALYSECYSE1EGULILEU1A1A1AGLU 200
DB 765 CTGCAGAGCATCATCCACTCAATTTTGAAGAAGTCTGCAATCGAAATTTAGACAGCTGAA 824
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DB 825 CCATCCACCAATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGGAAACGGCTTCGA 884
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DB 885 CAGTCCCGGACGTGACAGGGGTCTGTGACGCTTCAAGATCAATGACTGGTCACTC 944
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Qy 241 AsnGluYsEProPheSerValGluAspThrTyrlleuLeuCySProlAproIleLeuLys 260
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Qy 261 GluValGlyMetCysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 1005 GAAGTTGGCATGAAGCTGCACCTCCAGGTGACATGAACGATGGCCCTCTTTATCTCC 1064
Qy 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
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RESULT 3

US-10-159-563-58
Sequence 58, Application US/10159563
Publication No. US20040009154A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Rinsner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
FILE REFERENCE: 11613.56US11
CURRENT APPLICATION NUMBER: US/10/159,563
PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
NUMBER OF SEQ ID NOS: 444
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:

Pred. No.: 6 61e-185 Length: 1454
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-10-159-563-58 (1-1454)

Qy 1 GlnGlyGlyArgArgGluAspGlyGlyProAlaCysEtyrGlyGlyPheAspLeuTyrrPhe 20
Db 225 CAAGGGGAGCGAGGAGGATGGGGGCTCCAGCCGTCAAGCGGATTTGACCTGACTTC 284
Qy 21 IleLeuAspIysSerGlySerValLeuHisIleThrAsnGluIleTyrrPheValGlu 40
Db 285 ATTTGGACAATCAGAGAGTGTGCTGCACCACTGCAATGAATCTATTACTTTGTGAA 344
Qy 41 GlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
Db 345 CAGTTGGCTCAAAATTCATCAGCCACAGCTGGAATGCTCTTATTGTTTCTCCACC 404
Qy 61 ArgGlyThrThrIleuMetCysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
Db 405 CGAGGAACAACTTAATGAATGACAGAAACAGAAACAAATCCCTCAAGGCTTGAA 464
Qy 81 GluLeuGlnIlyValLeuProGlyGlyAspThrTyrrMetHisGluGlyPheGluArgAla 100
Db 465 GAACCTCCAGAAAGTTCTGCAGAGGAGACACTTAATCATGATGAAGATTGAAGGCC 524
Qy 101 SerGlnGlnIleTyrrGlyAsnArgGlnGlyTyrrArgThrAlaSerValIleIleAla 120
Db 525 AGTGAAGCATTTATTTATGAACAGACAGGCTACAGACAGCCGTCATCATTCCT 584
Qy 121 LeuThrAspGlyGluLeuHisIleGluAspLeuPhePheTyrrSerGluArgGluAlaAsnArg 140

Db 585 TTGACTAGTGAAGAACTCCATGAAGATCTTTTCTATTTCAGAGAGGAGCTAATAG 644
Qy 141 SerArgAsnLeuGlyAlaIleValTyrrCysValGlyValIysAspPheAsnGluThrGln 160
Db 645 TCTGAGATCTTGTGTGAATTTGTTACTGTGTGTGTGTGAAGATTTCAATGAACACAG 704
Qy 161 LeuAlaArgIleAlaAspSerIysAspHisValPheProValAsnAspGlyPheGlnAla 180
Db 705 CTGACCCGGATGGGACAGTMAAGATCATGTGTTCCCGTAATGACGGCTTCAGGCT 764
Qy 181 LeuGlnGlyIleIleHisSerIleLeuAllySerCysIleGluIleLeuAlaGlu 200
Db 765 CTGCAAGGCATCATCCACTCAATTTGAAAGAGTCTGCATCGAAATTTTACAGCTGAA 824
Qy 201 ProSerThrIleCysAlaGlyGlyIleSerPheGlnValValAlaArgGlyAsnGlyPheArg 220
Db 825 CCATCCACCATATGTGAGAGAGATCTTTCAATGTTCTGTGAAGAGAAACGGCTTCGA 884
Qy 221 HisAlaArgAsnValAspArgValLeuCysSerPheIysIleAsnAspSerValThrIleu 240
Db 885 CATCCCGCAACGTGGACAGGGTCTTGCAGCTTCAGATCAATGACTCGGTACACTC 944
Qy 241 AsnGluYsEProPheSerValGluAspThrTyrlleuLeuCySProlAproIleLeuLys 260
Db 945 AATGAGAAAGCCCTTTCTGTGGAGACACTTATTACTGTGTCCAGGCCCTATTTAAAA 1004
Qy 261 GluValGlyMetCysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 1005 GAAGTTGGCATGAAGCTGCACCTCCAGGTGACATGAACGATGGCCCTCTTTATCTCC 1064
Qy 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
Db 1065 AGTTCTGTCAATCACCACCACTGTTCTGACGCT 1103

RESULT 4

US-10-038-307-17
Sequence 17, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Englin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1674
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-17

Alignment Scores:

Pred. No.: 8 28e-185 Length: 1674
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-10-038-307-17 (1-1674)

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Db 94 CAAGGGGAGCGAGGAGGATGGGGGCTCCAGCCGTCAAGCGGATTTGACCTGACTTC 153
Qy 21 IleLeuAspIysSerGlySerValLeuHisIleThrAsnGluIleTyrrPheValGlu 40
Db 154 ATTTGGACAATCAGAGAGTGTGCTGCACCACTGCAATGAATCTATTACTTTGTGAA 213

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QY 41 GlnLeuAlaHisIleuPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
Db 214 CAGTTGGCTCACAAATTCATACGCCACGTTGAGAAATGCTTTATTTGTTTCTCCACC 273
QY 61 ArgGlyThrThrLeuMetLeuSerLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
Db 274 CGAGGAAACAACCTTAATGAACTGACAGAAACAGAGAAACAATCCGTCAGAGCCCTAGAA 333
QY 81 GluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluAlaGla 100
Db 334 GAACCTCCAGAAAGTTCTGCACAGAGAGACACTTACATGATGAAAGATTGAAAGGCC 393
QY 101 SerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
Db 394 AGTGACCAATTTATTTATGAAAACAGCAAGGTTACAGACAGCCAGCTCATCTGCT 453
QY 121 LeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
Db 454 TTGACTGATGGAGAACTCCATGAAAGATCTTTTCTAATTCAGAGAGGAGCTAATAGG 513
QY 141 SerArgAspLeuGlyAlaIleValTyrCybValGlyValIleAspPheAsnGluThrGln 160
Db 514 TCTCGAGATCTTGCTCAATGTTTACTGTGTGTGTAAGATTTCATAGAGACAG 573
QY 161 LeuAlaArgIleAlaAspSerLeuAspPheIleValPheProValAsnAspGlyPheGlnAla 180
Db 574 CTGGCCCGGATTCGGACACGTAAGATCATGTGTTCCCGTAATGACGGCTTCAAGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuValLeuSerCybIleGluIleLeuAlaIleGlu 200
Db 634 CTGCAGAGGATCATCCACTCAATTTGAAAGAGCTCCGATCGAAATTCAGACGCTGAA 693
QY 201 ProSerThrIleCybAlaGlyGlyLeuSerPheGlnValValArgGlyAsnGlyPheArg 220
Db 694 CCATTCACCACTAATGTGACAGAGAGTCAATTCAGATGTCGTGAGAGAGAAACGGCTTCCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCybSerPheIleValIleAsnAspSerValThrLeu 240
Db 754 CATGCCCGACAGCTGACAGAGGTCCTCTGACGCTTCAGATCATGACTGGCTCACACTC 813
QY 241 AsnGluIlePheProPheSerValGluAspThrTyrLeuLeuCybProAlaProIleLeuVal 260
Db 814 AATGAGAGAGCCCTTTCTGTGAAAGATCTTAATTTACTGTGTCAGAGCCCTATCTTAAA 873
QY 261 GluValGlyMetLeuValAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 874 GAAGTTGGCATGAAGCTGACCTCCAGTGACATGACATGACATGAGCCCTCTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCybSerAspGly 293
Db 934 AGTTCTGTATCATCACCAACACACTGTTCTGACGGT 972
RESULT 5
US-10-201-292-17
; Sequence 17, Application US/10201292
; Publication No US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-17
```

Alignment Scores:

| Pred. No.: | 8,286-185 | Length: | 1674 |
|------------------------|-----------|---------------|------|
| Score: | 1526.00 | Matches: | 293 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-970-076-2_copy_28_320 (1-293) x US-10-201-292-17 (1-1674)

```
QY 1 GlnGlyValArgArgGluAspGlyGlyProAlaCybTyrGlyGlyPheAspLeuTyrPhe 20
Db 94 CAGGGGGAGCGCAGGAGAGATGGGGTCCAGCTGCTAGGAGGATTTACCTGACTTC 153
QY 21 IleuAspIleSerGlySerValLeuHisIleTyrAsnGluIleTyrTyrPheValGlu 40
Db 154 ATTTTGACAAATTCAGAAAGTGTCTGCACCACTGAAATGAAATCTTTACTTTGGAA 213
QY 41 GlnLeuAlaHisIleuPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
Db 214 CAGTTGGCTCACAAATTCATACGCCACAGTTGAGAAATGCTTTATTTGTTTCTCCACC 273
QY 61 ArgGlyThrThrLeuMetLeuSerLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
Db 274 CGAGGAAACAACCTTAATGAACTGACAGAAACAGAGAAACAATCCGTCAGAGCCCTAGAA 333
QY 81 GluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluAlaGla 100
Db 334 GAACCTCCAGAAAGTTCTGCACAGAGAGACACTTACATGATGAAAGATTGAAAGGCC 393
QY 101 SerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
Db 394 AGTGACCAATTTATTTATGAAAACAGCAAGGTTACAGACAGCCAGCTCATCTGCT 453
QY 121 LeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
Db 454 TCTCGAGATCTTGCTCAATGTTTACTGTGTGTGTAAGATTTCATAGAGAGGAGCTAATAGG 513
QY 141 SerArgAspLeuGlyAlaIleValTyrCybValGlyValIleAspPheAsnGluThrGln 160
Db 514 TCTCGAGATCTTGCTCAATGTTTACTGTGTGTGTAAGATTTCATAGAGAGGAGCTAATAGG 573
QY 161 LeuAlaArgIleAlaAspSerLeuAspPheIleValPheProValAsnAspGlyPheGlnAla 180
Db 574 CTGGCCCGGATTCGGACACGTAAGATCATGTGTTCCCGTAATGACGGCTTCAAGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuValLeuSerCybIleGluIleLeuAlaIleGlu 200
Db 634 CTGCAGAGGATCATCCACTCAATTTGAAAGAGTCCGATCGAAATTCAGACGCTGAA 693
QY 201 ProSerThrIleCybAlaGlyGlyLeuSerPheGlnValValArgGlyAsnGlyPheArg 220
Db 694 CCATTCACCACTAATGTGACAGAGAGTCAATTCAGATGTCGTGAGAGAAACGGCTTCCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCybSerPheIleValIleAsnAspSerValThrLeu 240
Db 754 CATGCCCGACAGCTGACAGAGGTCCTCTGACGCTTCAGATCATGACTGGCTCACACTC 813
QY 241 AsnGluIlePheProPheSerValGluAspThrTyrLeuLeuCybProAlaProIleLeuVal 260
Db 814 AATGAGAGAGCCCTTTCTGTGAAAGATCTTAATTTACTGTGTCAGAGCCCTATCTTAAA 873
QY 261 GluValGlyMetLeuValAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 874 GAAGTTGGCATGAAGCTGACCTCCAGTGACATGACATGACATGAGCCCTCTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCybSerAspGly 293
Db 934 AGTTCTGTATCATCACCAACACACTGTTCTGACGGT 972
RESULT 6
US-09-918-715-176
; Sequence 176, Application US/09918715
```

```
/ Publication No. US20030017157A1
/ GENERAL INFORMATION:
/ APPLICANT: Brad St. Croix
/ APPLICANT: Bert Vogelstein
/ APPLICANT: Kenneth Kinzler
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00134
/ CURRENT APPLICATION NUMBER: US/09/918,715
/ PRIORITY FILING DATE: 2001-08-01
/ PRIORITY FILING DATE: 2000-08-02,599
/ PRIORITY FILING DATE: 2000-08-02,360
/ PRIORITY FILING DATE: 2000-08-11
/ PRIORITY FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 176
/ LENGTH: 5540
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-918-715-176
```

```
Alignment Scores:
Pred. No.: 5,576-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
```

US-09-970-076-2_COPY_28_320 (1-293) x US-09-918-715-176 (1-5540)

```
QY 1 GlnGlyGlyArgArgGlyuAspGlyGlyProAlaCySerGlyGlyPheAspLeuTyPhe 20
DB 225 CAAGGGGAGAGCGAGGAGGATGGGGGTCGACCGCTGACGCGGATTTGACCTGTACTTC 284
QY 21 IleuAspLysSerGlySerValLeuHisThrAsnGluIleTyTyPheValGlu 40
DB 285 ATTTGGACAAATGAGAAAGTGTCTGACCACTGGAATGAAATCTATTACTTTGTGAA 344
QY 41 GlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB 345 CAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATGCTCTTATTTGTTTCTCACC 404
QY 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGluIleArgGlnGlyLeuGlu 80
DB 405 CGAGGAACAACCTTAATGAAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTAGAA 464
QY 81 GlnLeuGlnLysValLeuProGlyGlyAspThrTyMetHisGluGlyPheGluArgAla 100
DB 465 GAACTCCAGAAAGTTCTGCGCAGGAGGAGACCTTAACATGCAATGAAAGATTTGAAAGGCC 524
QY 101 SerGlnGlnIleTyTyGlyuAsnArgGlnGlyTyArgThrAlaSerValIleIleAla 120
DB 525 AGTGAAGACATTTATTTATGAAACAGACAAAGGATGACAGACAGCCATCATATTGCT 584
QY 121 LeuThrAspGlyGlyLeuHisGluAspLeuPhePheTySerGluArgGluAlaAsnArg 140
DB 585 TTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGGAGGAGGCTTAATAG 644
QY 141 SerArgAspLeuGlyAlaIleValTyTyCysValGlyValLysAspPheAsnGluThrGln 160
DB 645 TCTGGAATCTTGTTGTCAAATGTTTACTGTGTGTGTGAAAGATTTCAATGAACACAG 704
QY 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 705 CTGGCCCGGATTTGGGACAGTAAGATCATGTGTTTCCGTGAATGACGGCTTTCAAGCT 764
QY 181 LeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIleGluIleLeuAlaIleGlu 200
DB 765 CTCGAAGGATCATCTCACTCAATTTTGAAGAAAGTCTGCATCGAAATTTCTAGCAGCTGAA 824
```

```
QY 201 ProSerThrIleCysAlaGlyGlyuSerPheGlnValValArgGlyuAsnGlyPheArg 220
DB 825 CCATCCACCATATATGACGAGAGACTCATTTCAATTTCTCGGAGAGAAAGCGCTTCCGA 884
QY 221 HisAlaArgAsnValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
DB 885 CATGCCCGCAACGTGACAGGGGTCTCTGACGCTTCAAGATCATGATGACGCTCACACTC 944
QY 241 AsnGluLysProPheSerValGluAspThrTyThrLeuLeuCysProAlaProIleLeuLys 260
DB 945 AATGAGAGCCCTTTTGTGGAAGATTAATTAATGTTGTCCAGCGCCCTATCTTAA 1004
QY 261 GluValGlyMetLysValAlaLeuGlnValSerMetAsnAspGlyLysSerPheIleSer 280
DB 1005 GAATTTGGCATGAAGCTGCACTCCAGGTGACATGAACATGAGCCCTCTTTATCTCC 1064
QY 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
DB 1065 AGTCTGTATCATCATCACACACACACTGTTCTGACCGT 1103
```

RESULT 7

```
US-09-918-715-231
/ Sequence 231, Application US/09918715
/ Publication No. US20030017157A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Brad St. Croix
/ APPLICANT: Kenneth Kinzler
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00134
/ CURRENT APPLICATION NUMBER: US/09/918,715
/ PRIORITY FILING DATE: 2001-08-01
/ PRIORITY FILING DATE: 2000-08-02,599
/ PRIORITY FILING DATE: 2000-08-02,360
/ PRIORITY FILING DATE: 2000-08-11
/ PRIORITY FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 231
/ LENGTH: 5540
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-918-715-231
```

```
Alignment Scores:
Pred. No.: 5,576-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
```

US-09-970-076-2_COPY_28_320 (1-293) x US-09-918-715-231 (1-5540)

```
QY 1 GlnGlyGlyArgArgGlyuAspGlyGlyProAlaCySerGlyGlyPheAspLeuTyPhe 20
DB 225 CAAGGGGAGAGCGAGGAGGATGGGGGTCGACCGCTGACGCGGATTTGACCTGTACTTC 284
QY 21 IleuAspLysSerGlySerValLeuHisThrAsnGluIleTyTyPheValGlu 40
DB 285 ATTTGGACAAATGAGAAAGTGTCTGACCACTGGAATGAAATCTATTACTTTGTGAA 344
QY 41 GlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB 345 CAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATGCTCTTATTTGTTTCTCACC 404
QY 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGluIleArgGlnGlyLeuGlu 80
DB 405 CGAGGAACAACCTTAATGAAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTAGAA 464
QY 81 GlnLeuGlnLysValLeuProGlyGlyAspThrTyMetHisGluGlyPheGluArgAla 100
```

```
DB 465 GAACTCCAGAAAGTTCTGCCAGAGAGACATTCATCATGAAAGATTGGAAGGCC 524
QY 101 SerGluGlnIleTyTyrGluAenArgInGlyTyrArgThrAlaSerValIleIleAla 120
DB 525 AGTGAGCAATTTATATGAAAAACAGACAAAGGTCACAGACGCCCTTCATTCATTGCT 584
QY 121 LeuThrAspGlyGluLeuHISegIuAAspLeuPhePheTyrSerGluArgGluAaenArg 140
DB 585 TTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCACAGAGGAGCTTAATAG 644
QY 141 SerArgAspLeuGlyValaIleValTyrCySvaIGlyValIlyAspPheAsnGluThrGln 160
DB 645 TCTCGAGATCTTGTCGTCATTTGTTTACTGTGTGGTGAAGATTTCATGAGACAG 704
QY 161 LeuAlaArgIleAlaAspSerIlyAspPheHISvalPheProValAenAspGlyPheGlnAla 180
DB 705 CTGGCCCGGATTCGGAGAGTAAGATCATGTGTTCCTCGTAATGACGGCTTTCAGGCT 764
QY 181 LeuGlnGlyIleIleHISerIleLeuIlyAspSerCySeliSegIuIleuAlaIleGlu 200
DB 765 CTGCAGAGCATCATCCATCAATTGTAAGAGTCTTCGATCGAAATTCCTAGCACTGAA 824
QY 201 ProSerThrIleCySvaIAGlyIuSerPheGlnValValaArgIlyAsnGlyPheArg 220
DB 825 CCATCCACCATATGTCAGAGAGAGTCAATTCAAGTTGTGTGAGAGAAACGGCTCCGA 884
QY 221 HIsAlaArgAenValAspArgValLeuCySerPheIlyIleAsnAspSerValThrLeu 240
DB 885 CATGCCCGCAACGTGACAGGGTCTCTCGACCTTCAGATCATGACCTCGGTCACACATC 944
QY 241 AsnGluIlyPhePheSerValIguAspThrTyrLeuLeuCySProAlaProIleLeuIly 260
DB 945 AATGAGAAAGCCCTTTCCTGGAAGATCTTATTTACTGTCTCAGAGGCTTAATCTTAAA 1004
QY 261 GluValIGlyMetIlySAlaIleGlnValaIserMeCAsnAspGlyLeuSerPheIleSer 280
DB 1005 GAAGTTGGCATGAAGCTGACCTCCAGGTACGATGAGATGAGCCCTCTTTTATCTCC 1064
QY 281 SerSerValIleIleThrThrThrHISCySerAspGly 293
DB 1065 AGTTCTGTCAATCATCACACACACACTGTTCTGACGGT 1103

RESULT 8
US-10-301-822-198
; Sequence 198, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, ShubhangI
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEMO1-029P2RMM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA
```

```
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)...(1838)
US-10-301-822-198

Alignment Scores:
Pred. No.: 5,576-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_copy_28_320 (1-293) x US-10-301-822-198 (1-5540)
QY 1 GlnGlyValArgArgGluAspGlyGlyProAlaCySyrGlyGlyPheAspLeuTyrPhe 20
DB 225 CAAGGGGACGAGAGAGATGGGGGTCCAGCTGTCTACGGCGGATTTGACCTGTACTTC 284
QY 21 IleuAspIlySerGlySerValLeuHISITrPAAsnGluIleTyrTyrPheValIGlu 40
DB 285 ATTITGACAAATCAGAAAGTGTCTGCACCACTGGAATGAAATCTAATTACTTTGTGGAA 344
QY 41 GlnLeuAlaHISlySphIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB 345 CAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATGTCTTTATTTGTTTCTCCACC 404
QY 61 ArgGlyThrThrLeuMetIlyLeuThrGluAAspArgGluGlnIleArgGlnIlyLeuGlu 80
DB 405 CGAGGAACAACCTTAATGAAGCTGACAGAAACAGAGAACAAATCCGTCAAGGCTTAGAA 464
QY 81 GluLeuGlnIlyValLeuProGlyIyAspThrTyrMetHISgluGlyPheGluArgAla 100
DB 465 GAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGATGAAGATTGAAAGGCC 524
QY 101 SerGluGlnIleTyTyrGluAenArgInGlyTyrArgThrAlaSerValIleIleAla 120
DB 525 AGTGAGCAATTTATATGAAAAACAGACAAAGGTCACAGACGCCCTTCATTCATTGCT 584
QY 121 LeuThrAspGlyGluLeuHISegIuAAspLeuPhePheTyrSerGluArgGluAaenArg 140
DB 585 TTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCACAGAGGAGGCTTAATAG 644
QY 141 SerArgAspLeuGlyValaIleValTyrCySvaIGlyValIlyAspPheAsnGluThrGln 160
DB 645 TCTCGAGATCTTGTCGTCATTTGTTTACTGTGTGGTGAAGATTTCATGAGACAG 704
QY 161 LeuAlaArgIleAlaAspSerIlyAspPheHISvalPheProValAenAspGlyPheGlnAla 180
DB 705 CTGGCCCGGATTCGGAGAGTAAGATCATGTGTTCCTCGTAATGACGGCTTTCAGGCT 764
QY 181 LeuGlnGlyIleIleHISerIleLeuIlyAspSerCySeliSegIuIleuAlaIleGlu 200
DB 765 CTGCAGAGCATCATCCATCAATTGTAAGAGTCTTCGATCGAAATTCCTAGCACTGAA 824
QY 201 ProSerThrIleCySvaIAGlyIuSerPheGlnValValaArgIlyAsnGlyPheArg 220
DB 825 CCATCCACCATATGTCAGAGAGAGTCAATTCAAGTTGTGTGAGAGAAACGGCTTCGA 884
QY 221 HIsAlaArgAenValAspArgValLeuCySerPheIlyIleAsnAspSerValThrLeu 240
DB 885 CATGCCCGCAACGTGACAGGGTCTCTCGACCTTCAGATCATGACCTCGGTCACACATC 944
QY 241 AsnGluIlyPhePheSerValIguAspThrTyrLeuLeuCySProAlaProIleLeuIly 260
DB 945 AATGAGAAAGCCCTTTCCTGGAAGATCTTATTTACTGTGTCTCAGAGGCTTAATAAA 1004
QY 261 GluValIGlyMetIlySAlaIleGlnValaIserMeCAsnAspGlyLeuSerPheIleSer 280
DB 1005 GAAGTTGGCATGAAGCTGACCTCCAGGTACGATGAGATGAGCCCTCTTTTATCTCC 1064
QY 281 SerSerValIleIleThrThrThrHISCySerAspGly 293
```



```
Db 405 CGAGGACAACTTATGAAATGACAGAGACAGAACAAATCCGTCAAGGCTTAGAA 464
Qy 81 GtluuGlnlyValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAla 100
Db 465 GAACCTCCAGAAAGTTCTGCGAGAGAGACACTTATCATCATGAAAGATTTGAAAGGGCC 524
Qy 101 SerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
Db 525 AGTGACGACATTTATTTATGAAAACAGACAAAGGTTACAGACACCGCTCATCTGCT 584
Qy 121 LeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
Db 585 TTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTTCAGAGAGGAGGCTTAATAG 644
Qy 141 SerArgAspLeuGlyValAlaIleValTyrCysValGlyValLysAspPheAsnGluThrGln 160
Db 645 TCTCGAGATCTGTGGCAATTGTTTACTGTGTGGTGAAGATTTCATATGACACAG 704
Qy 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
Db 705 CTGGCCCGAATTGCGGACAGTAAAGATCATGTGTTCCCGTGAATGACGGCTTTCAAGCT 764
Qy 181 LeuGlnGlyIleIleHisSerIleLeuLysSerCysIleGluIleLeuAlaAlaGlu 200
Db 765 CTGCAAGCATCATCCACTCAATTTTGAAGAAGTCTCGCATCGAAATTCAGACAGCTGAA 824
Qy 201 ProSerThrIleCysValAlaGlyLysSerPheGlnValValArgGlyLysGlyPheArg 220
Db 825 CCATCCACCATATGTGCAGAGAGAGTCAATTCAGGTGCGTGAAGAAACGGCTTCCGA 884
Qy 221 HisAlaArgAsnValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
Db 885 CATGCCCGCAAGCTGACAGGGTCTCTGCAAGCTTCAAGATCATATGATCGGTCAACATC 944
Qy 241 AsnGluLysProPheSerValGluAspThrTyrLeuLeuCysProAlaProIleLeuLys 260
Db 945 AATGAGAAAGCCCTTTCTGTGGAAGATATTATTTACTGTGTCACAGGCTTCTTAAAA 1004
Qy 261 GluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLysSerPheIleSer 280
Db 1005 GAAGTTGGCATGAAGACTGCACTCCAGGTGACATGATGAACGATGGCTCTCTTTATCTCC 1064
Qy 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
Db 1065 AGTTCTGTCTATCTACACCAACACACTGTTCTGACGGT 1103

RESULT 11
US-10-979-159-176
; Sequence 176, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107 00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-10-979-159-176
Alignment Scores:
Pred. No.: 5,576-184
Score: 1526.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9
Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-10-979-159-176 (1-5540)
Qy 1 GlnGlyTyrArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyrPhe 20
Db 225 CAAGGGGAGCGCAGAGGAGGATGGGGGTCCAGCTGCTGACGGCGGATTTGACCTGTACTTC 284
Qy 21 IleuAspLysSerGlySerValLeuHisGluPheAsnGluIleTyrTyrPheValGlu 40
Db 285 ATTTTGGACAAATCCAGAAAGTGTGCTGCACCACTGGAATGAATCTTATCTTTGTGGA 344
Qy 41 GlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
Db 345 CAGTTGGCTCAAAATTCATTCAGCCACAGTTGAAATGTCCTTTATTTGTTCTGCACC 404
Qy 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
Db 405 CGAGGACAACTTAAATGAATCTGACAGAAACAGAGAAACAAATCCGTCAAGGCTTAGAA 464
Qy 81 GtluuGlnlyValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAla 100
Db 465 GAACCTCCAGAAAGTTCTGCGAGAGAGACACTTATCATCATGAAAGATTTGAAAGGGCC 524
Qy 101 SerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
Db 525 AGTGACGACATTTATTTATGAAAACAGACAAAGGTTACAGACACCGCTCATCTGCT 584
Qy 121 LeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
Db 585 TTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTTCAGAGAGGAGGCTTAATAG 644
Qy 141 SerArgAspLeuGlyValAlaIleValTyrCysValGlyValLysAspPheAsnGluThrGln 160
Db 645 TCTCGAGATCTGTGGCAATTGTTTACTGTGTGGTGAAGATTTCATATGACACAG 704
Qy 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
Db 705 CTGGCCCGAATTGCGGACAGTAAAGATCATGTGTTCCCGTGAATGACGGCTTTCAAGCT 764
Qy 181 LeuGlnGlyIleIleHisSerIleLeuLysSerCysIleGluIleLeuAlaAlaGlu 200
Db 765 CTGCAAGCATCATCCACTCAATTTTGAAGAAGTCTCGCATCGAAATTCAGACAGCTGAA 824
Qy 201 ProSerThrIleCysValAlaGlyLysSerPheGlnValValArgGlyLysGlyPheArg 220
Db 825 CCATCCACCATATGTGCAGAGAGTCAATTCAGGTGCGTGAAGAAACGGCTTCCGA 884
Qy 221 HisAlaArgAsnValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
Db 885 CATGCCCGCAAGCTGACAGGGTCTCTGCAAGCTTCAAGATCATATGATCGGTCAACATC 944
Qy 241 AsnGluLysProPheSerValGluAspThrTyrLeuLeuCysProAlaProIleLeuLys 260
Db 945 AATGAGAAAGCCCTTTCTGTGGAAGATATTATTTACTGTGTCACAGGCTTCTTAAAA 1004
Qy 261 GluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLysSerPheIleSer 280
Db 1005 GAAGTTGGCATGAAGACTGCACTCCAGGTGACATGATGAACGATGGCTCTCTTTATCTCC 1064
Qy 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
Db 1065 AGTTCTGTCTATCTACACCAACACACTGTTCTGACGGT 1103

RESULT 12
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US-10-979-159-231
; Sequence 231, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/919,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-979-159-231

Alignment Scores:
Pred. No.: 5.57e-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-10-979-159-231 (1-5540)
QY 1 GlnGlyValArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyrPhe 20
Db 225 CAAAGGGAGAGCGAGGAGGATGGGGGTCACAGCTGCTACGGCGATTTGACCTGATCTTC 284
QY 21 IleuAspLysSerGlySerValLeuHsiStrPaangLuietyrTyrPheValGlu 40
Db 285 ATTTTGACAATCAGGAAGTGTCTGACACACTGGAATGAATCTTTATTTGTTCTCCACC 344
QY 41 GlnLeuAlaHsiLysPheHsiLysSerProGlnLeuArgMetSerPheHsiLysSerThr 60
Db 345 CAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGTCCTTTATTTGTTCTCCACC 404
QY 61 ArgGlyThrThrLeuMetLysLeuThrGlnAspArgGlnLysGlnLysGlnLysGln 80
Db 405 CGAGGAACAACCTTAATGAACCTGACAGAAAGACAGAAACAATCCCTCAAGGCTTAGAA 464
QY 81 GlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHsiGlnGlyPheGluArgAla 100
Db 465 GAATCTCAGAAAGTTCGCGAGAGAGACACTACATGATGAGAGATTTGAAAGGCC 524
QY 101 SerGlnGlnLysTyrTyrGlnAspArgGlnLysTyrArgThrAlaSerValHsiLeuAla 120
Db 525 AGTGAGCAGATTTTATTTGAAAACAGACAAGGGTACAGACAGCCGATCATCATTTGCT 584
QY 121 LeuThrAspGlyGlnLysHsiGlnAspLeuPheHsiLysSerGlnLysGlnLysAlaAspArg 140
Db 585 TTGACTATGAGAACTCCATGAAGATCTTTTTCATTCAGAGAGGAGGCTTAATAGG 644
QY 141 SerArgAspLeuGlyAlaHsiLysValTyrCysValGlyValLysAspPheAspGlnLysGln 160
Db 645 TCTGGAATCTTGGTGGCAATTTGTTACTGTGTGTTGTTGAAAGATTTCAATGAGACACAG 704
QY 161 LeuAlaArgGlnLysAspSerLysAspHsiValPheProValLysAspGlyPheGlnAla 180
Db 705 CTGGCCCGGATGGGAGCAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCAGGCT 764
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QY 181 LeuGlnGlyLysLysHsiSerLysLeuLysLysCysValGlnLysLeuAlaAlaGlu 200
Db 765 CTCGAAGCATCATCTCAATTTTGAAGAACTCCGATCGAAATTTGACAGCTGAA 824
QY 201 ProSerThrLysCysAlaGlyLysSerPheGlnValValAlaArgGlyAspGlyPheArg 220
Db 825 CCATCCACCACTATGTCAGAGAGAGTCAATTTCAAGTTGTCGTGAGAGAAACGGCTTCCGA 884
QY 221 HsiAlaArgAspValAlaAspArgValLeuCysSerPheLysLysLysAspSerValThrLeu 240
Db 885 CATGCCCGACAGCTGAGCAGAGGCTCTGACGCTTCAAGATCATGATGATCGATCACTC 944
QY 241 AsnGlnLysProPheSerValGlnAspThrTyrLeuLeuCysProAlaProLysLeuLys 260
Db 945 AATGAGAGCCCTTTCTGTGGAATATCTTATTTACTGTGTCAACGGCTTATCTTAAAA 1004
QY 261 GlnValGlyMetLysAlaAlaLeuGlnValSerMetAspAspGlyLysSerPheHsiLys 280
Db 1005 GAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGCATGAAAGATGGCTCTTTTATCTCC 1064
QY 281 SerSerValLysLysThrThrHsiCysSerAspGly 293
Db 1065 AGTTGTCTATCATCATCACACACACTGTTCTGACGCT 1103

RESULT 13
US-11-047-278-5
; Sequence 5, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mordridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)..(1835)
US-11-047-278-5

Alignment Scores:
Pred. No.: 5.57e-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-11-047-278-5 (1-5540)
QY 1 GlnGlyValArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyrPhe 20
Db 225 CAAAGGGAGAGCGAGGAGGATGGGGGTCACAGCTGCTACGGCGATTTGACCTGATCTTC 284
QY 21 IleuAspLysSerGlySerValLeuHsiStrPaangLuietyrTyrPheValGlu 40
Db 285 ATTTTGACAATCAGGAAGTGTCTGACACACTGGAATGAATCTTTATTTGTTCTCCACC 344
QY 41 GlnLeuAlaHsiLysPheHsiLysSerProGlnLeuArgMetSerPheHsiLysSerThr 60
Db 345 CAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGTCCTTTATTTGTTCTCCACC 404
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QY 61 ArgGlyThrThreumetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
DB 405 CAGAGAACAACTTATGAACTGACAGAAAGACAGAAACAATCCGTCAAGCCCTAGAA 464
QY 81 GluLeuGlnIlyValLeuProGlyGlyAspThrTyrMetHisGlnGlyPheGluArgAla 100
DB 465 GAACTCCAGAAAGTTCTGCGAGAGAGACACTTATCATGATGAAAGATTGAAAGGCGC 524
QY 101 SerGluGlnIleTyrGlyuAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
DB 525 AGTACAGCAATTTATATGAAAACAGACAAAGGCTACAGACCGCATCATTTGCT 584
QY 121 LeuThrAspGlyGluLeuHisGlnAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
DB 585 TTGACATGATGAGAACTCCATGAAAGATCTTTTCTATTTCAGAGAGGAGGCTATTAAG 644
QY 141 SerArgAspLeuGlyValIleValTyrCysValGlyValIlyAspPheAsnGluThrGln 160
DB 645 TCTCGAGATCTTGTCGAATTTGTTACTGTGTGTGTAAGATTTCATATGAGACACAG 704
QY 161 LeuAlaArgIleAlaAspSerIlyAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 705 CTGGCCCGAATTCGAGACAGTAAGATCATGTGTTCCTGTAATACGCTTTCAGGCT 764
QY 181 LeuGlnGlyIleIleHisSerIleLeuIlyAspSerCysIleGluIleLeuAlaIleGlu 200
DB 765 CTGCAGAGCATCATCCACTCAATTTTGAAGAACTCCTGCATCGAAATTCAGACGTGA 824
QY 201 ProSerThrIleCysAlaGlyGlySerPheGlnValValIlyArgGlyAsnGlyPheArg 220
DB 825 CCATCCACCATATGTGCAGAGAGATCATTTCAAGTTGTCGTGAGAGAAACGGCTTCCGA 884
QY 221 HisAlaArgAsnValAspArgValLeuCysSerPheIlyIleAsnAspSerValThrLeu 240
DB 885 CAGCCCGCAACCTGACAGGGGTCTCTGCAGCTTCAGATCATGACTGCGACACATC 944
QY 241 AsnGlyAspProPheSerValGluAspThrTyrLeuLeuCysProIleLeuIly 260
DB 945 AATGAGAAAGCCCTTTCTGTGGAAGATCTTATTACTGTCTCAAGCGCTATCTTAA 1004
QY 261 GluValGlyMetIlyAlaIleGlnIlyValSerMetAsnAspGlyLeuSerPheIleSer 280
DB 1005 GAAGTTGGCATGAAGCTGCATCCAGTCCAGATGACATGCGCTCTTTTATCTCC 1064
QY 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
DB 1065 AGTTCTGTATCATCACACCACTGTTCTGACGCT 1103
RESULT 14
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Englin OZAKYAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ. ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23
Alignment Scores:
Pred. No.: 1,39e-183 Length: 1056
Score: 1514.00 Matches: 291

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.21% Indels: 0
DB: 6 Gaps: 0
US-09-970-076-2_COPY_28_320 (1-293) x US-10-038-307-23 (1-1056)
QY 1 GlnGlyIlyArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyrPhe 20
DB 94 CAAGGGGGAGCGAGGAGGATGGGGGTCCAGCTCTCAAGGGGATTTGACTGTACTTC 153
QY 21 IleuAspIlySerGlySerValLeuHisGlnPheAsnGluIleTyrTyrPheValGlu 40
DB 154 ATTTTGGCAAAATTCAGAAAGTGTCTGCACCACTGAAATGAAATCTATTACTTTGGAA 213
QY 41 GlnLeuAlaHisIlyPheIleSerProGlnLeuAspMetSerPheIleValPheSerThr 60
DB 214 CAGTTGGCTCACAAATTCATCTACGCCACGTTGAAAGTCTTTATGTCTTTCTCCACC 273
QY 61 ArgGlyThrThreumetLysLeuThrGluAspArgGluGlnIleArgGlnIlyLeuGlu 80
DB 274 CAGAGAACAACTTATGAACTGACAGAAACAGAAACAATCCGTCAAGGCGCTAGAA 333
QY 81 GluLeuGlnIlyValLeuProGlyGlyAspThrTyrMetHisGlnGlyPheGluArgAla 100
DB 334 GAACCTCCAGAAAGTTCTGCGAGAGAGACACTTACATGACAGAAAGATTGAAAGGCGC 393
QY 101 SerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
DB 394 AGTGAACAAATTTATATGAAAACAGACAAAGGCTACAGACAGCCGCTCATCTTGGT 453
QY 121 LeuThrAspGlyGluLeuHisGlnAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
DB 454 TTGACATGATGAGAACTCCATGAAAGATCTTTTCTATTTCAGAGAGGAGCTAATTAAG 513
QY 141 SerArgAspLeuGlyValIleValTyrCysValGlyValIlyAspPheAsnGluThrGln 160
DB 514 TCTCGAGATCTTGTCGAATTTGTTACTGTGTGTGTAAGATTTCATAGACACAG 573
QY 161 LeuAlaArgIleAlaAspSerIlyAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 574 CTGGCCCGAATTCGAGACAGTAAGATCATGTGTTCCTGTAATACGCGCTTTCAGGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuIlyAspSerCysIleGluIleLeuAlaIleGlu 200
DB 634 CTGCAGAGCATCATCCACTCAATTTTGAAGAGTCTGATCGAAATTCAGACGTGA 693
QY 201 ProSerThrIleCysAlaGlyGlySerPheGlnValValIlyArgGlyAsnGlyPheArg 220
DB 694 CCATCCACCATATGTGCAGAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCysSerPheIlyIleAsnAspSerValThrLeu 240
DB 754 CAGCCCGCAACCTGAGACAGGGTCTCTGCAGCTTCACATCATATGATCTCGTCAACATC 813
QY 241 AsnGlyAspProPheSerValGluAspThrTyrTyrLeuLeuCysProIleLeuIly 260
DB 814 AATGAGAAAGCCCTTTCTGTGGAAGATCTTATTACTGTGTCCAGCGCTATCTTAA 873
QY 261 GluValGlyMetIlyAlaIleGlnIlyValSerMetAsnAspGlyLeuSerPheIleSer 280
DB 874 GAAGTTGGCATGAAGCTGCATCCAGTCCAGATGACAGATGAGATGCGCTCTTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCysSer 291
DB 934 AGTTCTGTATCATCACACCACTGTTCTGACGCT 966
RESULT 15
US-10-201-292-23
; Sequence 23, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN

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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201.292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1056
TYPE: DNA
ORGANISM: Homo sapiens
US-10-201-292-23

Alignment Scores:
Pred. No.: 1,39e-183 Length: 1056
Score: 1514.00 Matches: 291
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.21% Indels: 0
Gaps: 0
DB:

US-09-970-076-2_copy_28_320 (1-293) x US-10-201-292-23 (1-1056)

QY 1 GlnGlyGlyArgArgGlyuAspGlyGlyProAlaCysGlyGlyPheAspLeuTyrPhe 20
DB 94 CAGGGGGAGCCGAGGAGAGAGGGGGGCTCAGCCCTGCTACGGGAGTTGACCTGTACTTC 153
QY 21 lleuAspLysSerGlySerValleuHisIleTrrPheGlnIleTyrTyrPheValGlu 40
DB 154 ATTTGGACAATCAGGAGAGTGTCTGCACACCTGAAATGAAATCTTACTTTGTGAA 213
QY 41 GlnLeuAlaHisIleLysPheIleSerProGlnLeuArgWecSerPheIleValPheSerThr 60
DB 214 CAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGCTTTATTTGTTTCTCCACC 273
QY 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGlnIleArgGlnIleuGlu 80
DB 274 CGAGGAACACCTTAATGAACCTGACAGACAGACAGAACAAATCCGTCAGAGGCTAGAA 333
QY 81 GluLeuGlnLysValleuProGlyGlyAspThrTyrMetHisGlnGlyPheGluArgAla 100
DB 334 GAATCTCCAGAAAGTCTGCGCAGAGAGACCTTACATGCAATGAAGATTTGAAGGGCC 393
QY 101 SerGlnGlnIleTyrTyrGluAsnArgGlnIleTyrArgThrAlaSerValIleIleAla 120
DB 394 AGTAGACAGATTTATTAAGAAACAGACAGAGGTACAGACAGCCAGCTCATCATGCT 453
QY 121 LeuThrAspGlyGluLeuHisGluAspLeuPheThrTyrSerGluArgGluAlaAsnArg 140
DB 454 TTGACTGATGAGAACTCCATGAAGATCTTTTTCATTAATCAGAGGAGGCTAATAGG 513
QY 141 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAspPheAsnGluThrGln 160
DB 514 TCTGAGATCTGTGGTCAATGTTTACTGTGTGTGTGAAAGATTTCAATGAGACACAG 573
QY 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 574 CTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTCAGGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuLysSerCysIleGlnIleLeuAlaIleGlu 200
DB 634 CTGCAGGCAATCATCCACTCAATTTTGAAGAGTCTGCAATCGAAATTTAGCAGCTGAA 693
QY 201 ProSerThrIleCysAlaGlyGlySerPheGlnValValAlaArgGlyAsnGlyPheArg 220
DB 694 CCATCCACCAATATGTGACGAGAGATCATTTCAAGTTGTGCGAGAGAAAGCGCTTCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
DB 754 CATGCCCGCAACGTGACAGGGGTCTCTGACGCTTCAAGATCAATGACTCGGTCAACATC 813
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QY 241 AsnGluLysProPheSerValGluAspThrTyrLeuLeuCysProAlaProIleLeuLys 260
DB 814 AATGAGAGGCCCTTTCTGTGGAAGATCTTATTTACTGTGTCAGCGCTTACTTAAAA 873
QY 261 GluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
DB 874 GAAATTGGCATGAAAGCTGCACTCCAGGTCCAGCATGAAAGCATGCGCTCTCTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCysSer 291
DB 934 AGTTCTGTCAATCAACACACACACACTGTAGC 966
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 236.436 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526
Sequence: 1 OCGRRBDCGACGAGFPLYF.....DGLSFSSVITTHCSDG 293

Scoring table: BLOSUM62

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| Ygapop 10.0 | Ygapext 0.5 |
| Fgapop 6.0 | Fgapext 7.0 |
| Delop 6.0 | Delext 7.0 |

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Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.cdt -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 -CGN_1_1_675 -runac_14122005_111853_21065
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database: Published Applications NA New:*

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| 4: | /cg2_6/ptodaca/1/pubpna/US08_NEW_PUB.seq:* |
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| 6: | /cg2_6/ptodaca/1/pubpna/US10_NEW_PUB.seq:* |
| 7: | /cg2_6/ptodaca/1/pubpna/US11_NEW_PUB.seq:* |
| 8: | /cg2_6/ptodaca/1/pubpna/US11_NEW_PUB.seq2:* |
| 9: | /cg2_6/ptodaca/1/pubpna/US11_NEW_PUB.seq3:* |
| 10: | /cg2_6/ptodaca/1/pubpna/US60_NEW_PUB.seq:* |

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1526 | 100.0 | 5540 | 7 | US-11-186-284-198 |
| 2 | 145.5 | 9.5 | 4740 | 7 | US-11-080-026-3 |
| 3 | 131 | 8.6 | 11447 | 7 | US-11-186-284-25 |
| 4 | 122 | 8.0 | 2834 | 6 | US-10-750-185-39040 |
| 5 | 113.5 | 7.4 | 1325 | 6 | US-10-750-185-56394 |
| 6 | 113.5 | 7.4 | 2501 | 6 | US-10-821-234-182 |
| 7 | 113.5 | 7.4 | 3449 | 6 | US-10-131-826A-293 |
| 8 | 111 | 7.3 | 3564 | 6 | US-10-601-368-20 |

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|----|-------|-----|-------|---|---------------------|---------------------|
| 9 | 111 | 7.3 | 4858 | 6 | US-10-601-368-19 | Sequence 19, Appl |
| 10 | 107.5 | 7.0 | 3175 | 6 | US-10-995-561-464 | Sequence 464, Appl |
| 11 | 107.5 | 7.0 | 3464 | 6 | US-10-995-561-465 | Sequence 465, Appl |
| 12 | 107.5 | 7.0 | 3468 | 6 | US-10-995-561-466 | Sequence 466, Appl |
| 13 | 107 | 7.0 | 3564 | 6 | US-10-601-368-2 | Sequence 2, Appl1 |
| 14 | 107 | 7.0 | 3967 | 7 | US-11-000-463-574 | Sequence 574, Appl |
| 15 | 107 | 7.0 | 3969 | 7 | US-11-000-463-102 | Sequence 102, Appl |
| 16 | 107 | 7.0 | 5042 | 6 | US-10-601-368-1 | Sequence 1, Appl1 |
| 17 | 103.5 | 6.8 | 2765 | 6 | US-10-750-185-2575 | Sequence 2575, A |
| 18 | 101.5 | 6.7 | 3868 | 6 | US-10-995-561-404 | Sequence 404, Appl |
| 19 | 101.5 | 6.7 | 47572 | 6 | US-10-995-561-13356 | Sequence 13356, A |
| 20 | 100 | 6.6 | 2773 | 7 | US-11-102-240-33 | Sequence 33, Appl1 |
| 21 | 96 | 6.3 | 3884 | 6 | US-10-601-368-17 | Sequence 17, Appl1 |
| 22 | 94 | 6.2 | 1062 | 7 | US-11-137-465-11 | Sequence 11, Appl1 |
| 23 | 94 | 6.2 | 1347 | 7 | US-11-137-465-12 | Sequence 12, Appl1 |
| 24 | 91.5 | 6.0 | 1881 | 6 | US-10-467-657-5431 | Sequence 5431, Appl |
| 25 | 84.5 | 5.5 | 2715 | 6 | US-10-507-275-4 | Sequence 4, Appl1 |
| 26 | 82 | 5.4 | 3189 | 7 | US-11-137-465-10 | Sequence 10, Appl1 |
| 27 | 81.5 | 5.3 | 1688 | 6 | US-10-510-386-157 | Sequence 157, Appl |
| 28 | 81 | 5.3 | 11115 | 6 | US-10-513-786-6 | Sequence 6, Appl1 |
| 29 | 81 | 5.3 | 11115 | 6 | US-10-513-786-8 | Sequence 8, Appl1 |
| 30 | 79.5 | 5.2 | 2317 | 6 | US-10-793-626-4357 | Sequence 4357, Appl |
| 31 | 79.5 | 5.2 | 2987 | 6 | US-10-793-626-3398 | Sequence 3398, Appl |
| 32 | 79.5 | 5.2 | 3366 | 6 | US-10-467-657-6111 | Sequence 6111, Appl |
| 33 | 78.5 | 5.1 | 1895 | 6 | US-10-750-185-42451 | Sequence 42451, A |
| 34 | 78 | 5.1 | 1329 | 6 | US-10-467-657-3293 | Sequence 3293, Appl |
| 35 | 78 | 5.1 | 1443 | 6 | US-10-467-657-7037 | Sequence 7037, Appl |
| 36 | 77.5 | 5.1 | 960 | 6 | US-10-793-626-1039 | Sequence 1039, Appl |
| 37 | 77.5 | 5.1 | 1311 | 6 | US-10-763-712A-178 | Sequence 178, Appl |
| 38 | 77.5 | 5.1 | 20600 | 6 | US-10-829-826B-91 | Sequence 91, Appl1 |
| 39 | 77.5 | 5.1 | 28586 | 6 | US-10-829-826B-89 | Sequence 89, Appl1 |
| 40 | 77.5 | 5.1 | 28586 | 6 | US-10-829-826B-90 | Sequence 90, Appl1 |
| 41 | 76.5 | 5.0 | 1548 | 6 | US-10-467-657-7037 | Sequence 7037, Appl |
| 42 | 76 | 5.0 | 1407 | 6 | US-10-467-657-4369 | Sequence 4369, Appl |
| 43 | 75.5 | 4.9 | 8157 | 6 | US-10-523-912-1 | Sequence 1, Appl1 |
| 44 | 75 | 4.9 | 3445 | 6 | US-10-793-626-3648 | Sequence 3648, Appl |
| 45 | 74.5 | 4.9 | 2361 | 6 | US-10-467-962B-102 | Sequence 102, Appl |

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Sequence 198, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA

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/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (144)...(1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 3.8e-179      Length: 5540
Score: 1526.00         Matches: 293
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 7                  Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-11-186-284-198 (1-5540)

QY 1 GINGLYGIVARGRGIGUABRGIVYPROALCYETRGIVGIPHEAPLEUTYPHE 20
DB 225 CAAGGGGAGCGCAGGAGGTGGGGGTCCAGCTGCTACGGCGGATTTGACCTGTACTTC 284
QY 21 ILEUABRPLYSERGLYSERVALLEUHIETRPANGLULETYRTPHEVALGU 40
DB 285 ATTTGGACAAATCAGAAAGTGTGTGACCACTGGAATGAATCTATTACTTTGTGGAA 344
QY 41 GINLEUALHIATYSPHEIIESEPRGGINLEUARGMESERPHETLEVALPHESETHR 60
DB 345 CAGTTGGCTACAAATTCATCAGCCCAAGTTGAGATGCTTTATTGTTTTCTCCACC 404
QY 61 ARGGLYTHRTHEUWETLYSEUTHRGIVABRPGIUGINILEARGGINGLILEUGLU 80
DB 405 CGAGGAACAACCTTAATGAAACTGACGAGAACAGAACAAATCCGTCAAGGCGTAAAGA 464
QY 81 GINLEUGLNUYVALLEUPROGIVGIVABRTHRTMECHISGLIUGIPHEGIUARGIA 100
DB 465 GAATCCAGAAATTTCTGCGAGAGAGACATTAACGTGATAGAGATTTGAAGGGCC 524
QY 101 SERGLUGINILETYRTRGIVUABNARGINGLYTRARGTHRLASERVALILEIALA 120
DB 525 AGTGACCAAGTTTATTATGAAACAGAACAGGATACAGCACCCGCTCATCATTTGCT 584
QY 121 LEUTHRABRGLYGLUENHISGLUABRLEUPHEPHEPHEPHEPHEPHEPHEPHEPHE 140
DB 585 TTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTACAGAGAGGCGCTTAATAG 644
QY 141 SERHARGPRLUENGLIALILEVALTYRCYVALGIVALLYABRPHABANGIUTRGIN 160
DB 645 TCTCGAGATCTGTGCAATGTTTACTGTGTGTGTGAAGATTTCAATGAGACACAG 704
QY 161 LEUALARGILEALABRSEITLYABRPHIEVALPHEPROVALABNBRGIPHEGINALA 180
DB 705 CTGGCCCGGATTCGCGACATTAAGATCATGTGTTCCCGTAATGACGGCTTTCAAGCT 764
QY 181 LEUGINGLYTLEIENHISERTILEUUYELYSERCYALLEGUULEUALAALAGLU 200
DB 765 CTCGAAAGGCATCATCCACTCAATTTTGAAAGATCCGTCGATCGAAATTTCAAGAGCTGA 824
QY 201 PROSERTHRTLECYVALAGIUGUSERPHEGINVALVALYALARGIYAANGIYPHEARG 220
DB 825 CCATCCACCAATATGTGAGAGAGTCAATTCAGTTGTCGTGAGAGGAAAGCGCTTCGGA 884
QY 221 HIALABRABNVALABRARGVALLEUCYSESRPHELYSILEABNABRSEITLTHRU 240
DB 885 CATGCCCGCAACGTGGACAGGGTCTTGACAGCTTCAAGATCAATGCTGGCTCACACTC 944
QY 241 ABRGILUABRPHRPHESERVALGUABRTHRTYRLEUENUCYSPROALAPROIILEUUY 260
DB 945 AATGAGAAAGCCCTTTCTGTGAAAGATCTTATTACTGTGTCCAGGCGCTTACTTAAAA 1004
QY 261 GLUVALGIVETLYSALALALEUGINVALSERHEFABNBRGIVLEUSRPHETIESE 280
DB 1005 GAAGTTGGCATGAAGGTGACATCCAGGTCAAGCATGAACATGCGCTCTCTTATCTCC 1064
QY 281 SERSERVALILEITHTHTHTHTHIECYSESRABPLY 293
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DB 1065 AGTCTGCATCATCACACACACATGTTCTGACGGT 1103

RESULT 2
US-11-080-026-3
/ Sequence 3, Application US/11080026
/ Publication No. US20050260192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shinooka, Motomu
/ APPLICANT: Lu, Chafen
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ FILE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
/ FILE REFERENCE: CPER-P02-021
/ CURRENT APPLICATION NUMBER: US/11/080,026
/ CURRENT FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: 09/945,265
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 4740
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-080-026-3

Alignment Scores:
Pred. No.: 1.15e-06      Length: 4740
Score: 145.50           Matches: 60
Percent Similarity: 45.85%      Conservative: 45
Best Local Similarity: 25.20%      Mismatches: 81
Query Match: 9.53%      Indels: 43
DB: 7                  Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-11-080-026-3 (1-4740)

QY 17 ABPLUUTYRPHDILEUABRPLYSERGLYSERVALLEU---HIETRPANGLUILE 35
DB 520 GACATTCCTTTGATTATGCTGTGTGACATCATCCACATGACTTTGGCGGAG 579
QY 36 TYRTRYRPHVALGUGINLEUALHATYSPHEIIESEPRGGINLEUARGMESERPHE 55
DB 580 AAGGAGTTTGTCTCAACT-----GTGATGAGCAATTAATAAAGTCCAA 624
QY 56 ILEVALPHESETHRARGGLYTHRTHEUWETLYSEUTHRGIVABR----- 71
DB 625 ACCTGTGCTCT-----TTGATGCACTACTCTGAAGAAATTCGGAATTCAC 669
QY 72 -----ARGGLUGINILEARGINGLYLEUGIUGIUGIUGIN 83
DB 670 TTTACTTCAAGAGTTCAGAACAACTTAACCCAAAGTCACTGTGAAAGCAATTAAG 729
QY 84 LYVALLEUPROGLYGLYABRTHRTYRMECHISGLIUGIPHEGLUARGLASERGIN 103
DB 730 CAGCTGCTT-----GGGGGACACACACGGCCACGGGATCGCAAGGTGTAAGAG 783
QY 104 ILETYRTRYGLUABNARGINGLYTRARGTHRLA---SERVALILEIALALEUTHR 122
DB 784 CTGTTTACATCACCAACGAGGCCGAAAGAAATGCCCTTAAGATCTTACTGTGATCAG 843
QY 123 ABRGLIGLUENHISGLUABRLEUPHEPHEPHEPHEPHEPHEPHEPHEPHEPHEPHE 140
DB 844 GATGGGAAAGATTTGGCAATCCCTTGGATATGAGATGTATCCCTGAGCAGACAG 903
QY 141 SERHARGPRLUENGLIALILEVALTYRCYVALGIVALLYABRPHABANGIUTRGIN 160
DB 904 GAG-----GAGTCAATTCGCTACGTCAATTCGGGTGGAGATCCCTCCGACGTGAG 954
QY 161 LEUALARG-----ILEALABRSE-----LYABRPHISVALPHEPRO 173
DB 955 AATCCCGCAAGAGCTTAATACATGCATCCAAAGCCGCTGTATCAGTGTTCAG 1014
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Oy 174 ValaanaapgyPhgGlnAlaLeuGlnGlyIlelleHLeAserlleLeuLybLyserGys 193
Db 1015 GTGAATTAAC---TTTGAGGCTTGAAAGACATTCAAGACCAAGCTTCGGAGAG-- 1065
Oy 194 IleguileLeuAlaAlaGluProSerThrIleCyAlaGlyGluSerPhgGlnVal 213
Db 1066 -----ACTTTGGCATCGAGGGTACTCAGACAGAGAGTAGAGCTCTTGACATGAG 1119
Oy 214 ValArgGlyAenGlyPhaArgHtaIa 222
Db 1120 ATGCTCAGAGAGGCTTCAGCGCTGCC 1146

RESULT 3
US-11-186-284-25
; Sequence 25, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (9192)
US-11-186-284-25

Alignment Scores:
Pred. NO.: 0.000288 Length: 11447
Score: 131.00 Matches: 59
Percent Similarity: 48.98% Conservative: 38
Best Local Similarity: 29.80% Mismatches: 75
Query Match: 8.58% Indels: 26
DB: Gaps: 13

US-09-970-076-2_COPY_28_320 (1-293) x US-11-186-284-25 (1-11447)
Oy 17 AepLeuYrPhelleLeuAspLySerGlySerVal---LeuHnHnHtPraSndGlnIle 35
Db 1318 GAAATGCTGCTTTGGATGGTGGCTCTCAATGCAATGGAGATTCGCAAACTTGTAAAGTT 1377
Oy 36 TyrTyrPhaValGluGlnLeuAlaHbLybPhe---IleSerPro---GlnLeuArgMet 53
Db 1378 AGAGGCTTTTGGAAAGCTCTGTAAAAAAGTTTGAATTTCACCAAAATAGAGGTCAAGTT 1437
Oy 54 SerPheIleValPheSerThr-----ArgGlyThrThrLeuMetLybLeuThGlu 70
Db 1438 AGCTTTGCAATACAGCCGGAGATCTCATACTGATTCACCTTTGAAAAAATTCACCAAA 1497

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OY      71  AsparGluGlnIleArgGlnGlyLeuGluGluLeuGlnIleValLeuPro-----Gly 88
Db      1498 GTTGAAGATATAATT-----GAGCAATAAACAACCTTCCCTTACAGAGGA 1542
OY      89  GlyAspThrTyrMetHisIleGluGlyPheGluIArgAlaSerGluGlnIleTyrTyrGluAsn 108
Db      1543 GGATCTACAAATACATCGCAAAAGCAATGACTTATGTCAAGAGAAATATTTGTGCTAG 1602
OY      109  ArgGlnGlyTyrArgThr-----AlaSerValIleIleAlaLeuThrAspGlyGluLeu 126
Db      1603 AAG--GGATCAAGAACGATGTGCCAAGGCTATGATTCTTATCACCGATGGGAAA-- 1656
OY      127  HisGluAspLeuPhePheTyrSerGluArgGluIuAlaAsnAspSerArgAspLeuGlyAla 146
Db      1657 TCATCAGATGCTTTC-----AGAGATCCTGGATTAACATGAGGAATTCAGATCTT 1707
OY      147  IleValTyrCysValGlyValIleAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp 166
Db      1708 GAATTCCTTGGAGTTGGTGGTGAAGATGCCCTTGCTCAGAAATTGGAAGCATTTGCCCT 1766
OY      167  -----SerTyrAspHisValIlePheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 184
Db      1768 CCTCCTGACAGAGACCCATGCTTCAAGTGAAGAT--TTTGATGCTTTTCAAGAGATA 1824
OY      185  IleHisSerIleLeuIleGlySerCysIleGluIle-----LeuAlaAla 199
Db      1825 TCTTTGGAATCACACAGCTTATCTGCTTGAATTGAGCAAGAAATTGGCAGCT 1878

RESULT 4
US-10-750-185-39040/C
; Sequence 39040, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64822
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39040
; LENGTH: 2834
; TYPE: DNA
; ORGANISM: Bovine 19866880867914
US-10-750-185-39040

Alignment Scores:
Pred. No.: 0.000453 Length: 2834
Score: 122.00 Matches: 54
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 29.03% Mismatches: 71
Query Match: 7.99% Indels: 24
Gaps: 10

US-09-970-076-2_COPY_28_320 (1-293) x US-10-750-185-39040 (1-2834)

OY      17  AspleuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTPAsnGlu----- 34
Db      2115 GACATTAATCTCTTATGACGGGCTTCGGCAGTACC-----CACCAAGACGACTTCTC 2062
OY      35  ---IleTyrTyrPheValIleGluIleuAlaHisLysPhe---IleSerProGlnLeuArg 52
Db      2061 GCGATGAAGGTTTCATGAATGAGTGTATGAAGATGTTCCACGTTGACCGGAC--AGA 2005
OY      53  MetSerPheIleVal-PheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspAr 72

```

Db 2004 GTCCAGTTTGGAGTGTGTCAGTACTGGATGAAGTCAAGTCCCAAGTTTAACTCCAGCCAG 1945
Qy 72 gGluglnIleArgGlnGlyLeuGlu-----GluLeuGlnIlyValIleuProG1 88
Db 1944 CACTCCAGGTGTGGCAGAGGCTTGGAGGTAGCCGCTTACAGCATCCAGCAG-----AAGGG 1891
Qy 88 yG1yAspThrTyxMetHisGluGlyPheGluArgAlaSerGluGlnIleTyxTyrGluAs 108
Db 1890 AGGGGGGCACCAAGATGGGTGGAGGCCCTG---GGCAGCATGATCCAGGCTTTGGACAGATC 1834
Qy 108 nArgGlnGlyTyxArgThrAlaSerValIleIleAlaLeuThrAspGlyyGluLeuHisG1 128
Db 1833 TGCTCGCAGCAA-GETGCCTT-GGTATGTCAATTTGTTGTCTCACTAGCGCCAAATCTATGGA 1776
Qy 128 uAspLeuPhePheTyxSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleVal 148
Db 1775 CCCCGETG-----GCTGATGCTGCAGAGGCCCTGAGGGGCCATGGACATC 1728
Qy 148 lTyxTyxValGlyValIlyAspPheAsnGluThxGlnIleuAlaArgIleAlaAspSerIy 168
Db 1727 TTATGCAAGTTGGAGTCAGAGATGCAATATATGTGTGATGAGCTTCAAGAGATGCTGAA----- 1673
Qy 168 sAspHisValPheProValaAsnArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerI 188
Db 1672 -GACAGAAATGTTTTCGTGATGAT---TTTGAAGTCTTGAAGACCAATCCAAAGAAAGT 1617
Qy 188 eLeuIlyLeuSerCys 193
Db 1616 GGTACAAAGACATCTGT 1601

```

RESULT 5
US-10-750-185-56394
; Sequence 56394, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56394
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-56394
19866880505724

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| | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No.: | 0.00163 |
| Score: | 113.50 |
| Percent Similarity: | 42.63% |
| Best Local Similarity: | 23.11% |
| Query Match: | 7.44% |
| DB: | 6 |
| | |
| | |
| Length: | 1325 |
| Matches: | 58 |
| Conservative: | 49 |
| Mismatches: | 93 |
| Indels: | 51 |
| Gaps: | 15 |

US-09-970-076-2_COPY_28_320 (1-293) x US-10-750-185-56394 (1-1325)

QY 9 GLYPROMALACYSTYLYL---GLYPHEADPLEUITYRPHILLEUASPLYSSECDILSER 27
 DB 456 GGGAGCCCTGTAGAACACAGCAGCGGACGTCGTTCATTATGACACGCTCCAGAGC 515
 QY 28 VAL---LEUHSISHSTRPANGSILULEITYRYTPHE---VALGIUGINLEUADLHILYLE 45

[illegible]

RESULT 6
US-10-821-234-182/c
; Sequence 182, Application US/10821234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A

```

; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq Version 1.0
; SEQ ID NO: 182

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ORGANISM: Homo sapiens
US-10-821-234-182

| | | | |
|-------------------|---------|---------------|------|
| Alignment Scores: | 0.00432 | Length: | 2501 |
| Pred. No.: | 113.50 | Matches: | 66 |
| Score: | 38.288 | Conservative: | 63 |


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QY 54 SerPheIleValPheSerThrArgIleuThrThleu-----MetLysLeu 68
   ::::
Db 492 GGCCTGCTCAATAT-----GCCAGACATCTCAAGAAATAGTTCCTCCCAAGACC 542
QY 69 ThrGluAspArgGluGlnIleArgGlnIleGluGlnIleGluGlnIleValLeuProGly 88
   ::::
Db 543 TTCAGAGAGAAATGCCAGAGTGGAGCGTCTGTCAGAGAGATGGCGATCTGCACGGGC 602
QY 89 GlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsn 108
   ::::
Db 603 ACCATGACTGGCGTGCATCCAGTAT-----GCCCTGAACATCGCATTCACAGA 653
QY 109 ArgGlnIleTyrArg-----ThrAlaSerValIleIleAlaLeuThrAsp 123
   ::::
Db 654 GCGAGAGGGGGCCCGCCCTGAGAGGAAATGTCACAGGCTCATATGATCGAGACAGAT 713
QY 124 GlyIleLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 143
   ::::
Db 714 GGGAGACCTCAGGACTCCGTG-----GCCGAGGTGGCTCTAAGCGCACGGGAC 761
QY 144 LeuGlyAlaIleValTyrCysValGlyVal-----LysAspPheAsnGluThrGlnLeu 161
   ::::
Db 762 ACCGGCATCTCTATCTTGGCATGTGTGGCCAGGTACCTTCAACACCTTGAAATGCC 821
QY 162 AlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeu 181
   ::::
Db 822 ATGGAGAGTAGCCCGCCATGAGACATGCTTCTTGTGGCCAAT---TTCACCAAGATT 878
QY 182 GlnGlyIleIleHisSerIleLeuLysCysIleGluIleLeuAlaGluPro 201
   ::::
Db 879 GAGACCTGACCTCCGCTTCCAGAGAAATGTGTGACGGCCACATGTGTCACACCCCTG 938
QY 202 SerThrIleGlyAlaGlyIleGlySerPheGlnValValArgIleGlnIlePheAsnHis 221
   ::::
Db 939 GACCATTAATCTGTC-----CACTTCTGCATCAACATCCCTGCTCATACGTTCTGAGG 992
QY 222 AlaArg-----AsnValAspArgValLeuCysSerPheLysIleAsnAsp 236
   ::::
Db 993 TGCAGAACAGCTACATCTTCACACTCGATCGATCAGACGACTTGC-----AGAAATCCAGGAT 1046
QY 237 SerValThrLeuAsnGlu 242
   ::::
Db 1047 CTGTGTCATGGAGGAC 1064

RESULT 8
US-10-601-368-20
/ Sequence 20, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 20
/ LENGTH: 3564
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.0153 Length: 3564
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Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.27% Indels: 38
Gaps: 9
US-09-970-076-2_COPY_28_320 (1-293) x US-10-601-368-20 (1-3564)
QY 12 CysTyrGlnGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHis 31
   ::::
Db 475 TCCAGACTTAAATGACATCTCTCATGTCTTAAGTGGTCCAAACAGATC---TACCC 531
QY 32 TTPAENGILLETyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 49
   ::::
Db 532 TGGGTGAGGTCCACACTTCTCATCAATATCTCAAAAAGTTCTACATTTGCGCCGCG 591
QY 50 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 69
   ::::
Db 592 CAGATCCAGTGGAAATAGTCCAGTATGGAGAAATGCCGTCCATGATTCACCTT--- 648
QY 70 GluAspArgGluGlnIleArgGlnIleGluGlnIleGluGlnIleValLeuProGly 89
   ::::
Db 649 AATGACTACAGTCTGTAAAGATGTGTGAAAGCCGACGACATTCAGACAGAGA 708
QY 90 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyr 106
   ::::
Db 709 GGGACAGAGACCCGACCGCATTTGGCATTTGATTTGACAGGCTCGGAGGCTTCCAGAA 768
QY 107 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGlu 126
   ::::
Db 769 GGTGAAGAAAGGGCCCAAG-----AAAGTATGATTTGTATTCAGGACGGGAAATCC 822
QY 127 HisGluAsp----- 129
   ::::
Db 823 CACGACAGCCAGACCTGAGAAAGTATCCGGCAGAGGAGAGACAACGTGACAG 882
QY 130 -----LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeu 144
   ::::
Db 883 TAGCTGTGCGCGTTTGTGGCTATCAACCCAGGGGATGATCAACAGACTTTTCTCA 942
QY 145 GlyAlaIleValTyrCysValGlyValAsp-----PheAsnGluThrGln 160
   ::::
Db 943 AATGAATCAAAATACATCCGCCAGCAGCCTTGACGACAGACACTTTCACACGACAGAT 1002
QY 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
   ::::
Db 1003 GAGCGCGCCCTG-----AAGACATTTGTGATGCCCTTGGGACAGAGATCTTCAG 1053
QY 181 LeuGlnGly 183
   ::::
Db 1054 TTGGAAGGC 1062

RESULT 9
US-10-601-368-19
/ Sequence 19, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 19
/ LENGTH: 4858
/ TYPE: DNA
/ ORGANISM: Mus musculus
```

```
FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.0245 Length: 4858
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.27% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-601-368-19 (1-4858)

Qy 12 CyetYrGlyglYpHeaPLeuTYrPheleLeuApLySeRgLySeRValLeuHiHIs 31
Db 502 TGCCAGACTTACATGACATGTCATTTGTCTTAGTGCCCAACAGCATC---TACCC 558
Qy 32 TrpAengluIeTYrTYrPheValgluInLeuAlaHIsLyPhe---IleSeRPro--- 49
Db 559 TGGGTGAAGGTCCACACATCTCTCATCAATTCCTCAAAAGTCTTACATTGCCCGCC 618
Qy 50 GluLeuArgMetSerPheIleValPheSerThraRgLyThrThrLeuMetLySeuThr 69
Db 619 CAGATCCAGTCGGGAATGATGCAGATGAGAGAATGCCCGTCATGATTCACCTT--- 675
Qy 70 GluAbaRgLygluInIleArgGlyLeuGlulLeuGlyValLeuProGlyGly 89
Db 676 AATACATCAACAGCTGTAAAGATGTGTGGAAGCCGCCACCATTCAGCAGAGAAGA 735
Qy 90 AsPThrTYrMetHIsGlulYpHeGlU-----ArgAlaSerGlulHIsIeTYrTYr 106
Db 736 GGGACAGAGACCCCGACGGCATTTGGCATTAATTGCAAGCTCGAGAGCTTCCAGAG 795
Qy 107 GluAbaRgLygluInLYrTYrArgThraLaseRValIleIleAlaLeuThraSPgLyglu 126
Db 796 GGTGAAGAAAGAGGGCCAG---AAAGTATGATGTTGCATCAGCAGAGGGGAATCC 849
Qy 127 HIsGlulAbaP----- 129
Db 850 CACGACAGCCCGACCTGGAGAGAGTATCCGGCAGAGCAGAAAGCAACATGACCGA 909
Qy 130 -----LeuPhePheTYrSerGlulArgGlulAlaAbaRgSerArgAbaPLeu 144
Db 910 TACGCTGTGCCCTTTGGCTACTACACCGCAGGGGATCAATCCAGACATTTTCTA 969
Qy 145 GlYAlaIleValTYrCYrValglYValLyAbaP-----PheAenGlulThrGln 160
Db 970 AATGAATCAAAATCATGCGCAGGAGACCTGACGACAGACATCTTCACTGACAGAT 1029
Qy 161 LeuAlaArgIleAlaBaPSeRlyAbaPHisValPheProValAbaBaPglYpHeGlAla 180
Db 1030 GAGCGCGCCCTG-----AAGGACATGTGTATGCCCTTGAGGAGACAGATCTTACG 1080
Qy 181 LeuGlyngly 183
Db 1081 TTGGAAGGC 1089

RESULT 10
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 464
; LENGTH: 3175
; TYPR: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.035 Length: 3175
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.04% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-995-561-464 (1-3175)

Qy 18 LeuTYrPheIleLeuAbaPlySeRgLySeRVal----- 28
Db 243 GTGTACTTCGTCGACACCTCGAGAGCGTCACATGACAGTCCCGACGACATCCTG 302
Qy 29 LeuHIsHIsTrpAenglu---IleTYrTYrPheValgluInLeuAlaHIsLyPheIle 47
Db 303 CTCTTCACATGAAGACAGTTCGTCGACGATTCATGACGACGTCGAGAAAGAGTCTAC 362
Qy 48 SerProGluLeuArgMetSerPhe-----IleValPheSerThraRgLyThr 63
Db 363 CTGACACAGGTGGCGCTGAGCTGAGCTTANAGCGGCTGACATCTCTGACAGGTGAG 422
Qy 64 ThrLeuMetLySeuThraRgLygluInIleArgGlyLeuGlulLeuGlyValLeuGln 83
Db 423 GTGTTACGCCACCGGCGAGGACCGGCGCTCTTCAAGAAACCTGACGAGGCATCAGC 482
Qy 84 LySeValLeuProGlyglYbaPThrTYrMetHIsGlulYpHeGlulArgAlaSerGluln 103
Db 483 TCCTTCCGCGCGCGC-----ACCTTCACGACTGCGCGCTGCGCAACATGACGAGCAG 536
Qy 104 IleTYrTYrGluAbaRgLygluInLYrTYrArgThraLaseRValIleIleAlaLeuThraSP 123
Db 537 ATCCGACAGACCGCAGCAGAGGC-----ACGTCACATTCGCGCGTGCATACCGAC 590
Qy 124 GlYgluLeuHIsGlulAbaPLeuPheTYrSerGlulArgGlulAlaAbaRgSerArgAbaP 143
Db 591 GGCACGCTCACCGGACCGCCCTGGCGGGGATCAAGCTGACGAGCGGCGCGCGAG 650
Qy 144 LeuGlYAlaIleValTYrCYrVal-----GlyValLyA 154
Db 651 GAGGCGATCCGCGCTTCGCGCGGCCCGCAACCGAAGCTGAAGAGCAGAGGCTTCGG 710
Qy 155 AsPheAenGlulThr-----GlnLeuAlaRgIleAlaBaPSeRlyAbaPHisValPhe 172
Db 711 GACATGCCCGACGCGCGCAGAGCTTACCGC-----AAGCACTAGCCACACC 758
Qy 173 ProValAbaBaPglYpHeGlAlaLeuGlnIleIleHIsSerIleLeu----- 189
Db 759 ATGCTGCCYATCTCCACGAGATGACAGACCAACCATCAACGCAATCAAGGTGATG 818
Qy 190 -----LyLySeRcySIlleGluIle 196
Db 819 AAACACGAGACTACGAGAGTGTACTCAAGGTGAGTGTGCTCGGAATTC 866

RESULT 11
US-10-995-561-465
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 3464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-465
```

```
Alignment Scores:
Pred. No.: 0.04 Length: 3464
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.04% Indels: 45
DB: Gaps: 9
```

US-09-970-076-2_COPY_28_320 (1-293) x US-10-995-561-465 (1-3464)

```

QY 18 LeuTYrPheIleuAspIysSerGlySerVal----- 28
DB 243 GTGTAATTGCTGCTGGACACCTCGAGAGCGTCACCATGCAATCCCCACGACATCTTG 302
QY 29 LeuHisIeTpaSnglu---IleTYrTYrPheValGluGluLeuAlaHisIysPheIle 47
DB 303 CTCCTCCACATGAAGAGTTCGTGCGCAGATTCATCAGCCAGCTCGAGAACGAGTCTTAC 362
QY 48 SerProGluLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 63
DB 363 CTGACACAGGTGGCTGTGAGCTGCGCTATGAGCGCGCTGACCTTCTGTACCAAGTGGAG 422
QY 64 ThrLeuMetIysLeuThrGluAspArgGluGlnIleArgGlnIlyLeuGluLeuGln 83
DB 423 GTGTTACAGCCACCGGCGACGACCGGCGCTCTTCATCAAGAACCTGCAAGGCGATCAGC 482
QY 84 LysValLeuProGlyGlyAspThrTYrMetHisGluGlyPheGluArgAlaSerGluGln 103
DB 483 TCCTTCGCGCGCGGC-----ACCTTCACCGACCTGCGCGCTGCGCAACATGAGGAGCAG 536
QY 104 IleTYrTYrGluAsnArgGlnIlyTYrArgThrAlaSerValIleIleAlaLeuThrAsp 123
DB 537 ATCCGCGAGGACCGGCGACCAAGGCG-----ACCGTCACCTCGCGCGTGTGATCACCAGC 590
QY 124 GlyGluLeuHisGluAspLeuPhePheTYrSerGluArgGluAlaAsnArgSerArgAsp 143
DB 591 GCGCAGCTCAACCGGACCGCCCTGCGGCGGATCAAGCTGCAAGCGCGAGCGGCGCGAG 650
QY 144 LeuGlyAlaIleValTYrCysVal-----GlyValLys 154
DB 651 GAGGGCATCCGCGCTCTTCCGCGTGGCCCCAACCAAGAACTGAAGAGCAGGCGCTGCGG 710
QY 155 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerIysAspHisValPhe 172
DB 711 GACATGCCACGACGCGCGACGAGCTTACCGC-----AACGACTACGCCACC 758
QY 173 ProValAsnAspGlyPheGlnAlaLeuGlnIlyIleHisSerIleLeu----- 189
DB 759 ATGCTGCCTGACTCCACCGAGATRACACGAGACACCATCAACCGCATCATCAAGTTCATG 818
QY 190 -----LysLysSerCysIleGluIle 196
DB 819 AAACACGAGGCTACGAGAGTGTCTACAAAGGTGAGTGGCTGTGAATTC 866

RESULT 12
US-10-995-561-466
; Sequence 466, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
```

```
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-466
```

```
Alignment Scores:
Pred. No.: 0.0401 Length: 3468
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.04% Indels: 45
DB: Gaps: 9
```

US-09-970-076-2_COPY_28_320 (1-293) x US-10-995-561-466 (1-3468)

```

QY 18 LeuTYrPheIleuAspIysSerGlySerVal----- 28
DB 243 GTGTAATTGCTGCTGGACACCTCGAGAGCGTCACCATGCAATCCCCACGACATCTTG 302
QY 29 LeuHisIeTpaSnglu---IleTYrTYrPheValGluGluLeuAlaHisIysPheIle 47
DB 303 CTCCTCCACATGAAGAGTTCGTGCGCAGATTCATCAGCCAGCTCGAGAACGAGTCTTAC 362
QY 48 SerProGluLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 63
DB 363 CTGACACAGGTGGCTGTGAGCTGCGCTATGAGCGCGCTGACCTTCTGTACCAAGTGGAG 422
QY 64 ThrLeuMetIysLeuThrGluAspArgGluGlnIleArgGlnIlyLeuGluLeuGln 83
DB 423 GTGTTACAGCCACCGGCGACGACCGGCGCTCTTCATCAAGAACCTGCAAGGCGATCAGC 482
QY 84 LysValLeuProGlyGlyAspThrTYrMetHisGluGlyPheGluArgAlaSerGluGln 103
DB 483 TCCTTCGCGCGCGGC-----ACCTTCACCGACCTGCGCGCTGCGCAACATGAGGAGCAG 536
QY 104 IleTYrTYrGluAsnArgGlnIlyTYrArgThrAlaSerValIleIleAlaLeuThrAsp 123
DB 537 ATCCGCGAGGACCGGCGACCAAGGCG-----ACCGTCACCTCGCGCGTGTGATCACCAGC 590
QY 124 GlyGluLeuHisGluAspLeuPhePheTYrSerGluArgGluAlaAsnArgSerArgAsp 143
DB 591 GCGCAGCTCAACCGGACCGCCCTGCGGCGGATCAAGCTGCAAGCGGCGCGCGAG 650
QY 144 LeuGlyAlaIleValTYrCysVal-----GlyValLys 154
DB 651 GAGGGCATCCGCGCTCTTCCGCGTGGCCCCAACCAAGAACTGAAGAGCAGGCGCTGCGG 710
QY 155 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerIysAspHisValPhe 172
DB 711 GACATGCCACGACGCGCGACGAGCTTACCGC-----AACGACTACGCCACC 758
QY 173 ProValAsnAspGlyPheGlnAlaLeuGlnIlyIleHisSerIleLeu----- 189
DB 759 ATGCTGCCTGACTCCACCGAGATRACACGAGACACCATCAACCGCATCATCAAGTTCATG 818
QY 190 -----LysLysSerCysIleGluIle 196
DB 819 AAACACGAGGCTACGAGAGTGTCTACAAAGGTGAGTGGCTGTGAATTC 866

RESULT 13
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
```

```

; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (3564)
US-10-601-368-2

Alignment Scores:
Pred. No.: 0.0483 Length: 3564
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.01% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-601-368-2 (1-3564)
QY 12 CyeTyrGlyGlyPheAerPLeuYrPheIleuAerLySerGlySerValIleuHis 31
DB 475 TGCACAGCTTACATGACATCGTCATCTGATGCTCCCAACAGCATC---TACCCC 531
QY 32 TTPAaNgLuIleYrYrPheValGluGlnLeuAlaHisPhe---IleSerPro--- 49
DB 532 TGGGTGAGGTTGACGATCTTCATCAACATCTGTAAGAAAGTTTACATTGGCCCAAG 591
QY 50 GlnLeuAerGlySerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThr 69
DB 592 CAGATCCAGGTTGAGTTGTGAGTATGCGAAGATGTGTCATGATTCACCTC--- 648
QY 70 GluAerArgGluGlnIleArgGlnGlyLeuGluGlnLeuValIleuProGlyGly 89
DB 649 AACGACTACAGCTCTGAAGAAGATGTGTGAGCTGCCAGCCATGACAGAGAGA 708
QY 90 AspThrTyrmethIleGlnGlyPheGlu-----ArgAlaSerGluGlnIleYrTy 106
DB 709 GGAACAGAGACCCGAGCGCATTTGGCATTAATTTCAGAGCTTCAGAGCTTCCAGA 768
QY 107 GluAerArgGlnGlyYrArgThrAlaSerValIleIleAlaLeuThrAerGlyGlu 126
DB 769 GGTGAAGAGAAAGAGCCAAAG-----AAGTGTATGATTGTATCAAGATGGGAGTCC 822
QY 127 HisGluAerP----- 129
DB 823 CACGACAGCCCAAGCTCGAAGAAAGTATCCAGCAAGAGAAAGACAAGCTTAACA 882
QY 130 -----LeuPhePheTySerGlyuArgGluAlaAerGlySerArgAerPLeu 144
DB 883 TATCGCGTGGCCGCTCGGCTACTACACCGCAGGGGAGTCAATCCAGAAACTTTTCT 942
QY 145 GlyAlaIleValIleYrCyValIleGlyValIleAerP-----PheAerGluThrGln 160
DB 943 AATGAATCAAAATATACATCGCCAGTACCCGATGACAAAGACATTCCTCAATGTCACTGAT 1002
QY 161 LeuAlaArgIleAlaAerSerLyAerPheIleValPheProValAerAerGlyPheGlnAla 180
DB 1003 GAGGCTGCCTTG-----AAGGACATTGTGATGCTCGGAGGACAGAAATCTTCAGC 1053
QY 181 LeuGlnGly 183
DB 1054 CTGGAAGGC 1062

RESULT 14
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 574
; LENGTH: 3967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-574

Alignment Scores:
Pred. No.: 0.0569 Length: 3967
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.01% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) x US-11-000-463-574 (1-3967)
QY 12 CyeTyrGlyGlyPheAerPLeuYrPheIleuAerLySerGlySerValIleuHis 31
DB 524 TGCACAGCTTACATGACATCGTCATCTGATGCTCCCAACAGCATC---TACCCC 580
QY 32 TTPAaNgLuIleYrYrPheValGluGlnLeuAlaHisPhe---IleSerPro--- 49
DB 581 TGGGTGAGGTTGACGATCTTCATCAACATCTGTAAGAAAGTTTACATTGGCCCAAG 640
QY 50 GlnLeuAerGlySerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThr 69
DB 641 CAGATCCAGGTTGAGTTGTGAGTATGCGAAGATGTGTCATGATTCACCTC--- 697
QY 70 GluAerArgGluGlnIleArgGlnGlyLeuGluGlnLeuValIleuProGlyGly 89
DB 698 AACGACTACAGCTCTGAAGAAGATGTGTGAGCTGCCAGCCATGACAGAGAGA 757
QY 90 AspThrTyrmethIleGlnGlyPheGlu-----ArgAlaSerGluGlnIleYrTy 106
DB 758 GGAACAGAGACCCGAGCGCATTTGGCATTAATTTCAGAGCTTCAGAGCTTCCAGA 817
QY 107 GluAerArgGlnGlyYrArgThrAlaSerValIleIleAlaLeuThrAerGlyGlu 126
DB 818 GGTGAAGAGAAAGAGCCAAAG-----AAGTGTATGATTGTATCAAGATGGGAGTCC 871
QY 127 HisGluAerP----- 129
```

Db 872 CACGACAGCCAGACCTGGAGAGGTGATCCAGAAAGGAAAGAGACAACGTAACAAGA 931
|||
|||
Qy 130 -----LeuphetherYrserGIuArGIuAlaAsnArgerArgeArleu 144
|||
|||
Db 932 TATGCGGTGCCGTCTGGCTACTACAAACGAGGGGATGATCCAGAACTTTTCTA 991
|||
|||
Qy 145 GYAAlaIleValTyrCyValGlyValIyAsp-----PheAsnGIuThrGIu 160
|||
|||
Db 992 AATGAATCAATACATCCCGCACTGACCTGATGACAGACATCTTCAATGCTCAT 1051
|||
|||
Qy 161 LeuAlaArgIleAlaAspserIyAspHisValPheProValAsnAspGlyPheGlnAla 180
|||
|||
Db 1052 GAGGCGCTCTG-----AAGACATTTGATGATCCCTGGGGAGACAAATCTTCAGC 1102
|||
|||
Qy 181 LeuGlnGly 183
|||
|||
Db 1103 CTGGAAGGC 1111

RESULT 15

US-11-000-463-102
/ Sequence 102, Application US/11000463
/ Publication No. US20050266423A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Qian, Xiaohong B.
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhou, Ping
/ APPLICANT: Cao, Yi-Cheng
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
/ FILE REFERENCE: 785CIP4CN
/ CURRENT APPLICATION NUMBER: US/11/000,463
/ PRIOR FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: 10/291,265
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/922,279
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 09/617,746
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/631,451
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 09/633,870
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 3969
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3618)
US-11-000-463-102

Alignment Scores:

Pred. No.: 0.0569 Length: 3969
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Beet Local Similarity: 24.14% Mismatches: 88
Query Match: 7.01% Indels: 38
DB: 7 Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) x US-11-000-463-102 (1-3969)

Qy 12 CysTyrGIyGlyPheAspLeuTyrPheIleLeuAspIySserGlySerValLeuHisHis 31
|||
|||
Db 526 TCCAGACCTCATGATGACATGCTCATTTGCTCGATGGCTCCAGAGCATC---TACCCC 582
|||
|||
Qy 32 TTPAnGluIleTyrTyrPheValGluGlnLeuAlaHisIyPhe---IleSerPro--- 49
|||
|||
Db 583 TGGGTGGAGGTTTCACACATCTCTCATCAACATCCGMAAAAGTTTACATTTGGCCAGG 642
|||
|||
Qy 50 GlnLeuArgMetSerPheIleValPheSerThrArGlyThrThrIleuMetIySleuThr 69
|||
|||
Db 643 CAGATCCAGGTGGAGTTTGAGTTGTCAGTATGGCGAAAGATGTGTCATGATTCACCTC--- 699
|||
|||
Qy 70 GluAspArgGluGlnIleArgGlnIyLeuGlnIyLeuGlnIyValLeuProGIyGIy 89
|||
|||
Db 700 AACGACTACAGCTCTGTAAAGATGATGGTGAAGCTGCCAGCCACATTTAGCAGAGAGA 759
|||
|||
Qy 90 AspThrTyrMechIeGIyGlyPheGlu-----ArgAlaSerGIuGlnIleTyrTyr 106
|||
|||
Db 760 GGAACAGAGACCCGAGCGCATTTGGCATTTGCAATTTGCAAGCTCAGAGGCTTTCCAGAA 819
|||
|||
Qy 107 GluAsnArgGlnIyTyrArgThrAlaSerValIleIleAlaLeuThrAspGIyGluLeu 126
|||
|||
Db 820 GGTGAGAGGAAAGAGCCAAAG-----AAGGTGATGATTTGTATCATCAATGGGAGTCC 873
|||
|||
Qy 127 HisGIuAsp----- 129
|||
|||
Db 874 CACGACAGCCAGACCTGGAGAGGTGATCCAGAAAGGAAAGAGACAACGTAACAAGA 933
|||
|||
Qy 130 -----LeuphetherYrserGIuArGIuAlaAsnArgerArgeArleu 144
|||
|||
Db 934 TATGCGGTGCCGTCTGGCTACTACAAACGAGGGGATGATCCAGAACTTTTCTA 993
|||
|||
Qy 145 GYAAlaIleValTyrCyValGlyValIyAsp-----PheAsnGIuThrGIu 160
|||
|||
Db 994 AATGAATCAATACATCCCGCACTGACCTGATGACAGACATCTTCAATGCTCAT 1053
|||
|||
Qy 161 LeuAlaArgIleAlaAspserIyAspHisValPheProValAsnAspGlyPheGlnAla 180
|||
|||
Db 1054 GAGGCGCTCTG-----AAGACATTTGATGATCCCTGGGGAGACAAATCTTCAGC 1104
|||
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Qy 181 LeuGlnGly 183
|||
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Db 1105 CTGGAAGGC 1113

Search completed: December 19, 2005, 02:30:09
Job time : 258.436 secs


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APPLICANT: Baif, Mary L.
TITLE OF INVENTION: MAC-1 I-DOMAIN PROTEIN USEFUL IN
TITLE OF INVENTION: BLOCKING ADHESION AND MIGRATION OF NEUTROPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: The Upjohn Company, Intellectual Property Law
STREET: 301 Henrietta
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Gateway 2000 P5-90
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04439
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Darnley, James D., Jr.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4767.P CNL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/385-5210
TELEFAX: 616/385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04439-1

Query Match 14.7%; Score 142.5; DB 4; Length 435;
Best Local Similarity 26.9%; Pred. No. 9,4e-08;
Matches 54; Conservative 41; Mismatches 67; Indels 39; Gaps 11

QY 1 GGFQDLYFLDKSGSYL-HHWNIIYFVEQLAKFISPOLRMSFIYSTRGTLYMKLTED- 58
DB GGSDFALFLIDSGSIIPHDFRMRKEFVS-----VMEQLKSKTIPS-----LMQYSEF 278
QY 59 -----REQIRQGLEELQKYLPGGDIYMHGFEFASBOIYENRQYRTA-SVIT 106
DB 279 RHIFPFKEFQNNPNRSLVKPIITQLL-GRTHYATGIRKVRVRELFINITGAKNAFKILV 336
QY 107 ALTDGELHEDLFYSB--REANRSKDLAIYCVGKQFNEQLAR-----IADS--KDH 157
DB 337 VITDEKRPDPLGYEDVJPEADRE--GVIRYVIGVGAFRSEKSRQELINTIASKPRDH 393
QY 158 VEPVNDGFOALGGIIHSILKK 178
DB 394 VFQVNN-PEALKTIONQLREK 413

RESULT 3
US-08-286-889-37
Sequence 37, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

```

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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-37

Query Match          14.6% Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 5e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

OY      4 DLYTLKSGSV-LAHNNEIYYFPBQLAKHFISQLMSEFLVFSTRGTTMKLTE----- 57
DB      142 DIAFLIGSGSINORDPAOMKDFFVKALMGFERASTSTLSIMQYSNIUKHTFTPEFNIL 201
OY      58 DRDRIQGLEGELQVLDGGDTVMHGEFRASSEQUYENRQGYRTA-SVIIALTGTGELHD 116
DB      202 DPGLVLDPITVOLQ----GLTYTAGIRTWHEELFHSSNGSRKSARKILLVTDGQRDR 256
OY      117 LFFPSE--REANRSRDICATAYVCVVND-FNE-TOLARI-----ADSKDHVPYNDFQA 167
DB      257 PLERSDVIPADKA---GIIRYAIGVDARFGEPITALKEMLNTGSAPQDDHYFKGN-PAA 312
OY      168 LGIIHSILKK 178
DB      313 LRSIROLOLQEK 323

RESULT 4
US-08-485-618-37
Sequence 37, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-605-672-37

Query Match          14.6%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. Se-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 4 DLYFLDKSGSV-LHHNMEIYFVEQLAHKFI SPQLRMSFIVSTRGTTLMKLT----- 57
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 142 DIAFLIDSGSINQRFQAKMDVFKALMGFEFASTLFLSMQYSLNLTHTFTTFEKNIL 201
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 58 DREQIRQGLEELQKVLPGGDTYMHGFEFASQIYENRGYRTA-SVIALTDGELHED 116
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 202 DPQSLVDPIVQLQ-----GLTYATGIRTYMEELFHSKSGSKSAKKILVITDQCKYND 256
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 117 LFPEYS--REANRSRLGAIYVCVKVD-FNE-TQLARI-----ADSKDHVPVNDGFOA 167
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 257 PLEYSVDVIPADKA---GIIRYALGVDAFQEPFLAKELNTIGSAPPODHVKVGN-FAA 312
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 168 LOGIHSILKK 178
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 313 LRSIORLOEK 323
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 7
/ US-08-482-293A-37
/ Sequence 37, Application US/08482293A
/ Patent No. 5831029
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-482-293A-37

Query Match          14.6%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. Se-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 4 DLYFLDKSGSV-LHHNMEIYFVEQLAHKFI SPQLRMSFIVSTRGTTLMKLT----- 57
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 142 DIAFLIDSGSINQRFQAKMDVFKALMGFEFASTLFLSMQYSLNLTHTFTTFEKNIL 201
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 58 DREQIRQGLEELQKVLPGGDTYMHGFEFASQIYENRGYRTA-SVIALTDGELHED 116
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 202 DPQSLVDPIVQLQ-----GLTYATGIRTYMEELFHSKSGSKSAKKILVITDQCKYND 256
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 117 LFPEYS--REANRSRLGAIYVCVKVD-FNE-TQLARI-----ADSKDHVPVNDGFOA 167
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 257 PLEYSVDVIPADKA---GIIRYALGVDAFQEPFLAKELNTIGSAPPODHVKVGN-FAA 312
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 168 LOGIHSILKK 178
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 313 LRSIORLOEK 323
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 8
/ US-08-943-363-37
/ Sequence 37, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
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[illegible][illegible]

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-55

Query Match 14.6%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 5.1e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 4 DLYFILDKSGSV-LHNNELIYVVEQLAHKFIQPMSPFVSTRTGTLMLKTE----- 57
DB 152 DIAFLIDGSSGINSORDFAQMKDFKALMGEPASTSTLFSIMQYSNLIKHTFTFEFNIL 211
DB 58 DREGIRGLEBLQVLPQGDVTYMEGFERASEQIYYENRQGYRTA-SVIALTDGELHED 116
QY 212 DPGSLVDPVQLQ-----GLTYATGIRTYWELFHSKNGSRSAKXILLVITDGOXYRD 266
DB 117 LFYSSE--REANRSDIGAIYVCVVD-FNE-TQLARI-----ADSKDHFVPNDGFOA 167
QY 267 PLEYSVDVIPADKA--GIRYALVGDAFOEPALKEMLTIGSAPPDHFVKGN-FAA 322
DB 168 LQGIHSILKK 178
QY 323 LRSIORQLQEK 333
DB

RESULT 14
US-08-605-672-55
Sequence 55, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-55

Query Match 14.6%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 5.1e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 4 DLYFILDKSGSV-LHNNELIYVVEQLAHKFIQPMSPFVSTRTGTLMLKTE----- 57
DB 152 DIAFLIDGSSGINSORDFAQMKDFKALMGEPASTSTLFSIMQYSNLIKHTFTFEFNIL 211
DB 58 DREGIRGLEBLQVLPQGDVTYMEGFERASEQIYYENRQGYRTA-SVIALTDGELHED 116
QY 212 DPGSLVDPVQLQ-----GLTYATGIRTYWELFHSKNGSRSAKXILLVITDGOXYRD 266
DB 117 LFYSSE--REANRSDIGAIYVCVVD-FNE-TQLARI-----ADSKDHFVPNDGFOA 167
QY 267 PLEYSVDVIPADKA--GIRYALVGDAFOEPALKEMLTIGSAPPDHFVKGN-FAA 322
DB 168 LQGIHSILKK 178
QY 323 LRSIORQLQEK 333
DB

RESULT 15
US-08-482-293A-55
Sequence 55, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:07 ; Search time 56.3373 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970

Sequence: 1 GGFDFLYILDKSGSVLHHMN.....LQGIHSILKSCIEILAE 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
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| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 970 | 100.0 | 328 | 4 US-10-038-307-26 | Sequence 26, Appl |
| 2 | 970 | 100.0 | 328 | 4 US-10-201-292-26 | Sequence 26, Appl |
| 3 | 970 | 100.0 | 333 | 3 US-09-796-753-12 | Sequence 12, Appl |
| 4 | 970 | 100.0 | 333 | 4 US-10-038-307-2 | Sequence 2, Appl |
| 5 | 970 | 100.0 | 333 | 4 US-10-201-292-2 | Sequence 2, Appl |
| 6 | 970 | 100.0 | 333 | 6 US-11-047-278-8 | Sequence 8, Appl |
| 7 | 970 | 100.0 | 342 | 4 US-10-038-307-22 | Sequence 22, Appl |
| 8 | 970 | 100.0 | 342 | 4 US-10-201-292-22 | Sequence 22, Appl |
| 9 | 970 | 100.0 | 345 | 4 US-10-038-307-24 | Sequence 24, Appl |
| 10 | 970 | 100.0 | 345 | 4 US-10-201-292-24 | Sequence 24, Appl |
| 11 | 970 | 100.0 | 368 | 6 US-11-047-278-2 | Sequence 2, Appl |
| 12 | 970 | 100.0 | 403 | 3 US-09-833-245-621 | Sequence 621, Appl |
| 13 | 970 | 100.0 | 460 | 4 US-10-201-292-28 | Sequence 28, Appl |
| 14 | 970 | 100.0 | 479 | 4 US-10-201-292-32 | Sequence 32, Appl |
| 15 | 970 | 100.0 | 504 | 4 US-10-201-292-34 | Sequence 34, Appl |
| 16 | 970 | 100.0 | 529 | 4 US-10-201-292-36 | Sequence 36, Appl |
| 17 | 970 | 100.0 | 551 | 4 US-10-038-307-18 | Sequence 18, Appl |
| 18 | 970 | 100.0 | 551 | 4 US-10-201-292-18 | Sequence 18, Appl |
| 19 | 970 | 100.0 | 564 | 3 US-09-918-715-187 | Sequence 187, App |
| 20 | 970 | 100.0 | 564 | 3 US-09-918-715-232 | Sequence 232, App |
| 21 | 970 | 100.0 | 564 | 4 US-10-038-307-20 | Sequence 20, Appl |
| 22 | 970 | 100.0 | 564 | 4 US-10-201-292-20 | Sequence 20, Appl |
| 23 | 970 | 100.0 | 564 | 4 US-10-301-822-199 | Sequence 199, App |
| 24 | 970 | 100.0 | 564 | 4 US-10-408-765A-1823 | Sequence 1823, App |
| 25 | 970 | 100.0 | 564 | 4 US-10-474-794-187 | Sequence 187, App |
| 26 | 970 | 100.0 | 564 | 4 US-10-474-794-232 | Sequence 232, App |
| 27 | 970 | 100.0 | 564 | 5 US-10-979-159-187 | Sequence 187, App |

| | | | | | |
|----|-----|-------|-----|---------------------|-------------------|
| 28 | 970 | 100.0 | 564 | 5 US-10-979-159-232 | Sequence 232, App |
| 29 | 970 | 100.0 | 564 | 6 US-11-047-278-6 | Sequence 6, Appl |
| 30 | 965 | 99.5 | 403 | 3 US-09-833-245-620 | Sequence 620, App |
| 31 | 961 | 99.1 | 562 | 3 US-09-918-715-194 | Sequence 194, App |
| 32 | 961 | 99.1 | 562 | 3 US-09-918-715-301 | Sequence 301, App |
| 33 | 961 | 99.1 | 562 | 4 US-10-474-794-194 | Sequence 194, App |
| 34 | 961 | 99.1 | 562 | 4 US-10-474-794-301 | Sequence 301, App |
| 35 | 961 | 99.1 | 562 | 5 US-10-979-159-194 | Sequence 194, App |
| 36 | 961 | 99.1 | 562 | 5 US-10-979-159-301 | Sequence 301, App |
| 37 | 960 | 99.0 | 460 | 4 US-10-201-292-30 | Sequence 30, App |
| 38 | 949 | 97.8 | 534 | 4 US-10-038-307-12 | Sequence 12, Appl |
| 39 | 949 | 97.8 | 534 | 4 US-10-201-292-12 | Sequence 12, Appl |
| 40 | 949 | 97.8 | 543 | 4 US-10-038-307-10 | Sequence 10, Appl |
| 41 | 949 | 97.8 | 543 | 4 US-10-038-307-14 | Sequence 14, Appl |
| 42 | 949 | 97.8 | 543 | 4 US-10-038-307-16 | Sequence 16, Appl |
| 43 | 949 | 97.8 | 543 | 4 US-10-201-292-10 | Sequence 10, Appl |
| 44 | 949 | 97.8 | 543 | 4 US-10-201-292-14 | Sequence 14, Appl |
| 45 | 949 | 97.8 | 543 | 4 US-10-201-292-16 | Sequence 16, Appl |

ALIGNMENTS

```

RESULT 1
US-10-038-307-26
; Sequence 26, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OR INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-26

Query Match      100.0%; Score 970; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 6,6e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYILDKSGSVLHHNMEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 60
   |||||
Db 41 GGFDFLYILDKSGSVLHHNMEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 100
   |||||

QY 61 QIRGGELELOKVLPGSDTYNHBGFERSAQIYENRGYRTASVIALTDGEIHEDLFY 120
   |||||
Db 101 QIRGGELELOKVLPGSDTYNHBGFERSAQIYENRGYRTASVIALTDGEIHEDLFY 160
   |||||

QY 121 SEREARSRLGAIYVCVGYKDPNETQLARIASKXHVFPVNDGFQALQGIHISILKSC 180
   |||||
Db 161 SEREARSRLGAIYVCVGYKDPNETQLARIASKXHVFPVNDGFQALQGIHISILKSC 220
   |||||

QY 181 IETILAE 187
   |||||
Db 221 IETILAE 227
   |||||

RESULT 2
US-10-201-292-26
; Sequence 26, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK

```

```
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-201-292-26

Query Match      100.0%; Score 970; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 6,6e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFYFLDKSGSVLHNNELIYFVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 60
DB 41 GGFDFYFLDKSGSVLHNNELIYFVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 100
QY 61 QIRQGLEELQKVLPGSDTYMHGFEFASERQIYYENRQGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGSDTYMHGFEFASERQIYYENRQGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSC 180
DB 161 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSC 220
QY 181 IETLAEE 187
DB 221 IETLAEE 227

RESULT 3
US-09-796-753-12
/ Sequence 12, Application US/09796753
/ Publication No. US20030027998A1
/ GENERAL INFORMATION:
/ APPLICANT: McCarthy, Sean A.
/ TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
/ FILE REFERENCE: 7853-227-999
/ CURRENT APPLICATION NUMBER: US/09/796,753
/ CURRENT FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/183,175
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 09/223,094
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/223,546
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/224,246
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/259,388
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/122,458
/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: 09/312,359
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/336,536
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 09/342,687
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 09/345,464
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/365,164
/ PRIOR FILING DATE: 1999-07-30
/ PRIOR APPLICATION NUMBER: 09/399,723
/ PRIOR FILING DATE: 1999-09-20
/ PRIOR APPLICATION NUMBER: 09/409,634
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 09/471,179
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 09/474,071
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/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/474,072
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/514,010
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 09/516,745
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/572,002
/ PRIOR FILING DATE: 2000-05-14
/ PRIOR APPLICATION NUMBER: 09/597,993
/ PRIOR FILING DATE: 2000-06-19
/ PRIOR APPLICATION NUMBER: 09/599,596
/ PRIOR FILING DATE: 2000-06-22
/ PRIOR APPLICATION NUMBER: 09/630,334
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: 09/606,565
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/606,317
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/665,666
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: 09/677,751
/ PRIOR FILING DATE: 2000-09-30
/ NUMBER OF SEQ ID NOS: 162
/ SEQ ID NO 12
/ LENGTH: 333
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-796-753-12

Query Match      100.0%; Score 970; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFYFLDKSGSVLHNNELIYFVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 60
DB 41 GGFDFYFLDKSGSVLHNNELIYFVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 100
QY 61 QIRQGLEELQKVLPGSDTYMHGFEFASERQIYYENRQGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGSDTYMHGFEFASERQIYYENRQGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSC 180
DB 161 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSC 220
QY 181 IETLAEE 187
DB 221 IETLAEE 227

RESULT 4
US-10-038-307-2
/ Sequence 2, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 333
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-038-307-2

Query Match      100.0%; Score 970; DB 4; Length 333;
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Db 230 IETIAAE 236

RESULT 8

US-10-201-292-22
; Sequence 22, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-22

Query Match 100.0%; Score 970; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 6, 9e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMKLTEDRE 60
DB 50 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMKLTEDRE 109
DB 61 QIRQGLEELQKVLPGGDTYMHGFERASEQIYENRGYRTASVIALTDGELHEDLFFY 120
QY 110 QIRQGLEELQKVLPGGDTYMHGFERASEQIYENRGYRTASVIALTDGELHEDLFFY 169
DB 121 SEREANSRDLGAIYVCVGDVFNFTQIARIADSKDHFVPVNDGFQALOGIHSILKSC 180
QY 170 SEREANSRDLGAIYVCVGDVFNFTQIARIADSKDHFVPVNDGFQALOGIHSILKSC 229
DB 181 IETIAAE 187
QY 230 IETIAAE 236

RESULT 9

US-10-038-307-24
; Sequence 24, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-24

Query Match 100.0%; Score 970; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMKLTEDRE 60

Db 41 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMKLTEDRE 100

QY 61 QIRQGLEELQKVLPGGDTYMHGFERASEQIYENRGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGFERASEQIYENRGYRTASVIALTDGELHEDLFFY 160

QY 121 SEREANSRDLGAIYVCVGDVFNFTQIARIADSKDHFVPVNDGFQALOGIHSILKSC 180
DB 161 SEREANSRDLGAIYVCVGDVFNFTQIARIADSKDHFVPVNDGFQALOGIHSILKSC 220

QY 181 IETIAAE 187
DB 221 IETIAAE 227

RESULT 10

US-10-201-292-24
; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-24

Query Match 100.0%; Score 970; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMKLTEDRE 60
DB 41 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMKLTEDRE 100
QY 61 QIRQGLEELQKVLPGGDTYMHGFERASEQIYENRGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGFERASEQIYENRGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGDVFNFTQIARIADSKDHFVPVNDGFQALOGIHSILKSC 180
DB 161 SEREANSRDLGAIYVCVGDVFNFTQIARIADSKDHFVPVNDGFQALOGIHSILKSC 220
QY 181 IETIAAE 187
DB 221 IETIAAE 227

RESULT 11

US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481

PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
US-11-047-278-2

Query Match 100.0%; Score 970; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 7.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 100
QY 61 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTGGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTGGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
DB 161 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
QY 181 IETILAE 187
DB 221 IETILAE 227

RESULT 12

US-09-833-245-621
Sequence 621, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PPS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-621

Query Match 100.0%; Score 970; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 8.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 100
QY 61 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTGGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTGGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
DB 161 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
QY 181 IETILAE 187
DB 221 IETILAE 227

RESULT 13

US-10-201-292-28
Sequence 28, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-28

Query Match 100.0%; Score 970; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 100
QY 61 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTGGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTGGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
DB 161 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
QY 181 IETILAE 187
DB 221 IETILAE 227

RESULT 14

US-10-201-292-32
Sequence 32, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-32

Query Match 100.0%; Score 970; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLTEDRE 100

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QY 61 QIRQGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITALTGDELHEDLFFY 120
    |||
DB 101 QIRQGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITALTGDELHEDLFFY 160
    |||
QY 121 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 180
    |||
DB 161 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 220
    |||
QY 181 IEILAAE 187
    |||
DB 221 IEILAAE 227
    |||

```

```

RESULT 15
US-10-201-292-34
; Sequence 34, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-34

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Query Match      100.0%; Score 970; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGPDLFIILDKSGSVLHNMNEIYYFVQQLAHKFIISPOLRMSFTVFSRGTTLMKLTEDRE 60
    |||
DB 41 GGPDLFIILDKSGSVLHNMNEIYYFVQQLAHKFIISPOLRMSFTVFSRGTTLMKLTEDRE 100
    |||
QY 61 QIRQGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITALTGDELHEDLFFY 120
    |||
DB 101 QIRQGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITALTGDELHEDLFFY 160
    |||
QY 121 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 180
    |||
DB 161 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 220
    |||
QY 181 IEILAAE 187
    |||
DB 221 IEILAAE 227
    |||

```

Search completed: December 14, 2005, 11:59:00
 Job time : 56.504 secs

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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 : Search time 2.74816 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970
Sequence: 1 GGFGLYFLDKSGSVLHNMN.....LOGIHSILKKSCIEHLAE 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pap:*
2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pap:*
3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pap:*
4: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pap:*
5: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pap:*
6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pap:*
7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pap:*
8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 970 | 100.0 | 564 | 7 | US-11-186-284-199 |
| 2 | 132.5 | 13.7 | 1152 | 7 | US-11-080-026-4 |
| 3 | 131 | 13.5 | 3063 | 7 | US-11-186-284-26 |
| 4 | 111.5 | 11.5 | 739 | 7 | US-11-057-047-2 |
| 5 | 111.5 | 11.5 | 764 | 7 | US-11-057-047-1 |
| 6 | 111.5 | 11.5 | 798 | 6 | US-10-821-234-1034 |
| 7 | 109 | 11.2 | 955 | 6 | US-10-131-825A-294 |
| 8 | 109 | 11.2 | 956 | 7 | US-11-113-424-39 |
| 9 | 108 | 11.1 | 1141 | 6 | US-10-601-368-24 |
| 10 | 108 | 11.1 | 1166 | 6 | US-10-601-368-22 |
| 11 | 108 | 11.1 | 1166 | 6 | US-10-601-368-21 |
| 12 | 104.5 | 10.8 | 828 | 6 | US-10-995-561-983 |
| 13 | 104.5 | 10.8 | 918 | 6 | US-10-995-561-981 |
| 14 | 104.5 | 10.8 | 1019 | 6 | US-10-995-561-982 |
| 15 | 104 | 10.7 | 1141 | 6 | US-10-601-368-6 |
| 16 | 104 | 10.7 | 1166 | 6 | US-10-601-368-4 |
| 17 | 104 | 10.7 | 1188 | 6 | US-10-601-368-3 |
| 18 | 104 | 10.7 | 1188 | 7 | US-11-000-463-338 |
| 19 | 104 | 10.7 | 1188 | 7 | US-11-000-463-810 |
| 20 | 103.5 | 10.7 | 182 | 6 | US-10-601-368-25 |
| 21 | 103.5 | 10.7 | 761 | 7 | US-11-057-047-6 |
| 22 | 99.5 | 10.3 | 182 | 6 | US-10-601-368-7 |
| 23 | 95.5 | 9.8 | 1179 | 7 | US-11-097-125-1 |
| 24 | 95.5 | 9.8 | 1196 | 6 | US-10-995-561-921 |
| 25 | 94 | 9.7 | 678 | 7 | US-11-102-240-34 |

| | | | | | | |
|----|------|-----|------|---|--------------------|--------------------|
| 26 | 91.5 | 9.4 | 1167 | 7 | US-11-097-125-2 | Sequence 2, App1 |
| 27 | 90 | 9.3 | 1167 | 6 | US-10-601-368-18 | Sequence 18, App1 |
| 28 | 89.5 | 9.2 | 353 | 7 | US-11-137-465-44 | Sequence 44, App1 |
| 29 | 89.5 | 9.2 | 448 | 7 | US-11-137-465-45 | Sequence 45, App1 |
| 30 | 74 | 7.6 | 384 | 6 | US-10-510-386-158 | Sequence 158, App |
| 31 | 73.5 | 7.6 | 509 | 6 | US-10-793-626-2880 | Sequence 2880, App |
| 32 | 73.5 | 7.6 | 1804 | 6 | US-10-513-786-2 | Sequence 1, App1 |
| 33 | 73.5 | 7.6 | 3704 | 6 | US-10-513-786-1 | Sequence 1, App1 |
| 34 | 73 | 7.5 | 264 | 6 | US-10-793-626-388 | Sequence 388, App |
| 35 | 73 | 7.5 | 292 | 6 | US-10-793-626-2636 | Sequence 2636, App |
| 36 | 72 | 7.4 | 786 | 6 | US-10-467-962B-103 | Sequence 103, App |
| 37 | 71 | 7.3 | 629 | 6 | US-10-467-657-250 | Sequence 250, App |
| 38 | 71 | 7.3 | 629 | 6 | US-10-467-657-3084 | Sequence 3084, App |
| 39 | 70 | 7.2 | 468 | 6 | US-10-467-657-5696 | Sequence 5696, App |
| 40 | 69.5 | 7.2 | 489 | 6 | US-10-467-657-7846 | Sequence 7846, App |
| 41 | 69 | 7.1 | 242 | 6 | US-10-467-657-7306 | Sequence 7306, App |
| 42 | 69 | 7.1 | 1170 | 7 | US-11-080-026-2 | Sequence 2, App1 |
| 43 | 68.5 | 7.1 | 1734 | 7 | US-11-192-967-6 | Sequence 6, App1 |
| 44 | 68.5 | 7.1 | 1734 | 7 | US-11-193-715-6 | Sequence 6, App1 |
| 45 | 68 | 7.0 | 348 | 6 | US-10-674-767-4 | Sequence 4, App1 |

ALIGNMENTS

```
RESULT 1
US-11-186-284-199
; Sequence 199, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamekari, Shubhangi
; APPLICANT: Kamackar, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP001-0292PRM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-186-284-199

Query Match      100.0%  Score 970; DB 7; Length 564;
Best Local Similarity 100.0%; Pred No. 8.4e-87;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

1 GGFGLYFLDKSGSVLHNMNIIYFVEQLAKRIFSPQLRMSFIVSFGTITLKLTEDE 60
41 GGFGLYFLDKSGSVLHNMNIIYFVEQLAKRIFSPQLRMSFIVSFGTITLKLTEDE 100
QY 61 QIRGIEELQKVLPGSDITMHGFERASQIYYENRQGYRTASVIALTDGELHELFY 120
DB 101 QIRGIEELQKVLPGSDITMHGFERASQIYYENRQGYRTASVIALTDGELHELFY 160
QY 121 SREANRSDLAIVYCVGVDFNERQGLRIADSKDHVPVNDGFOALGIIHSILKSC 180

```
Db 161 SREANRSDLAIVYCVGVKDFNQTOLARLSDSDHVPVNDGQALGIIHSLKXSC 220
Qy 181 IEILAAE 187
Db 221 IEILAAE 227

RESULT 2
US-11-080-026-4
; Sequence 4, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CFBF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-026-4

Query Match 13.7%; Score 132.5; DB 7; Length 1152;
Best Local Similarity 26.3%; Pred. No. 3.6e-05;
Matches 52; Conservative 41; Mismatches 66; Indels 39; Gaps 11;

Qy 4 DLYFLIDKSGSV-LHHMNEIYFVEQLAKHF-ISPQLRMSFIVPST---RGTTLMKLTED---- 58
Db 150 DIAFLIDSGSIIIPHFRKRKEFVST---VMEQLKSKSTLPS---LMQYSEFRH 199
Qy 59 -----REQIQGLBELQKVLPGDPTVHGEFPERASEQIYENRQGYRTA-SVITIALT 109
Db 200 FTFRKQNNPNRPSLYKPIQQL--GRTHPATIRKVRLELPIITGARNAKILVIT 257
Qy 110 DGLHEDLFFYSF--REANRSDLAIVYCVGVKDFNQTOLAR----IADS--KHVPF 160
Db 258 DGEKFGDPLGYEDVPEADRE---GVIRYVIGVDAPRSEKRSQELNTIASKEPRDHVFO 314
Qy 161 VNDGQALGIIHSLKX 178
Db 315 VNN-PEALKTIOQLREK 331

RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Tribodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEM01-029P2RMM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
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```
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Query Match 13.5%; Score 131; DB 7; Length 3063;
Best Local Similarity 29.8%; Pred. No. 0.00018;
Matches 59; Conservative 38; Mismatches 75; Indels 26; Gaps 13;

Qy 4 DLYFLIDKSGSV-LHHMNEIYFVEQLAKHF-ISPQLRMSFIVPST---RGTTLMKLTED 57
Db 440 DIVFLVDSYSIGIANFVKRAFLVLYKSFISNRQVLSIVQSRDPHTEFTLKRTK 499
Qy 58 DREQIQGLBELQKVLPGDPTVHGEFPERASEQIYENRQGYRTA-SVITIALTDEL 113
Db 500 VEDIL-----EAINFPYRGGSTNTGKAMTYVREKIFVPSK-GSRSNPKWMLITDGR- 552
Qy 114 HEDLFFYSERANRSDLAIVYCVGVKDFNQTOLARLAD--SKHVPVNDGQALGII 171
Db 553 SSDAF---RDPALIKLRNSDVEIFAQVGDVARSLELAIASPPAEHVFVED-PDAFQRI 608
Qy 172 IHSILKSGCIEI---LAA 186
Db 609 SPFLTQSTICLRTEQELAA 626

RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Identification of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-047-2

Query Match 11.5%; Score 111.5; DB 7; Length 739;
Best Local Similarity 22.8%; Pred. No. 0.0022;
Matches 49; Conservative 44; Mismatches 77; Indels 45; Gaps 10;

Qy 1 GGFDLVFLIDKSGSV-----LHHMNEIYFVEQLAKHF-ISPQLRMSFIVPSTGTTLMLK 55
Db 242 GSNRIYLVLDGSDSIGASNFTGAKKCLVNLIERVASVGVKP--RYGLVYATYATPKIWKV 299
```



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OY      56 TE-----PREGROGIEEL-----OKVLPGSGDTVMHGEFPRASEOIYENR-----OQY- 99
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      300 SEADSSNADWVTKOLNEINVEDHKLKSTNT-----KKALQAVYSMMMSWPDDVPPBGON 353
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      100 RTASVIALTGD-----ELHEBDFPYSEBRANRSRLGAIVYCVG--VKDFN 144
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      354 RTRHVIIIMTGLNMGGDPIYVIDEIRDLLEYIGDKRONPREYLDVYVGVPLVNQVN 413
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : ~
OY      145 ETOLARIADSKOHVPVNDGFQALOGIITHSILIKS 179
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : ~
Db      414 INALASKKDNEQHVPKYKD-MENLEBDVEYQWIDDS 447
```

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RESULT 5
US-11-057-047-1
/ Sequence 1, Application US/11057047
/ Publication No. US20050260198A1
/ GENERAL INFORMATION:
/ APPLICANT: Holers, Vernon
/ APPLICANT: Thurman, Joshua
/ APPLICANT: Taube, Christian
/ APPLICANT: Gelfand, Erwin
/ APPLICANT: Gilkeson, Gary
/ TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
/ TITLE OF INVENTION: Methods Related Thereto
/ FILE REFERENCE: 2848-66
/ CURRENT APPLICATION NUMBER: US/11/057,047
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,594
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: 60/636,239
/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 764
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-11-057-047-1

```

| | | | | | |
|----|-----------------------|---|--------------------|--------------------|-------------------------|
| | Query Match | 11.8% | Score 111.5; | DB 7; | Length 764; |
| | Best Local Similarity | 22.8% | Pred. No. 0.0023; | | |
| | Matches | Conservative | 44; | Mismatches | 77; Indels 45; Gaps 10; |
| Qy | 1 | GGFDLYFLDKGSV---- | LHNNELIYFVEQLAHKFI | SPLRNSFVFSTRGTTMLK | 55 |
| | : | ::::: | : | : | : |
| Db | 267 | GSMNLYLVLDSDSDSGASNPFGAKKCLVLIEKVASYCKP-- | RGLTVATYATYPKIWKV | | 324 |
| Qy | 56 | TE-----DREOIROGIEEL-----OKVLPGDDPYMHGFBSAEIQIYYEKR-----OGY- | | | 99 |
| | : | ::::: | : | : | : |
| Db | 325 | SEADSNNDOWTKOLNEINVEDHKLKSGTNT-----KKALDAVSNMMSWDPDDVPBEGN | | | 378 |
| Qy | 100 | RTASVIALLTDG-----ELHADLFYSEREANSRDIGAIIVCVG--VKDFN | | | 144 |
| | : | ::::: | : | : | : |
| Db | 379 | RTRHVIILMTDGLHNMGDPITVIDEIRDLIYGDRKNRPREDYLDVVVGGLNVGN | | | 438 |
| Qy | 145 | ETOLARIDSKDHVPFVNDFQALOGIIHSLIKSS | | | 179 |
| | : | ::::: | : | : | : |
| Db | 439 | INALASKDNEQHAFKYKD--MENEDVVFQIMIDES | | | 472 |

RESULT 6
US-10-021-234-104
Sequence 104, Application US/10821234
Publication No. US2005025114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andatsman, Susan
APPLICANT: Tang, Y. Tom

```

OY      TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
Db      FILE REFERENCE: 821A
OY      CURRENT APPLICATION NUMBER: US/10/821,234
Db      PRIOR APPLICATION NUMBER: 2004-04-07
OY      PRIOR FILING DATE: 2003-04-07
Db      NUMBER OF SEQ ID NOS: 1704
OY      SOFTWARE: pc_seq_genes Version 1.0
Db      SEQ ID NO 1034
OY      LENGTH: 798
Db      TYPE: PRF
OY      ORGANISM: Homo sapiens
Db      US-10-821-234-1034

Query Match          11.5%; Score 111.5; DB 6; Length 798;
Best Local Similarity 22.8%; Pred. No. 0.0024;
Matches 49; Conservative 44; Mismatches 77; Indels 45; Gaps 10;

OY      1 GGPGPLTIDKSGGV-----LHHNNETTYVEQALAHFISPOLAMSTIVSTRGTTLMKL 55
Db      301 GSMNVIYVLDDGSISIGASNTFGAKKCIVNLIEKVASYGVAP--RYGLVATYAATPKIWKVK 358
OY      56 TE----DREQIRQGLEEL-----OKVLPGCGDTYMHGEFERASEQIYYENR-----OGY- 99
Db      359 SEADSSADAWVTQQLNEINYEHDHLKSGTWT-----KKLLQAIVSNMMSWPDVDVPEEGWN 412
OY      100 RTASVITIALTDG-----ELHEDLPFYSEFEARNRSRDLGAIYVCVG--VKDFN 144
Db      413 RTRRVIIILMTDGLHNMGGDPITYIDEIRDLLYTGKCRKRKNPREBDYLDTVVFEGVPLVNQVN 472
OY      145 ETOLARLADSNDHYFPVNDGFQALOGIHSILTKS 179
Db      473 INALASKDNQGHVFKYKD-MENTLEADVFGYMIDES 506

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1 RESULT 7
2 US-10-131-826A-294
3 : Sequence 294, Application US/10131826A
4 : Publication No. US20050245730A1
5 : GENERAL INFORMATION:
6 : APPLICANT: Baker, Kevin P.
7 : APPLICANT: Beresini, Maureen
8 : APPLICANT: DeForge, Laura
9 : APPLICANT: Desnoyers, Luc
10 : APPLICANT: Filvaroff, Ellen
11 : APPLICANT: Geo, Wei-Qiang
12 : APPLICANT: Geriltsen, Mary E.
13 : APPLICANT: Goddard, Audrey
14 : APPLICANT: Godowski, Paul J.
15 : APPLICANT: Gurney, Austin L.
16 : APPLICANT: Sherwood, Steven
17 : APPLICANT: Smith, Victoria
18 : APPLICANT: Stewart, Timothy A.
19 : APPLICANT: Tumas, Daniel
20 : APPLICANT: Watanabe, Colin K
21 : APPLICANT: Wood, William
22 : APPLICANT: Zhang, Zemin
23 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
24 : FILE REFERENCE: P330R1C128
25 : CURRENT APPLICATION NUMBER: US/10/131,826A
26 : CURRENT FILING DATE: 2002-04-24
27 : PRIOR APPLICATION NUMBER: 60/049911
28 : PRIOR FILING DATE: 1997-06-18
29 : PRIOR APPLICATION NUMBER: 60/056974
30 : PRIOR FILING DATE: 1997-08-26
31 : PRIOR APPLICATION NUMBER: 60/059113
32 : PRIOR FILING DATE: 1997-09-17
33 : PRIOR APPLICATION NUMBER: 60/059115
34 : PRIOR FILING DATE: 1997-09-17
35 : PRIOR APPLICATION NUMBER: 60/059117
36 : PRIOR FILING DATE: 1997-09-17
37 : PRIOR APPLICATION NUMBER: 60/059122

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1 TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
2 FILE REFERENCE: 07334-275001
3 CURRENT APPLICATION NUMBER: US/10/601,368
4 CURRENT FILING DATE: 2003-06-23
5 PRIOR APPLICATION NUMBER: US/09/561,263A
6 PRIOR FILING DATE: 2000-04-27
7 PRIOR APPLICATION NUMBER: US 09/322,790
8 PRIOR FILING DATE: 1999-05-28
9 NUMBER OF SEQ ID NOS: 40
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 22
12 LENGTH: 1166
13 TYPE: PR1
14 ORGANISM: Mus musculus
15 US-10-601-368-22

Query Match 11.1%; Score 108; DB 6; Length 1166;
Best Local Similarity 24.2%; Pred. No. 0.0088;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY 4 DLYFIIDKSGSVLHHNEIYFVEQLAHKE-ISP-QLRMSFIYFSTRGTTMLTDRDQ 61
DB 142 DIVIVDGSNSI-YPMVEVGHFLINILTKFYIGPGQIVGVGEDAVHEFL-NDYRS 199
QY 62 IROGLEBELQVLPBGDTYMEGFE---RASEQIYENRQGYRTASVIALTDDELHED-- 116
DB 200 VKDVVEASHIEBRCGETRTAFCIERASEAFQKGRKAK--KMIIVITDSESHDSP 257
QY 117 -----LFFYSERANRSDLAIVYCVGKD---FNETOLARIA 152
DB 258 LEKVIRQSEKDNTRYAVAVLGYNRRGINPETFLEIKYIASDPDKHFNVTDEAL- 316
QY 153 DSKDHVPVNDGFQALQG 170
DB 317 --KDIVDALGDRIFSLG 332

RESULT 11
US-10-601-368-21

1 Sequence 21, Application US/10601368
2 Publication No. US20050260702A1
3 GENERAL INFORMATION:
4 APPLICANT: Pan, Yang
5 APPLICANT: Lora, Jose M.
6 TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
7 FILE REFERENCE: 07334-275001
8 CURRENT APPLICATION NUMBER: US/10/601,368
9 CURRENT FILING DATE: 2003-06-23
10 PRIOR APPLICATION NUMBER: US/09/561,263A
11 PRIOR FILING DATE: 2000-04-27
12 PRIOR APPLICATION NUMBER: US 09/322,790
13 PRIOR FILING DATE: 1999-05-28
14 NUMBER OF SEQ ID NOS: 40
15 SOFTWARE: FastSeq for Windows Version 3.0
16 SEQ ID NO 21
17 LENGTH: 1188
18 TYPE: PR1
19 ORGANISM: Mus musculus
20 FEATURE:
21 NAME/KEY: SIGNAL
22 LOCATION: (1)...(22)
23 US-10-601-368-21

Query Match 11.1%; Score 108; DB 6; Length 1188;
Best Local Similarity 24.2%; Pred. No. 0.009;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY 4 DLYFIIDKSGSVLHHNEIYFVEQLAHKE-ISP-QLRMSFIYFSTRGTTMLTDRDQ 61
DB 164 DIVIVDGSNSI-YPMVEVGHFLINILTKFYIGPGQIVGVGEDAVHEFL-NDYRS 221
QY 62 IROGLEBELQVLPBGDTYMEGFE---RASEQIYENRQGYRTASVIALTDDELHED-- 116

DB 222 VKDVVEASHIEBRCGETRTAFCIERASEAFQKGRKAK--KMIIVITDSESHDSP 279
QY 117 -----LFFYSERANRSDLAIVYCVGKD---FNETOLARIA 152
DB 280 LEKVIRQSEKDNTRYAVAVLGYNRRGINPETFLEIKYIASDPDKHFNVTDEAL- 338
QY 153 DSKDHVPVNDGFQALQG 170
DB 339 --KDIVDALGDRIFSLG 354

RESULT 12
US-10-995-561-983
1 Sequence 983, Application US/10995561
2 Publication No. US20050272054A1
3 GENERAL INFORMATION:
4 APPLICANT: CARGILL, Michele et al.
5 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
6 TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
7 TITLE OF INVENTION: DETECTION AND USES THEREOF
8 FILE REFERENCE: CL001559
9 CURRENT APPLICATION NUMBER: US/10/995,561
10 CURRENT FILING DATE: 2004-11-24
11 NUMBER OF SEQ ID NOS: 85702
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 983
14 LENGTH: 828
15 TYPE: PR1
16 ORGANISM: Homo sapiens
17 US-10-995-561-983

Query Match

10.8%; Score 104.5; DB 6; Length 828;
Best Local Similarity 23.1%; Pred. No. 0.012;
Matches 50; Conservative 37; Mismatches 84; Indels 45; Gaps 9;

QY 5 LYFIIDKSGSV-----LHHWNE-IYFVEQLAHKEISPOLRMSF-----IVFSTRGT 50
DB 47 VYFVLDTSVYMQSPDTDLFLFMKQFVPOFISQGNERYLDQVALSMRWGLHFDQVE 106
QY 51 TLMKLTDEBQIRQGLEBELQVLPBGDTYMEGFEASQIYENRQGYRTASVIALTD 110
DB 107 VSPSPGSDRASFKXNLQGISFRRG--TFDCALANMTQIRDRSKG--TVHFAVVID 162
QY 111 GELHEDLFFYSERANRSDLAIVYCV-----GVKDFNET--OLARIADSKDHYF 159
DB 163 GHVTSPPCGGIRKIQARAREBGRIRPAVAPNOLKQGRADIASTHELXR-----NDYAT 218
QY 160 PVNDGFQALQGIHSTL-----KKSCTEI 183
DB 219 MLPDSTEIDQPTINRIKXMKHAYGECYKVSCTEI 254

RESULT 13

US-10-995-561-981
1 Sequence 981, Application US/10995561
2 Publication No. US20050272054A1
3 GENERAL INFORMATION:
4 APPLICANT: CARGILL, Michele et al.
5 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
6 TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
7 TITLE OF INVENTION: DETECTION AND USES THEREOF
8 FILE REFERENCE: CL001559
9 CURRENT APPLICATION NUMBER: US/10/995,561
10 CURRENT FILING DATE: 2004-11-24
11 NUMBER OF SEQ ID NOS: 85702
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 981
14 LENGTH: 918
15 TYPE: PR1
16 ORGANISM: Homo sapiens
17 US-10-995-561-981

Query Match 10.8%; Score 104.5; DB 6; Length 918;

Best Local Similarity 23.1%; Pred. No. 0.014;
Matches 50; Conservative 37; Mismatches 84; Indels 45; Gaps 9;

QY 5 LVPFLDKSGSV-----LHHMNE-IYFVEQLAHKFISSPOLRMSF-----IVFSTRGT 50
DB 47 VVFVLDTSSVTWQSTFDILLFPMKQFVPOFISQLONEFLDQVALSMRYGGHFSDDQVE 106
QY 51 TLMKLTDEBEQIRQGLEIELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTD 110
DB 107 VFSPPSDRASFIKNIQGISFRRG--TFTDCALAMTQDIRQDRSG--TVHFAVITD 162
QY 111 GELHEDLFFYSERANRSRDGAIVYCV-----GVKDFNET--QLARIADSKDHVF 159
DB 163 GHVTSGPCGGIKQLQARAREEGIRLFAVAPNQLKEQGLADIASTPHELYR----NDYAT 218
QY 160 PVNDGFOALQGIHSLI-----KKSCEI 183
DB 219 MLPDSTEIDQDTINRIIKWMKEAYGECYKVSCLDI 254

RESULT 14

US-10-995-561-982
; Sequence 982, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 982
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-982

Query Match 10.8%; Score 104.5; DB 6; Length 1019;
Best Local Similarity 23.1%; Pred. No. 0.016;
Matches 50; Conservative 37; Mismatches 84; Indels 45; Gaps 9;

QY 5 LVPFLDKSGSV-----LHHMNE-IYFVEQLAHKFISSPOLRMSF-----IVFSTRGT 50
DB 47 VVFVLDTSSVTWQSTFDILLFPMKQFVPOFISQLONEFLDQVALSMRYGGHFSDDQVE 106
QY 51 TLMKLTDEBEQIRQGLEIELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTD 110
DB 107 VFSPPSDRASFIKNIQGISFRRG--TFTDCALAMTQDIRQDRSG--TVHFAVITD 162
QY 111 GELHEDLFFYSERANRSRDGAIVYCV-----GVKDFNET--QLARIADSKDHVF 159
DB 163 GHVTSGPCGGIKQLQARAREEGIRLFAVAPNQLKEQGLADIASTPHELYR----NDYAT 218
QY 160 PVNDGFOALQGIHSLI-----KKSCEI 183
DB 219 MLPDSTEIDQDTINRIIKWMKEAYGECYKVSCLDI 254

RESULT 15

US-10-601-368-6
; Sequence 6, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-10-601-368-6

Query Match 10.7%; Score 104; DB 6; Length 1141;
Best Local Similarity 24.2%; Pred. No. 0.021;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY 4 DLVFLDKSGSVLHHMNEIYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDREQ 61
DB 164 DIVIVLDGNSI-YPMVEYQHFLINILKKFYIGPGQIQGVVQYGEDVHBEFL-NDYRS 221
QY 62 INQGLEIELQKVLPGGDTYMHGFE--RASEQIYYENRQGYRTASVIALTDGELHED-- 116
DB 222 VKDVEASHIEQRGSETETRTAFGIEPARSEAFQKGRGAK--KMWIVTDGESHSDPD 279
QY 117 -----LFFYSERANRSRDGAIVYCVGVD-----FNETOIARIA 152
DB 280 LEKVIOGSRDQVTRAYAAVAGLYNRRGINPETFINEIKYIASDPDDKHFFVITDEAL- 338
QY 153 DSKDHVPVNDGFOALQ 170
DB 339 --KDIVDALGDRIFSLIG 354

Search completed: December 14, 2005, 11:59:29
Job time : 3.74816 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:35:12 ; Search time 599.1 Seconds

(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970
Sequence: 1 GGFIDYFILDKSGSVLHMN.....LOGIHSILKKSCIEIILAAE 187

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Litering first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-O/cgn2_1/USPTO_bpool/US0970076/runat_14122005_11852_21035/app_query.fasta_1.2410
-DB=Published Applications NA Main -QPMF=fastcap -SUFFIX=trnphm -MINMATCH=0.1
-LOOCPU=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human4.ctd -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0970076@cgn_1_1_2715 @runat_14122005_11852_21035
-NCPU=6 -ICPU=3 -NO_MMAP -LAQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:*

1: /cgn2_6/ptoddata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptoddata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptoddata/1/pubpna/US09_PUBCOMB.seq:*
4: /cgn2_6/ptoddata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptoddata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptoddata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptoddata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptoddata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptoddata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptoddata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------|-------------------|
| 1 | 970 | 100.0 | 1008 | US-10-038-307-25 | Sequence 25, Appl |
| 2 | 970 | 100.0 | 1008 | US-10-201-292-25 | Sequence 25, Appl |
| 3 | 970 | 100.0 | 1047 | US-10-038-307-21 | Sequence 21, Appl |
| 4 | 970 | 100.0 | 1047 | US-10-201-292-21 | Sequence 21, Appl |
| 5 | 970 | 100.0 | 1056 | US-10-038-307-23 | Sequence 23, Appl |
| 6 | 970 | 100.0 | 1056 | US-10-201-292-23 | Sequence 23, Appl |
| 7 | 970 | 100.0 | 1401 | US-10-201-292-27 | Sequence 27, Appl |
| 8 | 970 | 100.0 | 1401 | US-10-201-292-29 | Sequence 29, Appl |

| | | | | | | |
|----|-----|-------|------|----|---------------------|--------------------|
| 9 | 970 | 100.0 | 1414 | 10 | US-11-047-278-1 | Sequence 1, Appl1 |
| 10 | 970 | 100.0 | 1436 | 10 | US-11-047-278-9 | Sequence 9, Appl1 |
| 11 | 970 | 100.0 | 1454 | 6 | US-10-133-937-58 | Sequence 58, Appl1 |
| 12 | 970 | 100.0 | 1454 | 6 | US-10-159-563-58 | Sequence 58, Appl1 |
| 13 | 970 | 100.0 | 1464 | 6 | US-10-201-292-31 | Sequence 31, Appl1 |
| 14 | 970 | 100.0 | 1534 | 6 | US-10-201-292-33 | Sequence 33, Appl1 |
| 15 | 970 | 100.0 | 1608 | 6 | US-10-201-292-35 | Sequence 35, Appl1 |
| 16 | 970 | 100.0 | 1609 | 5 | US-10-037-770-8 | Sequence 8, Appl1 |
| 17 | 970 | 100.0 | 1609 | 6 | US-10-117-722-8 | Sequence 8, Appl1 |
| 18 | 970 | 100.0 | 1609 | 9 | US-10-132-851-8 | Sequence 9, Appl1 |
| 19 | 970 | 100.0 | 1623 | 6 | US-10-038-307-11 | Sequence 11, Appl1 |
| 20 | 970 | 100.0 | 1623 | 6 | US-10-201-292-11 | Sequence 11, Appl1 |
| 21 | 970 | 100.0 | 1650 | 6 | US-10-038-307-9 | Sequence 9, Appl1 |
| 22 | 970 | 100.0 | 1650 | 6 | US-10-038-307-13 | Sequence 13, Appl1 |
| 23 | 970 | 100.0 | 1650 | 6 | US-10-038-307-15 | Sequence 15, Appl1 |
| 24 | 970 | 100.0 | 1650 | 6 | US-10-201-292-9 | Sequence 9, Appl1 |
| 25 | 970 | 100.0 | 1650 | 6 | US-10-201-292-13 | Sequence 13, Appl1 |
| 26 | 970 | 100.0 | 1650 | 6 | US-10-201-292-15 | Sequence 15, Appl1 |
| 27 | 970 | 100.0 | 1674 | 6 | US-10-038-307-17 | Sequence 17, Appl1 |
| 28 | 970 | 100.0 | 1674 | 6 | US-10-201-292-17 | Sequence 17, Appl1 |
| 29 | 970 | 100.0 | 1713 | 6 | US-10-038-307-19 | Sequence 19, Appl1 |
| 30 | 970 | 100.0 | 1713 | 6 | US-10-201-292-19 | Sequence 19, Appl1 |
| 31 | 970 | 100.0 | 1718 | 8 | US-10-357-930-30300 | Sequence 30300, A |
| 32 | 970 | 100.0 | 2112 | 10 | US-11-047-278-7 | Sequence 7, Appl1 |
| 33 | 970 | 100.0 | 2272 | 3 | US-09-796-753-11 | Sequence 11, Appl1 |
| 34 | 970 | 100.0 | 2272 | 6 | US-10-038-307-1 | Sequence 1, Appl1 |
| 35 | 970 | 100.0 | 2272 | 6 | US-10-201-292-1 | Sequence 1, Appl1 |
| 36 | 970 | 100.0 | 2353 | 5 | US-10-198-846-9957 | Sequence 9957, Ap |
| 37 | 970 | 100.0 | 5540 | 3 | US-09-918-715-176 | Sequence 176, App |
| 38 | 970 | 100.0 | 5540 | 3 | US-09-918-715-231 | Sequence 231, App |
| 39 | 970 | 100.0 | 5540 | 6 | US-10-301-822-198 | Sequence 198, App |
| 40 | 970 | 100.0 | 5540 | 8 | US-10-474-794-176 | Sequence 176, App |
| 41 | 970 | 100.0 | 5540 | 8 | US-10-474-794-231 | Sequence 231, App |
| 42 | 970 | 100.0 | 5540 | 9 | US-10-979-159-176 | Sequence 176, App |
| 43 | 970 | 100.0 | 5540 | 9 | US-10-979-159-231 | Sequence 231, App |
| 44 | 970 | 100.0 | 5540 | 10 | US-11-047-278-5 | Sequence 5, Appl1 |
| 45 | 961 | 99.1 | 5520 | 3 | US-09-918-715-186 | Sequence 186, App |

ALIGNMENTS

RESULT 1
US-10-038-307-25
; Sequence 25, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PASCSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:

Pred. No.: 7.35e-120 Length: 1008
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-038-307-25 (1-1008)

Gy 1 G[yG]yPheapsleuTyrrPheilleleuApplysSecl[ySeerValleuHstHrPAsn 20

```
DB 133 GGGGGATTGACCTGACTTTCATTTTGGACAAATTCAGAAAGTGTGCTGCACCTGGAAAT 192
QY 21 G|U|L|E|T|Y|T|P|H|E|V|A|G|U|G|I|N|L|E|U|A|A|H|I|S|Y|P|H|E|L|E|S|E|P|R|O|G|I|N|L|E|U|A|A|G|M|E|T 40
DB 193 GAAATCTATTAATCTTTGTGGAAACAGTTGGCTCACAATAATTCATCGCCACAGTTGGAAGAATG 252
QY 41 SerPheI|LevalPheSerThraSgI|YThrThleuMetLysLeuThrgL|UaSPaRgIu 60
DB 253 TCCCTTATTTGTTTCTTCCACCCGAGAACCACTTAAATGAATCTGACAGAAACAGAA 312
QY 61 G|N|I|E|A|R|G|I|N|L|E|U|G|I|U|E|U|G|I|U|E|V|A|L|L|E|U|P|R|O|G|I|Y|A|S|P|H|T|Y|R|M|E|T 80
DB 313 CAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCGACAGAGACACTTACATG 372
QY 81 H|S|G|U|G|I|P|H|E|L|U|A|R|G|I|A|S|E|R|G|U|G|I|N|L|E|T|Y|T|Y|R|G|I|U|A|S|P|A|R|G|I|N|G|I|Y|T|R|A|R|G 100
DB 373 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTTATTATGAAACAGACAAAGGGTACAG 432
QY 101 ThrAlaSerVal|I|L|E|I|A|L|E|U|ThraSPG|Y|G|I|U|E|U|H|I|S|G|I|U|A|S|P|L|E|U|P|H|E|P|H|E|Y|R 120
DB 433 ACAGCCAGGCTCATCATCTGTTGACTGATGAGAACTCATGAAGATCTTTTCTAT 492
QY 121 SerG|U|A|R|G|I|U|A|A|S|P|A|R|S|E|R|A|R|G|A|R|P|L|E|U|G|I|A|I|L|E|V|A|I|Y|R|C|Y|S|V|A|I|G|I|Y|V|A|I 140
DB 493 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTTG 552
QY 141 LysASPheAsnG|U|Thrg|I|N|L|E|U|A|A|R|G|I|L|E|A|A|S|P|S|E|R|Y|A|S|P|H|I|S|V|A|I|P|H|E|P|R|O 160
DB 553 AAAGATTTCAATAGACACACAGCTGGCCGGATGGCGACAGTAAATCATGTGTTTCCC 612
QY 161 ValAsnAspG|I|P|H|E|G|I|N|A|L|E|U|G|I|Y|I|E|I|H|I|S|E|R|I|L|E|U|L|Y|S|E|R|C|Y|S 180
DB 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCTGCG 672
QY 181 I|L|E|G|I|L|E|U|A|A|A|G|I|U 187
DB 673 ATCGAAATTTAGCAGCTGAA 693
```

RESULT 2

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US-10-201-292-25
/ Sequence 25, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTHMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 1008
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-25
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Alignment Scores:

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Pred. No.: 7,35e-120 Length: 1008
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-25 (1-1008)

```
QY 1 G|Y|G|I|P|H|A|S|P|L|E|U|T|Y|R|P|H|E|I|L|E|U|A|S|P|Y|S|E|R|G|I|S|E|R|V|A|L|L|E|U|H|I|S|I|S|T|R|P|A|S|N 20
DB 133 GGGGATTTGACCTGACTTTCATTTTGGACAAATTCAGAAAGTGTGCTGCACCACTGGAAAT 192
```

```
QY 21 G|U|L|E|T|Y|T|P|H|E|V|A|G|U|G|I|N|L|E|U|A|A|H|I|S|Y|P|H|E|L|E|S|E|P|R|O|G|I|N|L|E|U|A|A|G|M|E|T 40
DB 193 GAAATCTATTAATCTTTGTGGAAACAGTTGGCTCACAATAATTCATCGCCACAGTTGGAAGAATG 252
QY 41 SerPheI|LevalPheSerThraSgI|YThrThleuMetLysLeuThrgL|UaSPaRgIu 60
DB 253 TCCCTTATTTGTTTCTTCCACCCGAGAACCACTTAAATGAATCTGACAGAAACAGAA 312
QY 61 G|N|I|E|A|R|G|I|N|L|E|U|G|I|U|E|U|G|I|U|E|V|A|L|L|E|U|P|R|O|G|I|Y|A|S|P|H|T|Y|R|M|E|T 80
DB 313 CAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCGACAGAGACACTTACATG 372
QY 81 H|S|G|U|G|I|P|H|E|L|U|A|R|G|I|A|S|E|R|G|U|G|I|N|L|E|T|Y|T|Y|R|G|I|U|A|S|P|A|R|G|I|N|G|I|Y|T|R|A|R|G 100
DB 373 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTTATTATGAAACAGACAAAGGGTACAG 432
QY 101 ThrAlaSerVal|I|L|E|I|A|L|E|U|ThraSPG|Y|G|I|U|E|U|H|I|S|G|I|U|A|S|P|L|E|U|P|H|E|P|H|E|Y|R 120
DB 433 ACAGCCAGGCTCATCATCTGTTGACTGATGAGAACTCATGAAGATCTTTTCTAT 492
QY 121 SerG|U|A|R|G|I|U|A|A|S|P|A|R|S|E|R|A|R|G|A|R|P|L|E|U|G|I|A|I|L|E|V|A|I|Y|R|C|Y|S|V|A|I|G|I|Y|V|A|I 140
DB 493 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTTG 552
QY 141 LysASPheAsnG|U|Thrg|I|N|L|E|U|A|A|R|G|I|L|E|A|A|S|P|S|E|R|Y|A|S|P|H|I|S|V|A|I|P|H|E|P|R|O 160
DB 553 AAAGATTTCAATAGACACACAGCTGGCCGGATGGCGACAGTAAATCATGTGTTTCCC 612
QY 161 ValAsnAspG|I|P|H|E|G|I|N|A|L|E|U|G|I|Y|I|E|I|H|I|S|E|R|I|L|E|U|L|Y|S|E|R|C|Y|S 180
DB 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCTGCG 672
QY 181 I|L|E|G|I|L|E|U|A|A|A|G|I|U 187
DB 673 ATCGAAATTTAGCAGCTGAA 693
```

RESULT 3

```
US-10-038-307-21
/ Sequence 21, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTHMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 1047
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-038-307-21
```

Alignment Scores:

```
Pred. No.: 7,79e-120 Length: 1047
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-038-307-21 (1-1047)

```
QY 1 G|Y|G|I|P|H|A|S|P|L|E|U|T|Y|R|P|H|E|I|L|E|U|A|S|P|Y|S|E|R|G|I|S|E|R|V|A|L|L|E|U|H|I|S|I|S|T|R|P|A|S|N 20
DB 160 GGGGATTTGACCTGACTTTCATTTTGGACAAATTCAGAAAGTGTGCTGCACCACTGGAAAT 219
QY 21 G|U|L|E|T|Y|T|P|H|E|V|A|G|U|G|I|N|L|E|U|A|A|H|I|S|Y|P|H|E|L|E|S|E|P|R|O|G|I|N|L|E|U|A|A|G|M|E|T 40
```

```
Db 220 GAATCTATTACTTGTGGAAACAGTGGCTCACAAATTCAACGCCACAGTTGAGATG 279
Qy 41 SerPheIleValPheSerThrArgGlyThrThreumelysLeuThrGluaspArgGlu 60
Db 280 TCCCTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAAATGACAGAAACAGAA 339
Qy 61 GluIleArgGlnGlyLeuGlnGluLeuValLeuProGlyGlyAspThrTyrMet 80
Db 340 CAATCCGTCAAGGCTTAGAAGAACTCCAGAAATCTCCAGAGAGAGACATTACATG 399
Qy 81 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluaspArgGlnGlyTyrArg 100
Db 400 CAGGAAGGATTTGAAAGGGCCAGTACAGACAGTTTATTATGAAACAGACAGGTACAGG 459
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 120
Db 460 ACAGCCAGCGTCATCATGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 519
Qy 121 SerGluArgGluAlaaspArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db 520 TCAGAGAGGAGGCTTAATAGCTCTCGAGATCTTGTCATTTGTTACTGTGTGTGTG 579
Qy 141 LysAspPheaspGluThrGlnLeuAlaArgIleAlaaspSerLysAspHisValPhePro 160
Db 580 AAGATTTCATATGACACACAGCTGCCCGGATTCGGACAGTACATCATGTGTTCC 639
Qy 161 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 640 GTGATATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTGGAAGAAGTCTGCG 699
Qy 181 IleGluIleLeuAlaIleGlu 187
Db 700 ATCGAAATTCACGACTGAA 720
```

RESULT 4

```
US-10-201-292-21
; Sequence 21, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-21
```

```
Alignment Scores:
Pred. No.: 7,79e-120 Length: 1047
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-21 (1-1047)

```
Qy 1 GlyGlyPheaspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 20
Db 160 GGGGATTTGACCTGTACTTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCTGGAAT 219
Qy 21 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 220 GAATCTATTACTTGTGGAAACAGTGGCTCACAAATTCAACGCCACAGTTGAGATG 279
```

```
Qy 41 SerPheIleValPheSerThrArgGlyThrThreumelysLeuThrGluaspArgGlu 60
Db 280 TCCCTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAAATGACAGAAACAGAA 339
Qy 61 GluIleArgGlnGlyLeuGlnGluLeuValLeuProGlyGlyAspThrTyrMet 80
Db 340 CAATCCGTCAAGGCTTAGAAGAACTCCAGAAATCTCCAGAGAGAGACATTACATG 399
Qy 81 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluaspArgGlnGlyTyrArg 100
Db 400 CAGGAAGGATTTGAAAGGGCCAGTACAGACAGTTTATTATGAAACAGACAGGTACAGG 459
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 120
Db 460 ACAGCCAGCGTCATCATGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 519
Qy 121 SerGluArgGluAlaaspArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db 520 TCAGAGAGGAGGCTTAATAGCTCTCGAGATCTTGTCATTTGTTACTGTGTGTGTG 579
Qy 141 LysAspPheaspGluThrGlnLeuAlaArgIleAlaaspSerLysAspHisValPhePro 160
Db 580 AAGATTTCATATGACACACAGCTGCCCGGATTCGGACAGTACATCATGTGTTCC 639
Qy 161 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 640 GTGATATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTGGAAGAAGTCTGCG 699
Qy 181 IleGluIleLeuAlaIleGlu 187
Db 700 ATCGAAATTCACGACTGAA 720
```

RESULT 5

```
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23
```

```
Alignment Scores:
Pred. No.: 7,89e-120 Length: 1056
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-038-307-23 (1-1056)

```
Qy 1 GlyGlyPheaspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 20
Db 133 GGGGATTTGACCTGTACTTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCTGGAAT 192
Qy 21 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 193 GAATCTATTACTTGTGGAAACAGTGGCTCACAAATTCATCAGCCACAGTTGAGAAGT 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThreumelysLeuThrGluaspArgGlu 60
```

```
Db 253 TCCCTTATTGTTTCTCCACCAGAGAACAACTTATGAACTGACAGAGACAGAGAA 312
Qy 61 GlnlleArgInglYLeuGluGluLeuGlnlyValLeuProGlyGlyAspThrTyrMet 80
Db 313 CAATCCGTCACAGGCGCTGAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 372
Qy 81 HsGluGlyPheGluArgAlaSerGluGlnlleTyrTyrGluAsnArgInglYTyArg 100
Db 373 CATGAAGGATTTGAAAAGGGCCAGTACAGCATTTATTAAGAAAACAGACAGGTTACAG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHsGluAspLeuPhePheTyr 120
Db 433 ACAGCCAGCGCTCATCATGCTTTGACTGATGAGAACTCCATGAAGATCTTTTTCAT 492
Qy 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCyValGlyVal 140
Db 493 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGCGCAATGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAAGATTTCAATGACACACAGCTGCGCCGATTCGAGACAGTAAGATCATGTGTTCCC 612
Qy 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsSerIleLeuLysLysSerCys 180
Db 613 GTGAATGACGCGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAAGAGTCTGCG 672
Qy 181 IleGluIleLeuAlaAlaGlu 187
Db 673 ATCGAAATTTCTAGCAGCTGAA 693
```

RESULT 6

```
US-10-201-292-23
/ Sequence 23, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ. ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 23
/ LENGTH: 1056
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-23
```

```
Alignment Scores:
Pred. No.: 7,896-120 Length: 1056
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
```

US-09-970-076-2_copy_41_227 (1-187) x US-10-201-292-23 (1-1056)

```
Qy 1 GtlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHsIleTyrPaa 20
Db 133 GGGGAGATTGACCTGTACTTATTTTGACAAATCAGAAAGTGTGCGACCACTGGAAT 192
Qy 21 GtlyleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 193 GAAATCTATTACTTTGTGGAAACAGTTGGCTACAAATTCATCACCCACAGTTGAGAAATG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
Db 253 TCCTTTATTGTTTCTCCACCAGAGAAACAACCTTAATGAAGTGAAGAGACAGAGAA 312
```

```
Qy 61 GlnlleArgInglYLeuGluGluLeuGlnlyValLeuProGlyGlyAspThrTyrMet 80
Db 313 CAATCCGTCACAGGCGCTGAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 372
Qy 81 HsGluGlyPheGluArgAlaSerGluGlnlleTyrTyrGluAsnArgInglYTyArg 100
Db 373 CATGAAGGATTTGAAAAGGGCCAGTACAGCATTTTATTAAGAAAACAGACAGGTTACAG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHsGluAspLeuPhePheTyr 120
Db 433 ACAGCCAGCGCTCATCATGCTTTGACTGATGAGAACTCCATGAAGATCTTTTTCAT 492
Qy 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCyValGlyVal 140
Db 493 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGCGCAATGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAAGATTTCAATGACACACAGCTGCGCCGATTCGAGACAGTAAGATCATGTGTTCCC 612
Qy 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsSerIleLeuLysLysSerCys 180
Db 613 GTGAATGACGCGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAAGAGTCTGCG 672
Qy 181 IleGluIleLeuAlaAlaGlu 187
Db 673 ATCGAAATTTCTAGCAGCTGAA 693
```

RESULT 7

```
US-10-201-292-27
/ Sequence 27, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ. ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 1401
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-27
```

```
Alignment Scores:
Pred. No.: 1,226-119 Length: 1401
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
```

US-09-970-076-2_copy_41_227 (1-187) x US-10-201-292-27 (1-1401)

```
Qy 1 GtlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHsIleTyrPaa 20
Db 133 GGGGAGATTGACCTGTACTTATTTTGACAAATCAGAAAGTGTGCGACCACTGGAAT 192
Qy 21 GtlyleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 193 GAAATCTATTACTTTGTGGAAACAGTTGGCTACAAATTCATCACCCACAGTTGAGAAATG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
Db 253 TCCTTTATTGTTTCTCCACCAGAGAAACAACCTTAATGAAGTGAAGAGACAGAGAA 312
Qy 61 GlnlleArgInglYLeuGluGluLeuGlnlyValLeuProGlyGlyAspThrTyrMet 80
```



```
Db 313 CAATCCGTCAGCGCTAGAAAGAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATG 372
Qy 81 HIGLUGLYPHEGLUARGALASERGLUGNILETYRTYRGLUENARGINGLYTYRARG 100
Db 373 CATGAGAGATTGTAAGAGGCGCATGAGACAGATTATATGAAAACAGACAGAGGTACAGG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
Db 433 ACAGCCAGCGCTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTCTAT 492
Qy 121 SerGLUARGGLUALAENARGSERARGASPLEUGLYALALEVALTYRCYSVALIGLYVAL 140
Db 493 TCAGAGAGGAGGCTATATAGGTCTCGAGATCTTGTCACATTTGTTACTGTGTGTG 552
Qy 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAGATTTCATATGACACACAGCTGGCCCGATTGCGACAGTAAAGATCATGTGTCTCC 612
Qy 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 613 GTGATATGACGCTTTCAGGCTCTGCAGAGCATCATCTCAATTTTGAAGAAGTCTTGC 672
Qy 181 ILeGluIleLeuAlaAlaGlu 187
Db 673 ATCGAAATTCCTAGCAGCTGAA 693
```

RESULT 8

```
US-10-201-292-29
; Sequence 29, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYMAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-201-292-29
```

Alignment Scores:

| Pred. No.: | 1,226-119 | Length: | 1401 |
|------------------------|-----------|---------------|------|
| Score: | 970.00 | Matches: | 187 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-29 (1-1401)

```
Qy 1 GLyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisStrpAsn 20
Db 133 GCGGAGATTGACCTGATCTTTCATTTTGACAAATCAGAAAGTGTGCGACCACTGGAAT 192
Qy 21 GlnIleTyrrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 193 GAATCATTAATCTTGTGGAACAGTTGCTCACAAATTCATCAGCCACAGTTGAGATG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
Db 253 TCCCTTTATGTTTCTCCACCCAGAGAACAACTTAATGAACTGACAGAGACAGAGAA 312
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyLysAspThrTyMet 80
Db 313 CAATCCGTCAGCGCTAGAAAGAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATG 372
```

```
Qy 81 HIGLUGLYPHEGLUARGALASERGLUGNILETYRTYRGLUENARGINGLYTYRARG 100
Db 373 CATGAGAGATTGTAAGAGGCGCATGAGACAGATTATATGAAAACAGACAGAGGTACAGG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
Db 433 ACAGCCAGCGCTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTCTAT 492
Qy 121 SerGLUARGGLUALAENARGSERARGASPLEUGLYALALEVALTYRCYSVALIGLYVAL 140
Db 493 TCAGAGAGGAGGCTATATAGGTCTCGAGATCTTGTCACATTTGTTACTGTGTGTG 552
Qy 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAGATTTCATATGACACACAGCTGGCCCGATTGCGACAGTAAAGATCATGTGTCTCC 612
Qy 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 613 GTGATATGACGCTTTCAGGCTCTGCAGAGCATCATCTCAATTTTGAAGAAGTCTTGC 672
Qy 181 ILeGluIleLeuAlaAlaGlu 187
Db 673 ATCGAAATTCCTAGCAGCTGAA 693
```

RESULT 9

US-11-047-278-1

```
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047.278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970.076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251.481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
; US-11-047-278-1
```

Alignment Scores:

| Pred. No.: | 1,246-119 | Length: | 1414 |
|------------------------|-----------|---------------|------|
| Score: | 970.00 | Matches: | 187 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-09-970-076-2_COPY_41_227 (1-187) x US-11-047-278-1 (1-1414)

```
Qy 1 GLyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisStrpAsn 20
Db 224 GCGGAGATTGACCTGATCTTTCATTTTGACAAATCAGAAAGTGTGCGACCACTGGAAT 283
Qy 21 GlnIleTyrrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 284 GAATCATTAATCTTGTGGAACAGTTGCTCACAAATTCATCAGCCACAGTTGAGATG 343
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
```

Db 344 TCGTTATTGTTTTCACCCGAGGACCACTTATGAAACTGACAGAGACAGAA 403
Qy 61 GlnleargGlnGlyLeuGlnGluValLeuProGlyGlyAspThyTyrMet 80
Db 404 CAATTCGTCAGAGGCTTAAGAACTCCAGAAAGTTCTGCGAGGAGAGACCTTACATG 463
Qy 81 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGlnuAsnArgGlnGlyTyrArg 100
Db 464 CATGAAGATTGCAAAAGGCGCATGACGATTATTATGAAGACAGACAGGTTACAG 523
Qy 101 ThrAlaSerValIleIleAlaLeuThraSpGlyGlnuLeuHisGlnuAspLeuPhePheTyr 120
Db 524 ACAGCAGCGGTCACTTCCTTGTGACTGAGAACTCCATGAAATCATCTTTTCTAT 583
Qy 121 SerGlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db 584 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGGTCAATGTTTACCTGTGTGTGTG 643
Qy 141 LysAspPheAsnGlnuThraGlnuLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 644 AAAGATTTCATAGACACACAGCTGCGCCGATTCGCGACATGATCATGTGTTCCC 703
Qy 161 ValAsnAspGlyPheGlnuAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 704 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCATTTTGAAGAAGTCTGCG 763
Qy 181 IlegluIleLeuAlaIleGlu 187
Db 764 ATCGAAATTCTAGCAGCTGAA 784

RESULT 10

US-11-047-278-9
; Sequence 9, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-11-047-278-9

Alignment Scores:
Pred. No.: 1,27e-119 Length: 1436
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-11-047-278-9 (1-1436)

Qy 1 GylGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleSTrPaen 20
Db 263 GGGGGATTGACCTGTACTTCACTTTTGGACAAATCAGAAAGTGTGTCACCACTGGAAAT 322
Qy 21 GlnIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40

Db 323 GAAATCTTACTTGTGTGAACAGTTGGCTCCAAATTCATCAGCCACAGTTGAGAAAG 382
Qy 41 SerPheIleValPheSerThraArgGlyThraThrLeuMetLysLeuThraGluAspArgGlu 60
Db 383 TCGTTATTGTTTTCACCCGAGAGACACACTTAATGAATCTACAGAAACAGAGAA 442
Qy 61 GlnleargGlnGlyLeuGlnGluValLeuProGlyGlyAspThyTyrMet 80
Db 443 CAATTCGTCAGAGGCTTAAGAACTCCAGAAAGTTCTGCGAGGAGAGACCTTACATG 502
Qy 81 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGlnuAsnArgGlnGlyTyrArg 100
Db 503 CATGAAGATTGCAAAAGGCGCATGACGAGATTATTATGAAGACAGCAAGGTTACAG 562
Qy 101 ThrAlaSerValIleIleAlaLeuThraSpGlyGlnuLeuHisGlnuAspLeuPhePheTyr 120
Db 563 ACAGCAGCGGTCACTTCCTTGTGACTGAGAACTCCATGAAATCATCTTTTCTAT 622
Qy 121 SerGlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db 623 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGGTCAATGTTTACCTGTGTGTGTG 682
Qy 141 LysAspPheAsnGlnuThraGlnuLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 683 AAAGATTTCATAGACACACAGCTGCGCCGATTCGCGACATGATCATGTGTTCCC 742
Qy 161 ValAsnAspGlyPheGlnuAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 743 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCATTTTGAAGAAGTCTGCG 802
Qy 181 IlegluIleLeuAlaIleGlu 187
Db 803 ATCGAAATTCTAGCAGCTGAA 823

RESULT 11

US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 1,29e-119 Length: 1454
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-133-937-58 (1-1454)

Qy 1 GylGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleSTrPaen 20
Db 264 GGGGGATTGACCTGTACTTCACTTTTGGACAAATCAGAAAGTGTGTCACCACTGGAAAT 323
Qy 21 GlnIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40

```
DB 324 GAATCTATTACTTGTGGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGATG 383
QY 41 SerPheIleValIpheserThrArgGlyThrThreumelysLeuThrGluaspArgGlu 60
DB 384 TCCCTTAATTTGTTTCTCCACCCGAGAACAACTTAATGAACCTGACAGAAACAGAGAA 443
QY 61 GluIleArgGlnIleuGlnIleuGlnIleuValLeuProGlyGlyAspThrTyrMet 80
DB 444 CAAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTACATG 503
QY 81 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGluuaspArgGlnIlyTyrArg 100
DB 504 CATGAAGATTGTAAGAGGCGCAGTGAAGACATTTATATGAAAACAGACAAAGGTACAGG 563
QY 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGlnuaspLeuPhePheTyr 120
DB 564 ACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTAT 623
QY 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIlyTyrCyvaIglVal 140
DB 624 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCAAATGTTTACTGTTGGTGTG 683
QY 141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 684 AAGATTTCATATAGACACAGCTGGCCCGGATTCGGACAGTAAGATCATGTGTTTCCC 743
QY 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYsLysSerCy 180
DB 744 GTCAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTGAAAGAGTCTGCG 803
QY 181 IleGluIleLeuAlaIleGlu 187
DB 804 ATCGAAATTTCTAGCAGCTGAA 824
```

RESULT 12

US-10-159-563-58

Sequence 58, Application US/10159563

Publication No. US20040009154A1

GENERAL INFORMATION:

APPLICANT: Khan, Javed

APPLICANT: Ringner, Markus

APPLICANT: Peterson, Carsten

APPLICANT: Melzer, Paul

TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

FILE REFERENCE: 11613.56US11

CURRENT APPLICATION NUMBER: US/10/159,563

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: US 10/133,937

PRIOR FILING DATE: 2002-04-25

NUMBER OF SEQ ID NOS: 444

SOFTWARE: PatentIn version 3.1

SEQ ID NO 58

LENGTH: 1454

TYPE: DNA

ORGANISM: Homo sapiens

US-10-159-563-58

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1,296-119 | Length: | 1454 |
| Score: | 970.00 | Matches: | 187 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-970-076-2_COPY_41_227 (1-187) x US-10-159-563-58 (1-1454)

```
QY 1 GlyGlyPheAspLeuTyrPheIleLeuAlaAspLysSerGlySerValLeuHisIleSTPaaN 20
DB 264 GCGGAGATTGACCTGACTTCATTTGACAAATTCAGAAAGTGTGTCACCACTGGAAT 323
```

```
QY 21 GluIleTyrPhePheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
DB 324 GAATCTATTACTTGTGGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGATG 383
QY 41 SerPheIleValIpheserThrArgGlyThrThreumelysLeuThrGluaspArgGlu 60
DB 384 TCCCTTAATTTGTTTCTCCACCCGAGAACAACTTAATGAACCTGACAGAAACAGAGAA 443
QY 61 GluIleArgGlnIleuGlnIleuGlnIleuValLeuProGlyGlyAspThrTyrMet 80
DB 444 CAAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTACATG 503
QY 81 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGluuaspArgGlnIlyTyrArg 100
DB 504 CATGAAGATTGTAAGAGGCGCAGTGAAGACATTTATATGAAAACAGACAAAGGTACAGG 563
QY 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGlnuaspLeuPhePheTyr 120
DB 564 ACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTAT 623
QY 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIlyTyrCyvaIglVal 140
DB 624 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCAAATGTTTACTGTGTTGGTGTG 683
QY 141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 684 AAGATTTCATATAGACACAGCTGGCCCGGATTCGGACAGTAAGATCATGTGTTTCCC 743
QY 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYsLysSerCy 180
DB 744 GTCAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTGAAAGAGTCTGCG 803
QY 181 IleGluIleLeuAlaIleGlu 187
DB 804 ATCGAAATTTCTAGCAGCTGAA 824
```

RESULT 13

US-10-201-292-31

Sequence 31, Application US/10201292

Publication No. US2003014193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatSeq for Windows Version 4.0

SEQ ID NO 31

LENGTH: 1464

TYPE: DNA

ORGANISM: Homo sapiens

US-10-201-292-31

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1,316-119 | Length: | 1464 |
| Score: | 970.00 | Matches: | 187 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-31 (1-1464)

```
QY 1 GlyGlyPheAspLeuTyrPheIleLeuAlaAspLysSerGlySerValLeuHisIleSTPaaN 20
DB 133 GCGGAGATTGACCTGACTTCATTTGACAAATTCAGAAAGTGTGTCACCACTGGAAT 192
QY 21 GluIleTyrPhePheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
```

```
Db 193 GAATCTATTACTTTGTGGACAGTGGCTCAAAATTGATCGCCACAGTGTGAATG 252
Qy 41 SerpHeileValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
Db 253 TCCTTTATTGTTTCTCCACCCGAGGAAACAACCTTAATGAACTGACAGAAACAGAGAA 312
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 80
Db 313 CAATTCCTCAAGGCTTAGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATG 372
Qy 81 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArgGlnGlyTyrArg 100
Db 373 CATGAAGATTGAAAGGCCAGTGACAGATTATTAAGAAACAGACAGAGGTACAGG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 120
Db 433 ACAGCCAGCGTCATCATCTTGTGACTGAGTGAAGAACTCCATGAAAGATCTCTTTTCTAT 492
Qy 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db 493 TCAGAGAGGGAGGCTTAATAGGCTCTCGAGATCTTGCAATTGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAAGATTTCATAGACACACAGCTGGCCCGGATTGGCGACAGTAAAGATCATGTGTTCCC 612
Qy 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCTGCG 672
Qy 181 IlegIuIleLeuAlaIleGlu 187
Db 673 ATCGAAATTCTAGCAGCTGAA 693
```

RESULT 14
US-10-201-292-33

```
/ Sequence 33, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 1534
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-33
```

Alignment Scores:
Pred. No.: 1,4e-119 Length: 1534
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-33 (1-1534)

```
Qy 1 G|G|G|G|PheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrPAsn 20
Db 133 GGGGAAATTGACCTGTACTTATTTGGACAAATCAGAAAGTGTGCTGCACCACTGGAAAT 192
Qy 21 G|u|l|e|T|y|r|P|h|e|V|a|l|G|u|G|l|n|L|e|u|A|l|a|I|e|I|e|H|s|e|r|I|e|u|L|y|s|e|r|C|y|s 40
Db 193 GAATCTATTACTTTGTGGACAGTGGCTCAAAATTGATCGCCACAGTGTGAATG 252
```

```
Qy 41 SerpHeileValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
Db 253 TCCTTTATTGTTTCTCCACCCGAGGAAACAACCTTAATGAACTGACAGAAACAGAGAA 312
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 80
Db 313 CAATTCCTCAAGGCTTAGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATG 372
Qy 81 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArgGlnGlyTyrArg 100
Db 373 CATGAAGATTGAAAGGCCAGTGACAGATTATTAAGAAACAGACAGAGGTACAGG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 120
Db 433 ACAGCCAGCGTCATCATCTTGTGACTGAGTGAAGAACTCCATGAAAGATCTCTTTTCTAT 492
Qy 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db 493 TCAGAGAGGGAGGCTTAATAGGCTCTCGAGATCTTGTCAAATTGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAAGATTTCATAGACACACAGCTGGCCCGGATTGGCGACAGTAAAGATCATGTGTTCCC 612
Qy 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCTGCG 672
Qy 181 IlegIuIleLeuAlaIleGlu 187
Db 673 ATCGAAATTCTAGCAGCTGAA 693
```

RESULT 15
US-10-201-292-35

```
/ Sequence 35, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 1608
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-35
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Alignment Scores:
Pred. No.: 1,51e-119 Length: 1608
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-35 (1-1608)

```
Qy 1 G|G|G|G|PheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrPAsn 20
Db 133 GGGGAAATTGACCTGTACTTATTTGGACAAATCAGAAAGTGTGCTGCACCACTGGAAAT 192
Qy 21 G|u|l|e|T|y|r|P|h|e|V|a|l|G|u|G|l|n|L|e|u|A|l|a|I|e|I|e|H|s|e|r|I|e|u|L|y|s|e|r|C|y|s 40
Db 193 GAATCTATTACTTTGTGGACAGTGGCTCAAAATTGATCGCCACAGTGTGAATG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
```

```
Db      253 TCCTTATGTTTTCCTCACCAGAGAACACTTAATGAACCTGACAGAGACAGAA 312
Qy      61  GlnIleArgInglYleuGlnIleuGlnIleuProGlyAspThrTyrMet 80
Db      313 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGGAGAGACATTACATG 372
Qy      81  HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGlnAsnArgGlnGlyTyrArg 100
Db      373 CATGAAGGATTTGAAAGGCCACGTAGACAGATTATATGAAAACAGACAAAGGTACAGG 432
Qy      101 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPheTyr 120
Db      433 ACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAGATCTTTTCTAT 492
Qy      121 SerGlnArgGlnIleAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db      493 TCAGAGAGGAGGCTTAAGGTCTCGAGATCTTGGTCAATGTGTACTGTGTGTGTG 552
Qy      141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db      553 AAAGATTTCAATGAGACACACAGCTGCCCCGATTCGGACAGTAAAGATCATGTGTTCCC 612
Qy      161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 180
Db      613 GTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCCACTCAATTTGAAGAAAGTCTGTC 672
Qy      181 IleGlnIleLeuAlaIleGln 187
Db      673 ATCGAATCTACGACGCTGAA 693
```

Search completed: December 19, 2005, 02:10:22
Job time : 606.1 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_pzn model

Run on: December 18, 2005, 07:41:36 ; Search time 150.899 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970
Sequence: 1 GCRDLYFILDKSGSVLHMN.....LQGIHSILKKSCEIILAE 187

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 416131 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09970076/runat_14122005_111853_21065/app_query.fasta_1_2410
-DB=Published Applications NA New -QFMT=fastcap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=tblowsum62
-TRANS=human40.csl -LIST=45 -DOCALL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076@cgn_1_1_675/runat_14122005_111853_21065
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New:

1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1 | 970 | 100.0 | 5540 | 7 US-11-186-284-198 | Sequence 198, App |
| 2 | 132.5 | 13.7 | 4740 | 7 US-11-080-026-3 | Sequence 3, Appl |
| 3 | 131 | 13.5 | 11447 | 7 US-11-186-284-25 | Sequence 25, Appl |
| 4 | 122 | 12.6 | 2834 | 6 US-10-750-185-39040 | Sequence 39040, A |
| 5 | 111.5 | 11.5 | 2501 | 6 US-10-821-234-182 | Sequence 182, App |
| 6 | 109 | 11.2 | 3449 | 6 US-10-131-826A-293 | Sequence 293, App |
| 7 | 108 | 11.1 | 3564 | 6 US-10-601-368-20 | Sequence 20, Appl |
| 8 | 108 | 11.1 | 4858 | 6 US-10-601-368-19 | Sequence 19, Appl |

| | | | | | |
|----|-------|------|-------|-----------------------|--------------------|
| 9 | 107.5 | 11.1 | 3175 | 6 US-10-995-561-464 | Sequence 464, App |
| 10 | 107.5 | 11.1 | 3464 | 6 US-10-995-561-465 | Sequence 465, App |
| 11 | 107.5 | 11.1 | 3468 | 6 US-10-995-561-466 | Sequence 466, App |
| 12 | 107 | 11.0 | 1325 | 6 US-10-750-185-56394 | Sequence 56394, A |
| 13 | 104 | 10.7 | 3564 | 6 US-10-601-368-2 | Sequence 2, Appl |
| 14 | 104 | 10.7 | 3967 | 7 US-11-000-463-574 | Sequence 574, App |
| 15 | 104 | 10.7 | 3969 | 7 US-11-000-463-102 | Sequence 102, App |
| 16 | 104 | 10.7 | 5042 | 6 US-10-601-368-1 | Sequence 1, Appl |
| 17 | 101.5 | 10.5 | 47572 | 6 US-10-995-561-13356 | Sequence 13356, A |
| 18 | 95.5 | 9.8 | 3864 | 6 US-10-995-561-404 | Sequence 404, App |
| 19 | 95 | 9.8 | 3884 | 6 US-10-601-368-17 | Sequence 17, Appl |
| 20 | 94 | 9.7 | 2773 | 7 US-11-102-240-33 | Sequence 33, Appl |
| 21 | 89.5 | 9.2 | 1062 | 7 US-11-137-465-11 | Sequence 11, Appl |
| 22 | 89.5 | 9.2 | 1347 | 7 US-11-137-465-12 | Sequence 12, Appl |
| 23 | 79.5 | 8.2 | 3366 | 6 US-10-467-657-6111 | Sequence 6111, App |
| 24 | 75 | 7.7 | 3435 | 6 US-10-793-626-3648 | Sequence 3648, App |
| 25 | 74 | 7.6 | 1688 | 6 US-10-510-386-157 | Sequence 157, App |
| 26 | 73.5 | 7.6 | 1530 | 6 US-10-793-626-2879 | Sequence 2879, App |
| 27 | 73.5 | 7.6 | 2996 | 6 US-10-793-626-3563 | Sequence 3563, App |
| 28 | 73.5 | 7.6 | 3092 | 6 US-10-793-626-3559 | Sequence 3559, App |
| 29 | 73.5 | 7.6 | 3900 | 6 US-10-793-626-4177 | Sequence 4177, App |
| 30 | 73.5 | 7.6 | 1115 | 6 US-10-513-786-6 | Sequence 6, Appl |
| 31 | 73.5 | 7.6 | 1115 | 6 US-10-513-786-8 | Sequence 8, Appl |
| 32 | 73 | 7.5 | 795 | 6 US-10-793-626-387 | Sequence 387, App |
| 33 | 73 | 7.5 | 876 | 6 US-10-793-626-2635 | Sequence 2635, App |
| 34 | 73 | 7.5 | 2657 | 6 US-10-793-626-3472 | Sequence 3472, App |
| 35 | 73 | 7.5 | 3281 | 6 US-10-793-626-4324 | Sequence 4324, App |
| 36 | 73 | 7.5 | 3290 | 6 US-10-793-626-3960 | Sequence 3960, App |
| 37 | 73 | 7.5 | 3633 | 6 US-10-793-626-4307 | Sequence 4307, App |
| 38 | 73 | 7.5 | 4828 | 6 US-10-750-185-56813 | Sequence 56813, A |
| 39 | 72 | 7.4 | 2361 | 6 US-10-467-657-249 | Sequence 249, App |
| 40 | 71 | 7.3 | 1887 | 6 US-10-467-657-3083 | Sequence 3083, App |
| 41 | 71 | 7.3 | 1887 | 6 US-10-467-657-3083 | Sequence 3083, App |
| 42 | 70 | 7.2 | 1305 | 6 US-10-467-657-5693 | Sequence 5693, App |
| 43 | 70 | 7.2 | 1404 | 6 US-10-467-657-5695 | Sequence 5695, App |
| 44 | 70 | 7.2 | 96988 | 7 US-11-117-187-196 | Sequence 196, App |
| 45 | 69.5 | 7.2 | 730 | 6 US-10-750-185-61019 | Sequence 61019, A |

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Sequence 198, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITILE OF INVENTION: THERAPY FOR COLON CANCER
; FILE REFERENCES: MP01-029P2RM
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA

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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144) .. (1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 4,94e-117 Length: 5540
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-11-186-284-198 (1-5540)

QY 1 GYGLYPhEaSPLeuTYrPheIleuAspLYSeRgLYSeRValIeuhIshIstrPaen 20
   |||
Db 264 GGGGATTTCACCTTGTAACCTTCATTTGGCAATTCAGAAAGTGTGTCGACCACTGGAAAT 323

QY 21 GYLIeTYrTYrPheValGluGlnLeuAlaHisLYrPheIleSeRProGlnLeuAlaGmeC 40
   |||
Db 324 GAATCTATTAATCTTGCGAAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 383

QY 41 SeRPhelIeValPheSeRThrArgLYThrThrIeumetLYSeRThrgIuAPARgGlu 60
   |||
Db 384 TCCCTTAATGTTTCTCCACCCAGAACCACTTAATGAACTGACAGAGACAGAA 443

QY 61 GlnIleArgGlnLYeugGluGlnLeuGlnLYeValIeupRoGLYaSPThrTYrmet 80
   |||
Db 444 CAATCCGTCAAGCCGTAGAAAGAACTCCAGAAAGTTCTGCAAGAGAGACCTTACATG 503

QY 81 HisGluGlyPheGluArgAlaSeRgGluGlnIleTYrTYrGlnuAPARgGlnLYrYrAG 100
   |||
Db 504 CATGAAGAGATTGAAAGGGCCAGTGAACAGATTATTAATAACAGAAAGGGTACAGG 563

QY 101 ThrAlSeRValIleIleAlaLeuThrAPSPGLYLeuuhIseGluAPLeuPhePheTYr 120
   |||
Db 564 ACAGCCAGCCTCATCATTCCTTGACCTGATGAGAACTCCATGAAGATCTCTTTTCTAT 623

QY 121 SeRGLuArgGluAlaAsnArgSeRArgSPLeuGlyAlaIleValTYrCYsValGlyVal 140
   |||
Db 624 TCAGAGAGGAGGCTAATAGTGTCTCGAGATCTTGTCATATGTTTACTGTGTGGTGTG 683

QY 141 LYeAPheAPheAngluThrGlnLeuAlaArgIleAlaAspSeRLYsAPhIseValPhePro 160
   |||
Db 684 AAAGATTTCATATGACACACAGCTGGCCCGATTGGCGACAGTAAAGATCATGTGTTCCC 743

QY 161 ValAsnAPSPGLYPheGlnAlaLeuGlnGlyIleIleHisSeRtleuLYsLYsSeRCYs 180
   |||
Db 744 GTGAATACGCGCTTTCAGGCTGTGCAAGGCAATCATCATCATCATCATCATCATCATCAT 803

QY 181 IlegluIleuAlaAlaGlu 187
Db 804 ATCGAATTTCTAGCAGCTGAA 824

RESULT 2
US-11-080-026-3
; Sequence 3, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Lu, Chafen
; APPLICANT: Shimaoka, Motomu
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CBRF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; PRIOR FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
```

```

; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-026-3

Alignment Scores:
Pred. No.: 3,49e-06 Length: 4740
Score: 132.50 Matches: 52
Percent Similarity: 46.97% Conservative: 41
Best Local Similarity: 26.26% Mismatches: 66
Query Match: 13.66% Indels: 39
DB: 7 Gaps: 11

US-09-970-076-2_COPY_41_227 (1-187) x US-11-080-026-3 (1-4740)

QY 4 APLeuTYrPheIleuAspLYSeRgLYSeRValIeuhIshIstrPaenGluIle 22
   |||
Db 520 GACATTGCTCTTGATGATGATGCTGTGATGATCATCATCCATGACTTTCGGCGGATG 579

QY 23 TYrTYrPheValGluGlnLeuAlaHisLYrPheIleSeRProGlnLeuArgmeSeRphre 42
   |||
Db 580 AAGAGATTGCTCAACT-----GTGATGAGCAATTAATAAAGTCCAA 624

QY 43 IleValPheSeRThrArgLYThrThrIeumetLYSeRThrgIuAPARgGlu 58
   |||
Db 625 ACCCTGTTCTCT-----TTGATGCAAGTACTGAAAGATTCGGGATTCAC 669

QY 59 -----ArgGluGlnIleArgGlnLYeugGluGlnLeuGln 70
   |||
Db 670 TTACCTTCAGAGAGTTCAGAAACCTTAACCCAGATCATCGTGTGAAGCCAAATTAAG 729

QY 71 LYsValIeupRoGLYaSPThrTYrmetHisGluGlyPheGluArgAlaSeRgGluGln 90
   |||
Db 730 CAGCTGCTT-----GGGGGACACACACAGCCAGCGGAGATCCGCAAGTGTGACAGAG 783

QY 91 IleTYrTYrGluAPARgGlnLYrYrArgThrAla-----SeRValIleIleAlaLeuThr 109
   |||
Db 784 CTGTTTAACATCACCAAGGAGCCGAAAGAAATGCTTTAAATCTTAATGATTCATCAG 843

QY 110 APSPGLYLeuuhIseGluAPLeuPhePheTYrSeRgln-----ArgGluAlaAsnArg 127
   |||
Db 844 GATGAGAAAGAGTTGGCGATCCTTGATGAGATGATGATCCTCGAGAGACAGACA 903

QY 128 SeRArgSPLeuGlyAlaIleValTYrCYsValGlyValLYsAPheAPheAngluThrGln 147
   |||
Db 904 GAG-----GGAATCATGTGCTACGTATGGGTGGAGATGCTTCCGCAAGTGA 954

QY 148 LeuAlaArg-----IleAlaAspSeR-----LYsAPhIseValPhePro 160
   |||
Db 955 AAATCCCGCAAGAGCTTAATACATGCATGCATCCAGCCGCTGTATCATCGTGTCCAG 1014

QY 161 ValAsnAPSPGLYPheGlnAlaLeuGlnGlyIleIleHisSeRtleuLYsLYs 178
Db 1015 GTGAATPAC---TTGAGGCTGTGAAGACCATTCAGAACAGCTTGGGAGAGAG 1065

RESULT 3
US-11-186-284-25
; Sequence 25, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamackar, Shubhang1
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
```


TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEMO1-0292RM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 11447
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(9192)
US-11-186-284-25

Alignment Scores:
Pred. No.: 2,02e-05 Length: 11447
Score: 131.00 Matches: 59
Percent Similarity: 48.99% Conservative: 38
Best Local Similarity: 29.80% Mismatches: 75
Query Match: 13.51% Indels: 26
Gaps: 13

US-09-970-076-2_COPY_41_227 (1-187) x US-11-186-284-25 (1-11447)

QY 4 AspleutyRheilleuapRlySeGlySeVal---leuHsiStrPaenglu 22
DB 1318 GATATTCGTTTGGTGTGATGCTCATATGCGATGCAAACTTTGTTAAAGTT 1377
QY 23 TyTyRheValGluGluInleuAlaHsiLysPhe---IleSerPro---GlnLeuArgMet 40
DB 1378 AGAGCTTTTGGAAAGTTCTGTAAAGTTGAAATTCACCAAAATGAGGTCACAGTT 1437
QY 41 SerPheIleValPheSerThr-----ArgGlyThrPheMetLysLeuThrGlu 57
DB 1438 AGCTTGTGCAATACACCCGAGATCTCATATGAGTTCACTTGAAGAAATTCACCAAA 1497
QY 58 AsparGluGlnIleArgGlnGlyLeuGluGluLeuValLeuPro-----Gly 75
DB 1498 GTTGAAGATATTAATT-----GAGCAATAAACACCTTCCCTTACAGAGA 1542
QY 76 GlyAspThrTyRheHsiGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAsn 95
DB 1543 GGAATCTAACAATCTGGCAAGCAATGATTATGTCAGAGAAATTTGTGCTTAC 1602
QY 96 ArgGlnIleTyTyRgluThr-----AlaSerValIleIleAlaLeuThrAspGlyLeu 113
DB 1603 AAG---GGATCAGACAGCAATGTCGCAAGAGTCATGATTCTTATCAGCGATGGAAA--- 1656
QY 114 HsiGluapRlyPhePheTyRserGluArgGluAlaAsnArgSerArgAspLeuGlyAla 133
DB 1657 TCATCAGATGCTTTC-----AGAGATCTGTCGATTAACAGAGAAATTCAGAGTT 1707
QY 134 IleValTyRcyValAlaGlyValLysAspPheAsnGluThrGlnLeuAlaGlyIleAlaAsp 153
DB 1708 GAAATCTTTCAGTGTGTGAGATGCGCTTCCGATGCAATTTGAAAGCTATTGCTCT 1767
QY 154 -----SerLysAspHsiValAlaPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 171
DB 1768 CTCCTTCAGAGACCAATGCTGTTTACAGTGAAGAT---TTTATGCTTTTTCAGAGATA 1824
QY 172 IleHsiSerIleLeuLysLysSerCysIleGluIle-----IleuAlaAla 186
DB 1825 TCTTTGAATCTACACAGTCTATCTGCTTGAATGAGCAAGAAATGCGAGCT 1878

RESULT 4

US-10-750-185-39040/c
Sequence 39040, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39040
LENGTH: 2834
TYPE: DNA
ORGANISM: Bovine 19866880867914
US-10-750-185-39040

Alignment Scores:
Pred. No.: 4.03e-05 Length: 2834
Score: 122.00 Matches: 54
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 29.03% Mismatches: 71
Query Match: 12.58% Indels: 24
Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-10-750-185-39040 (1-2834)

QY 4 AspleutyRheilleuapRlySeGlySeValleuHsiStrPaenglu----- 21
DB 2115 GACATTTACTTCTTTATATGACGGGTCTGCGAGTACC-----CACCAAGCAGTTTCTC 2062
QY 22 ---IleTyRheValGluGluInleuAlaHsiLysPhe---IleSerProGlnLeuArg 39
DB 2061 GCCATGAAGGTGTCATGAAATGAGTGATTAAGATGTTCCAGTGGAGCGAGC---AGA 2005
QY 40 MetSerPheIleVal-PheSerThrArgGlyThrPheMetLysLeuThrGluAsp 59
DB 2004 GTCCAGTTTGGAGTCTGTCAGTCTCGAGTGAAGTCCAGATTACCTCAGCCAG 1945
QY 59 GgluGlnIleArgGlnGlyLeuGlu-----GluLeuGlnValLeuProGlu 75
DB 1944 CACTCAGTGTGGCAGGGCTTGGAGGTAGCCGTTGACAGCATCAGAG---AAGGG 1891
QY 75 YGlyAspThrTyRheHsiGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAs 95
DB 1890 AGGGGGGACCAAAATGAGGTAGGCGCTG---GGCAGATGATCCAGGTCTTTCAGAGCTC 1834
QY 95 nArgGlnGlyTyTyRgluThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHsiG 115
DB 1833 TGCTCGCAGCAA-CGTCGCTT-CGTATCTCATTTGTGTACACGAGCGCAATCTATGGA 1776
QY 115 uAspLeuPhePheTyRserGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleVal 135
DB 1775 CCGCGGTG-----GCTATGCTGCAAGAGCGCTGAGGGCCATGAGTACACAT 1728
QY 135 TyTyRcyValAlaGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLys 155
DB 1727 TTATGAGTGTGAGTCAAGATGCTAATATGCTGAGCTTCAAGAGATTCGTA----- 1673
QY 155 sAspHsiValAlaPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsiSerI 175
DB 1672 -GACAGAAATGTTTGTGTCATGAT---TTTATGCTCTTGAAGACCATCCAAAGAAAGT 1617
QY 175 eLeuLysLysSerCys 180


```
Db 372 GACCTGGTTTCATCATGACAGCTCCGACGTCTCAACACCATGACTATGCAAGATC 431
Qy 23 TyrTyrPhe---ValGluGlnLeuAlaHisIlePheIleSerProGlnLeu---ArgMet 40
Db 432 AAGAGATTCTATCTGGTACATCTTGCAATCTTGACATCTGCTGTATGTCACCCGAGTG 491
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeu-----MetValLeu 55
Db 492 GGGCTGCTCCAAAT-----GGCAGCATCTCAAGATGAGTTCTCCCTCAAGACC 542
Qy 56 ThrGluAspArgGluGlnIleArgGlnGlyLeuGlnLeuGlnValLeuProGly 75
Db 543 TTCAGAGAGAAAGTCCGAGGTGAGCGTCTCAAGAGATGCGGCATCTGTCAAGCGGC 602
Qy 76 GlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsn 95
Db 603 ACCATGACTGGGTGGGCATCCAGTAT-----GCCCTGAACATCGCATCTCAGAA 653
Qy 96 ArgGlnGlyTyrArg-----ThrAlaSerValIleIleAlaLeuThrAsp 110
Db 654 GCAGAGGGGGCCGGCCCTGAGGAGAAATGCCACGGCATATGATGATCGTACAGAT 713
Qy 111 GlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 130
Db 714 GGGAGACCTCAGACACTCGTG-----GCCAGGTGGCTGTCTAAGGACCGGAC 761
Qy 131 LeuGlyAlaIleValTyrCysValGlyVal-----LysAspPheAsnGlnThrGlnLeu 148
Db 762 ACCGGCATCTCTTAATCTTTCGTCATGTCGTGGCCAGGTAGATTCACACCTTGAAAGTCC 821
Qy 149 AlaArgIleAlaAspSerIleAspHisIleValPheProValAsnAspGlyPheGlnAlaLeu 168
Db 822 ATTGGAGTAGACCCCATGAGACCATGTCTCTTGTGCCAAT--TTCAGCCAGATT 878
Qy 169 GlnGlyIleIleHisSerIleLeuLysSerCys 180
Db 879 GAGACGCTGACCTCCGCTTCCAGAAAGATTGTGC 914

RESULT 7
US-10-601-368-20
; Sequence 20, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.00404 Length: 3564
Score: 108.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.13% Indels: 38
DB: Gaps: 9
```

```
US-09-970-076-2_COPY_41_227 (1-187) x US-10-601-368-20 (1-3564)
Qy 4 AspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleThrPheAsnGlnIleTyr 23
Db 490 GACATGCTCATTTCTTATGAGGCTCCACAGATC--TACCCTGGAGTGAAGTCSAA 546
Qy 24 TyrPheValGluGlnLeuAlaHisIlePhe---IleSerPro---GlnLeuArgMetSer 41
Db 547 CACTTCTCATCAATATCCCAAAAAGTTTACATTTGAGTGGCCCGGCGAGATCAGTGGGA 606
Qy 42 PheIleValPheSerThrArgGlyThrThrLeuMetIleValLeuThrGluAspArgGluGln 61
Db 607 ATAGTCAGATGAGAAAGATCGCTGCATGAGTTCCACCT--AATGACTACAGGCT 663
Qy 62 IleArgGlnGlyLeuGlnGluLeuGlnValLeuProGlyValAspThrTyrMetHis 81
Db 664 GTAAAAGATGTGGTGAAGCCGCGACCCACATTTAGACAGAGAGAGAGAGAGACCCGC 723
Qy 82 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 98
Db 724 ACCGCAATTTGGCATTTGATTTGACCGCTCGAGGCTTTCCAGAAAGGTGGAAGAAAGG 783
Qy 99 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 116
Db 784 GCCAAG-----AAAGTATGATTTGATCATCAGGAGGGAATCCACAGACCCAGAC 837
Qy 116 ----- 116
Db 838 CTGAGAAAGGTGATCCGGCAGACCGAGAGACACAGTGCAGATACGCTGGCCGTT 897
Qy 117 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 136
Db 898 TTGGCTACTTCAACCGCAGGGGATCAATCCAGAGACTTTTAAATGAATCAATAC 957
Qy 137 CysValGlyValLysAsp-----PheAsnGlnThrGlnLeuAlaArgIleAla 152
Db 958 ATGCCAGACACCTCGACGACAGACACTTCTTCAAGTCCACAGTACGAGCGCGCCCTG-- 1014
Qy 153 AspSerLysAspHisIleValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 170
Db 1015 -----AAGGACATTGTGATGCCCTTGGGAGAGAGATTTCACTTGGAAAGC 1062

RESULT 8
US-10-601-368-19
; Sequence 19, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.00638 Length: 4858
Score: 108.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
```


US-09-970-076-2_COPY_41_227 (1-187) x US-10-995-561-465 (1-3464)

```

QY      5 LeuTYRPhel1eLeuArylySerGlySerVal-----15
      243 GTGTAATTCCTGCTGGACACCTCGAGAGGTCCATGACATGCCCGGACATCTCTG 302
QY      16 LeuN1h1e1eTrranGlu---11eTYrTYrPhenAlGluGluLeuAlaH1slyrPhe1le 34
      303 CTCTTCCACATGAAGCAAGTTCTGTCGCCAGTTCACTACGCACTGCGAAGCAAGTTTAC 362
QY      35 SerProGluLeuArylyMetSerPhe-----11eValPheSerThrAryGlyThr 50
      363 CTGACACAGGTGGCGCTGACCTGCGCTGATAGCGCGCTGCACTCTCTGACAGAGTGAAG 422
QY      51 Th1eumetylyeuthrGluAryGluGluGluGluGluGluGluGluGluGluGlu 70
      423 GTGTTCAAGCCACCGGACGAGCGGCGCTCTTCATCAAGAACTGCGAGGCGATAGC 482
QY      71 LyValAlLeuProGlyGlyAerThrTYrMetH1eGluGlyPheGluAryAlaSerGluGln 90
      483 TCCTTCGCGCGCGGCGC-----ACCTTCAACGACCTGCGCGCTGCGCAATGACGAGAG 536
QY      91 11eTYrTYrGluAryGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 110
      537 ATCCGCGAGAGACCGGACGAGAGGCG-----ACGCTCACTTCGCGCGCTGCTATCACCGAC 590
QY      111 GlyGluLeuH1eGluAryPhePheTYrSerGluAryGluAlaArySerAryAry 130
      591 GGCACACTCAACCGGACCGCTGCGGCGGATCAAGCTGCGAGCGCGCGCGCGAG 650
QY      131 LeuGlyAla1eValTYrGlyVal-----GlyValLys 141
      651 GAGGCGATCCGCGCTTCCTGCGCGTGGCCCCAACCAAGCACTGAAGAGCGAGGCTTCGG 710
QY      142 AspPheAryGluThr-----GlnLeuAlaArg11eAlaArySerLysAryPhe 159
      711 GACATGCCGACGACCGCGGACGAGCTTACCGC-----AACGACTACGCCACC 758
QY      160 ProValAryAryGlyPheGluAlaLeuGluGly11eH1eSer11eLeu-----176
      759 ATCTGCTGATCTCCACCGAGATCTACAGACACCATCAACCGCATCATCAAGTCTAGT 818
QY      177 -----LyLysSerCysAl1eGlu11e 183
      819 AAACACGAGCCTTACGAGAGTCTACAGGTGAGTGCCTGGAAATC 866

```

RESULT 11

US-10-995-561-466
 ; Sequence 466, Application US/10995561
 ; Publication No. US20050272054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: C0001559
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: PasteSeq for Windows Version 4.0
 ; SEQ ID NO 466
 ; LENGTH: 3468
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-995-561-466

Alignment Scores:

Pred. No.: 0.00452 Length: 3468
 Score: 107.50 Matches: 50
 Percent Similarity: 40.28% Conservative: 37
 Best Local Similarity: 23.15% Mismatches: 84
 Query Match: 11.08% Indels: 45

DB: 6 Gaps: 9

US-09-970-076-2_COPY_41_227 (1-187) x US-10-995-561-466 (1-3468)

```

QY      5 LeuTYRPhel1eLeuArylySerGlySerVal-----15
      243 GTGTAATTCCTGCTGGACACCTCGAGAGGTCCATGACATGCCCGGACATCTCTG 302
QY      16 LeuN1h1e1eTrranGlu---11eTYrTYrPhenAlGluGluLeuAlaH1slyrPhe1le 34
      303 CTCTTCCACATGAAGCAAGTTCTGTCGCCAGTTCACTACGCACTGCGAAGCAAGTTTAC 362
QY      35 SerProGluLeuArylyMetSerPhe-----11eValPheSerThrAryGlyThr 50
      363 CTGACACAGGTGGCGCTGACCTGCGCTGATAGCGCGCTGCACTCTCTGACAGAGTGAAG 422
QY      51 Th1eumetylyeuthrGluAryGluGluGluGluGluGluGluGluGluGluGlu 70
      423 GTGTTCAAGCCACCGGACGAGCGGCGCTCTTCATCAAGAACTGCGAGGCGATAGC 482
QY      71 LyValAlLeuProGlyGlyAerThrTYrMetH1eGluGlyPheGluAryAlaSerGluGln 90
      483 TCCTTCGCGCGCGGCGC-----ACCTTCAACGACCTGCGCGCTGCGCAATGACGAGAG 536
QY      91 11eTYrTYrGluAryGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 110
      537 ATCCGCGAGAGACCGGACGAGAGGCG-----ACGCTCACTTCGCGCGCTGCTATCACCGAC 590
QY      111 GlyGluLeuH1eGluAryPhePheTYrSerGluAryGluAlaArySerAryAry 130
      591 GGCACACTCAACCGGACCGCTGCGGCGGATCAAGCTGCGAGCGCGCGCGCGAG 650
QY      131 LeuGlyAla1eValTYrGlyVal-----GlyValLys 141
      651 GAGGCGATCCGCGCTTCCTGCGCGTGGCCCCAACCAAGCACTGAAGAGCGAGGCTTCGG 710
QY      142 AspPheAryGluThr-----GlnLeuAlaArg11eAlaArySerLysAryPhe 159
      711 GACATGCCGACGACCGCGGACGAGCTTACCGC-----AACGACTACGCCACC 758
QY      160 ProValAryAryGlyPheGluAlaLeuGluGly11eH1eSer11eLeu-----176
      759 ATCTGCTGATCTCCACCGAGATCTACAGACACCATCAACCGCATCATCAAGTCTAGT 818
QY      177 -----LyLysSerCysAl1eGlu11e 183
      819 AAACACGAGCCTTACGAGAGTCTACAGGTGAGTGCCTGGAAATC 866

```

RESULT 12

US-10-750-185-56394
 ; Sequence 56394, Application US/10750185
 ; Publication No. US200502603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 56394
 ; LENGTH: 1325
 ; TYPE: DNA
 ; ORGANISM: Bovine
 ; US-10-750-185-56394

US-10-750-185-56394


```
Db      775 ACGGCATTGGCATTTGCAACGCTCAGAGGCTTTCAGAAAGGTGGAAGAAGA 834
Qy      99 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 116
Db      835 GCCAAG-----AAGGTGATGATTGTTCATCAGATGGGAGTCCACAGACAGCCAGAC 888
Qy      116 ----- 116
Db      889 CTGGAGAAAGTGATCCAGCAAAAGCAAGACAGTAACAAGATATGGCGTGGCCGTC 948
Qy      117 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 136
Db      949 CTGGGCTACTACAAACCGCAGGGGATCAATCCAGAAACTTTTCTAAATGAATCAATATAC 1008
Qy      137 CysValGlyValIysAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 152
Db      1009 ATGCCAGTGACCCCTGATGACAAAGCACTTCTTCAATGTCTCATGATGAGGCTGCTTG--- 1065
Qy      153 AspSerIysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 170
Db      1066 -----AAGGACATTTGTTCGATGCCCTGGGGGACAGAACTTTCAGCCTGGAAGGC 1113
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Search completed: December 19, 2005, 02:30:25
Job time : 166.899 secs

STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-37

Query Match 15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 3 DLYFLDKSGV-LHHMNEIYFVEQLAHKFI SPOLRMSPFIVSTRGTTLMKLT----- 56
DB 142 DIAFLDGGSSINQRFQAKMDPVKALMGSEFASTSLFSLMQSNLIKTHFTTEPKNLI 201
QY 57 DREQIRQGLEELQKVLPGDVTYMHGFEFASSEQIYENRQGYTA-SVIALTDGELHED 115
DB 202 DPQSLVDPIVQD-----GLTYTATGIRTYMBELFHSKXSRKSAKKILVITDGGKYRD 256
QY 116 LEFYSE--REANRSRLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
DB 257 PLEYSDVTPADKA--GIIRYAIQVGDAPFOEPTALKELNTIGSAPPQDHVFVGN-FAA 312
QY 167 LGGIHSILKK 177
DB 313 LRSIQROLOEK 323

RESULT 3
US-08-485-618-37
Sequence 37, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-37

Query Match 15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 3 DLYFLDKSGV-LHHMNEIYFVEQLAHKFI SPOLRMSPFIVSTRGTTLMKLT----- 56
DB 142 DIAFLDGGSSINQRFQAKMDPVKALMGSEFASTSLFSLMQSNLIKTHFTTEPKNLI 201
QY 57 DREQIRQGLEELQKVLPGDVTYMHGFEFASSEQIYENRQGYTA-SVIALTDGELHED 115
DB 202 DPQSLVDPIVQD-----GLTYTATGIRTYMBELFHSKXSRKSAKKILVITDGGKYRD 256
QY 116 LEFYSE--REANRSRLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
DB 257 PLEYSDVTPADKA--GIIRYAIQVGDAPFOEPTALKELNTIGSAPPQDHVFVGN-FAA 312
QY 167 LGGIHSILKK 177
DB 313 LRSIQROLOEK 323

RESULT 4
US-08-362-652-37
Sequence 37, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652

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: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,889
: FILING DATE: 5-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32391
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 37:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1151 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-605-672-37

```

```

Query Match          15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4,7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

```

```

QY 3 DLYFILDKSGSV-LHMHNEIYFVEQLAHKFISPOLMSPFIVSTGTTLMKLT-----56
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 142 DIAFLIDSGSINQRPQAKMDFKALMGFASTSTLFSIMQYSNILKHTFTPEFNIL 201
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 57 DRQIQGLELELQKVLPGDPTMHGEPERASQIYYENRGYRTA-SVITALDGELEHD 115
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 202 DPQSLVDPIYQLQ-----GLTYATGIRTYMEELFHSKNGSRKSAKKILVITDGOQYRD 256
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 116 LFFYSE--REANRSRDGAIVYCVGYD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 257 PLEYSVPIPADKA---GIIRYALGVDAFOEPTALKELNTIGSAPPQDHVFKGN-FAA 312
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 167 LQGIHSILKK 177
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 313 LRSTQRLQLEK 323

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RESULT 5
US-08-605-672-37
: Sequence 37, Application US/08605672
: Patent No. 5817515
: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Michael
: TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 103
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive, 6300 Sear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/605,672
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993

```

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,889
: FILING DATE: 5-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/362,652
: FILING DATE: 21-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32684
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 37:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1151 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-605-672-37

```

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Query Match          15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4,7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

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QY 3 DLYFILDKSGSV-LHMHNEIYFVEQLAHKFISPOLMSPFIVSTGTTLMKLT-----56
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 142 DIAFLIDSGSINQRPQAKMDFKALMGFASTSTLFSIMQYSNILKHTFTPEFNIL 201
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 57 DRQIQGLELELQKVLPGDPTMHGEPERASQIYYENRGYRTA-SVITALDGELEHD 115
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 202 DPQSLVDPIYQLQ-----GLTYATGIRTYMEELFHSKNGSRKSAKKILVITDGOQYRD 256
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 116 LFFYSE--REANRSRDGAIVYCVGYD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 257 PLEYSVPIPADKA---GIIRYALGVDAFOEPTALKELNTIGSAPPQDHVFKGN-FAA 312
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 167 LQGIHSILKK 177
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 313 LRSTQRLQLEK 323

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RESULT 6
US-08-482-293A-37
: Sequence 37, Application US/08482293A
: Patent No. 5831029
: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Michael
: TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 103
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive, 6300 Sear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,293A
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: APPLICATION NUMBER: US 08/286,889

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/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-482-293A-37

Query Match          15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFTVSTRTGTTMLKLT----- 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 142 DIAFLIDSGSINQRFQAKDFVAKLMGEFFASTSTLFSIMQYSNLKTHFTTFEKNIL 201
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 DREQIRQGLEELQKVLPGSDTYMHGFEFASRSEIYYENRQGYRTA-SVIALTDGELHED 115
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 202 DPQSLVDPIVQLQ-----GLTYRTATGIRTWMEELHSHKSKRSKAKILLVITDQKXND 256
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LFFYSE--REANRSRDGAIVYCVGKD-FNE-TQLARI-----ADSKDHVPVNDGFOA 166
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 257 PLEYSDVIPADAKA---GIRVAIGVGDAFQEPFLALKEINTIGSAPPQDHVFVGN-FAA 312
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 LQGIHSILKK 177
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 313 LRSIORLOEK 323

RESULT 7
US-08-943-363-37
/ Sequence 37, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-943-363-37

Query Match          15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFTVSTRTGTTMLKLT----- 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 142 DIAFLIDSGSINQRFQAKDFVAKLMGEFFASTSTLFSIMQYSNLKTHFTTFEKNIL 201
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 DREQIRQGLEELQKVLPGSDTYMHGFEFASRSEIYYENRQGYRTA-SVIALTDGELHED 115
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 202 DPQSLVDPIVQLQ-----GLTYRTATGIRTWMEELHSHKSKRSKAKILLVITDQKXND 256
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LFFYSE--REANRSRDGAIVYCVGKD-FNE-TQLARI-----ADSKDHVPVNDGFOA 166
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 257 PLEYSDVIPADAKA---GIRVAIGVGDAFQEPFLALKEINTIGSAPPQDHVFVGN-FAA 312
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 LQGIHSILKK 177
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 313 LRSIORLOEK 323

RESULT 8
US-09-193-043-37
/ Sequence 37, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ TITLE OF INVENTION: No. 6251395el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ EARLIER FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 37
/ LENGTH: 1151
/ TYPE: PRT
/ ORGANISM: Rattus rattus
/ US-09-193-043-37

Query Match          15.0%; Score 141.5; DB 2; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFTVSTRTGTTMLKLT----- 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 142 DIAFLIDSGSINQRFQAKDFVAKLMGEFFASTSTLFSIMQYSNLKTHFTTFEKNIL 201
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[illegible]

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RESULT 9
US-09-688-307A-37
Sequence 37, Application US/09688307A
Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/153,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
NUMBER OF FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 1151
TYPE: PRT
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: misc_feature
LOCATION: 361
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 486
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 506
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1117
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-688-307A-37

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| | | | | |
|--------------------------|--------|--------------------|------------|--------------|
| Query Match | 15.0%; | Score 141.5; | DB 2; | Length 1151; |
| Best Local Similarity | 27.7%; | Pred. No. 4.7e-07; | | |
| Matches 53; Conservative | 38; | Mismatches 75; | Indels 25; | Gaps 10; |

Qy 3 DLVFLIDKSGSV-LHHMNIYFVFLQALHKFTSPOLRMSPLVFSTGTGLMKLKE-----56
 Db 142 DIALFLDGGSGSIQGRFQAKMDPFVALNGCFRSTSTPLSMQYSNLIKTHPTTFEPFNIL 201
 Qy 57 DNEQIRQGLBELQKLVPGSDTYMHGFEFASQIYYENRQGYRTA-SVIALTDGLIEDH 115

Db 202 DQGLTADPITVQIQ-----GLTFTATGIRTWEEELFHSNGSRKSAKILLIVITDGGKYRD 256
 QY 116 LFFYSE--REANRSDLGAIYCVGKVD-FNE-TQLARI-----ADSKDHVPFYNDGFOA 166
 Db 257 PLEYSVIIPADKA---GIIRYAIQVGDAPFALPALKELNTIGSAPPQDHVFKVGN-FAA 312
 QY 167 LOGIHSILKK 177
 Db 313 LRSIQROLOEK 323

```

RESULT 10
US-09-350-259-37
; Sequence 37, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/352,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Rattus rattus
; US-09-350-259-37

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[illegible]

RESULT 11
US-08-485-618-55
Sequence 55, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-55

Query Match 15.0%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFLDKSGSV-LHMMNEIYFVEQLAHKFIISPOLMSFIVSTRGTLMLKTE----- 56
DB 152 DIAFLDSSGSINORDPAQMKDFKALMGEPASTSTLFSLMQYSNLKHTFTTERKNIL 211
QY 57 DREQIRQGLEBLQKVLPGDPTVMHGEFERASQIYYENRQGYRTA-SVIALTDGELHED 115
DB 212 DPQSLVDPIVQLQ-----GLTYTATGIRTYMELFHSKNGSRKSAKKILVITDGGCKYRD 266
QY 116 LFPEYSE--REANRSRLGAIYVCVKD-FNE-TOLARI-----ADSKDHFVPYNGFOA 166
DB 267 PLEYSVDVIPADKKA--GIIRYAIGVDADFQEPALKELNTIGSAPPQDHVFKVGN-FAA 322
QY 167 LOGIHSILKK 177
DB 323 LRSIORQLQEK 333

RESULT 12
US-08-362-652-55
Sequence 55, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago

STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-55

Query Match 15.0%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFLDKSGSV-LHMMNEIYFVEQLAHKFIISPOLMSFIVSTRGTLMLKTE----- 56
DB 152 DIAFLDSSGSINORDPAQMKDFKALMGEPASTSTLFSLMQYSNLKHTFTTERKNIL 211
QY 57 DREQIRQGLEBLQKVLPGDPTVMHGEFERASQIYYENRQGYRTA-SVIALTDGELHED 115
DB 212 DPQSLVDPIVQLQ-----GLTYTATGIRTYMELFHSKNGSRKSAKKILVITDGGCKYRD 266
QY 116 LFPEYSE--REANRSRLGAIYVCVKD-FNE-TOLARI-----ADSKDHFVPYNGFOA 166
DB 267 PLEYSVDVIPADKKA--GIIRYAIGVDADFQEPALKELNTIGSAPPQDHVFKVGN-FAA 322
QY 167 LOGIHSILKK 177
DB 323 LRSIORQLQEK 333

RESULT 13
US-08-605-672-55
Sequence 55, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:07 ; Search time 54.5297 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Perfect score: 943
Sequence: 1 GFDLYFLDKSGSVLHHMNE.....DGFQALQGIHSLKKSCE 181

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|---------------------|
| 1 | 943 | 100.0 | 328 | 4 US-10-038-307-26 | Sequence 26, Appl |
| 2 | 943 | 100.0 | 328 | 3 US-10-201-292-26 | Sequence 26, Appl |
| 3 | 943 | 100.0 | 333 | 3 US-09-796-753-12 | Sequence 12, Appl |
| 4 | 943 | 100.0 | 333 | 4 US-10-038-307-2 | Sequence 2, Appl |
| 5 | 943 | 100.0 | 333 | 4 US-10-201-292-2 | Sequence 2, Appl |
| 6 | 943 | 100.0 | 333 | 6 US-11-047-278-8 | Sequence 8, Appl |
| 7 | 943 | 100.0 | 342 | 4 US-10-038-307-22 | Sequence 22, Appl |
| 8 | 943 | 100.0 | 342 | 4 US-10-201-292-22 | Sequence 22, Appl |
| 9 | 943 | 100.0 | 345 | 4 US-10-038-307-24 | Sequence 24, Appl |
| 10 | 943 | 100.0 | 345 | 4 US-10-201-292-24 | Sequence 24, Appl |
| 11 | 943 | 100.0 | 368 | 6 US-11-047-278-2 | Sequence 2, Appl |
| 12 | 943 | 100.0 | 403 | 3 US-09-833-245-621 | Sequence 621, Appl |
| 13 | 943 | 100.0 | 460 | 4 US-10-201-292-28 | Sequence 28, Appl |
| 14 | 943 | 100.0 | 479 | 4 US-10-201-292-32 | Sequence 32, Appl |
| 15 | 943 | 100.0 | 504 | 4 US-10-201-292-34 | Sequence 34, Appl |
| 16 | 943 | 100.0 | 529 | 4 US-10-201-292-36 | Sequence 36, Appl |
| 17 | 943 | 100.0 | 551 | 4 US-10-038-307-18 | Sequence 18, Appl |
| 18 | 943 | 100.0 | 551 | 4 US-10-201-292-18 | Sequence 18, Appl |
| 19 | 943 | 100.0 | 564 | 3 US-09-918-715-187 | Sequence 187, Appl |
| 20 | 943 | 100.0 | 564 | 3 US-09-918-715-232 | Sequence 232, Appl |
| 21 | 943 | 100.0 | 564 | 4 US-10-038-307-20 | Sequence 20, Appl |
| 22 | 943 | 100.0 | 564 | 4 US-10-201-292-20 | Sequence 20, Appl |
| 23 | 943 | 100.0 | 564 | 4 US-10-301-822-199 | Sequence 199, Appl |
| 24 | 943 | 100.0 | 564 | 4 US-10-408-765A-1823 | Sequence 1823, Appl |
| 25 | 943 | 100.0 | 564 | 4 US-10-474-794-187 | Sequence 187, Appl |
| 26 | 943 | 100.0 | 564 | 4 US-10-474-794-232 | Sequence 232, Appl |
| 27 | 943 | 100.0 | 564 | 5 US-10-979-159-187 | Sequence 187, Appl |

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|----|-----|-------|-----|---------------------|--------------------|
| 28 | 943 | 100.0 | 564 | 5 US-10-979-159-232 | Sequence 232, Appl |
| 29 | 943 | 100.0 | 564 | 6 US-11-047-278-6 | Sequence 6, Appl |
| 30 | 938 | 99.5 | 562 | 3 US-09-833-245-620 | Sequence 620, Appl |
| 31 | 934 | 99.0 | 562 | 3 US-09-918-715-194 | Sequence 194, Appl |
| 32 | 934 | 99.0 | 562 | 3 US-09-918-715-301 | Sequence 301, Appl |
| 33 | 934 | 99.0 | 562 | 4 US-10-474-794-194 | Sequence 194, Appl |
| 34 | 934 | 99.0 | 562 | 4 US-10-474-794-301 | Sequence 301, Appl |
| 35 | 934 | 99.0 | 562 | 5 US-10-979-159-194 | Sequence 194, Appl |
| 36 | 934 | 99.0 | 562 | 5 US-10-979-159-301 | Sequence 301, Appl |
| 37 | 933 | 98.9 | 460 | 4 US-10-201-292-30 | Sequence 30, Appl |
| 38 | 922 | 97.8 | 534 | 4 US-10-038-307-12 | Sequence 12, Appl |
| 39 | 922 | 97.8 | 534 | 4 US-10-201-292-12 | Sequence 12, Appl |
| 40 | 922 | 97.8 | 543 | 4 US-10-038-307-10 | Sequence 10, Appl |
| 41 | 922 | 97.8 | 543 | 4 US-10-038-307-14 | Sequence 14, Appl |
| 42 | 922 | 97.8 | 543 | 4 US-10-038-307-16 | Sequence 16, Appl |
| 43 | 922 | 97.8 | 543 | 4 US-10-201-292-10 | Sequence 10, Appl |
| 44 | 922 | 97.8 | 543 | 4 US-10-201-292-14 | Sequence 14, Appl |
| 45 | 922 | 97.8 | 543 | 4 US-10-201-292-16 | Sequence 16, Appl |

ALIGNMENTS

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RESULT 1
US-10-038-307-26
; Sequence 26, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALRY
; TITLE OR INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-26

Query Match      100.0%; Score 943; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  IROGLELEQLVLRPGDVTYMEHGFERASEQIYYENRQGYRTASVIALTDGLHEDLFYS 120
DB      42  GFDLYFLDKSGSVLHHMNEIYFVEQLAKHFIISPOLRMSFIYFSTRGTTMLKLTREQ 101

QY      61  IROGLELEQLVLRPGDVTYMEHGFERASEQIYYENRQGYRTASVIALTDGLHEDLFYS 120
DB      102  IROGLELEQLVLRPGDVTYMEHGFERASEQIYYENRQGYRTASVIALTDGLHEDLFYS 161

QY      121  ERENANSRDGLAIVYCYGVKDFNETQLARLADSKDHVPVNDGFQALOGIHSILKKSCT 180
DB      162  ERENANSRDGLAIVYCYGVKDFNETQLARLADSKDHVPVNDGFQALOGIHSILKKSCT 221

QY      181  E 181
DB      222  E 222

RESULT 2
US-10-201-292-26
; Sequence 26, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
```

```

; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-201-292-26

Query Match      100.0%; Score 943; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSFVFSRGTTLMLKLTEDRQ 60
      42  GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSFVFSRGTTLMLKLTEDRQ 101
DB
QY      61  IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 120
      102  IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 161
DB
QY      121  EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 180
      162  EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 221
DB
QY      181  E 181
      222  E 222
DB
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; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-753-12

Query Match      100.0%; Score 943; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSFVFSRGTTLMLKLTEDRQ 60
      42  GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSFVFSRGTTLMLKLTEDRQ 101
DB
QY      61  IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 120
      102  IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 161
DB
QY      121  EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 180
      162  EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 221
DB
QY      181  E 181
      222  E 222
DB

RESULT 4
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-307-2

Query Match      100.0%; Score 943; DB 4; Length 333;
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Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 180
DB 162 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 221

QY 181 E 181
DB 222 E 222

RESULT 5

US-10-201-292-2
Sequence 2, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201.292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-2

Query Match 100.0%; Score 943; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 180
DB 162 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 221

QY 181 E 181
DB 222 E 222

RESULT 6

US-11-047-278-8
Sequence 8, Application US/11047278
Publication No. US20050196407A1
GENERAL INFORMATION:
APPLICANT: Young, John A. T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.97745

CURRENT APPLICATION NUMBER: US/11/047.278
CURRENT FILING DATE: 2005-01-31
PRIOR APPLICATION NUMBER: US/09/970.076
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-11-047-278-8

Query Match 100.0%; Score 943; DB 6; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 180
DB 162 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 221

RESULT 7

US-10-038-307-22
Sequence 22, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038.307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-22

Query Match 100.0%; Score 943; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 60
DB 51 GFDLYFLDKSGSVLHHMNEIYYFVEQLAHKFISPOLRMSFIVSTRTTLMKLTEDREQ 110
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 111 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 170
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 180
DB 171 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHFVPVNDGFOALOGIHSILKKSCT 230
QY 181 E 181

Db 231 E 231

RESULT 8

US-10-201-292-22
; Sequence 22, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-22

Query Match 100.0%; Score 943; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60

Db 51 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 110

QY 61 IRGLEELQKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 120

Db 111 IRGLEELQKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 170

QY 121 EREANRSRDIGAIYCVGVKDFNETQARIADSKDHFVPVNDGFQALOGIHSILKKSCT 180

Db 171 EREANRSRDIGAIYCVGVKDFNETQARIADSKDHFVPVNDGFQALOGIHSILKKSCT 230

QY 181 E 181

Db 231 E 231

RESULT 9

US-10-038-307-24
; Sequence 24, Application US/10038307
; Publication No. US20030134766A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-24

Query Match 100.0%; Score 943; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60

Db 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101

QY 61 IRGLEELQKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 120

Db 102 IRGLEELQKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 161

QY 121 EREANRSRDIGAIYCVGVKDFNETQARIADSKDHFVPVNDGFQALOGIHSILKKSCT 180

Db 162 EREANRSRDIGAIYCVGVKDFNETQARIADSKDHFVPVNDGFQALOGIHSILKKSCT 221

QY 181 E 181

Db 222 E 222

RESULT 10

US-10-201-292-24
; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-24

Query Match 100.0%; Score 943; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60

Db 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101

QY 61 IRGLEELQKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 120

Db 102 IRGLEELQKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 161

QY 121 EREANRSRDIGAIYCVGVKDFNETQARIADSKDHFVPVNDGFQALOGIHSILKKSCT 180

Db 162 EREANRSRDIGAIYCVGVKDFNETQARIADSKDHFVPVNDGFQALOGIHSILKKSCT 221

QY 181 E 181

Db 222 E 222

RESULT 11

US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481

PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
US-11-047-278-2

Query Match 100.0%; Score 943; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 2e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 ERENRRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOALOGIHSILKXSCI 180
DB 162 ERENRRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOALOGIHSILKXSCI 221
QY 181 E 181
DB 222 E 222

RESULT 12

US-09-833-245-621
Sequence 621, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PFS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-621

Query Match 100.0%; Score 943; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 2.3e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 ERENRRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOALOGIHSILKXSCI 180
DB 162 ERENRRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOALOGIHSILKXSCI 221
QY 181 E 181
DB 222 E 222

RESULT 13

US-10-201-292-28
Sequence 28, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-28

Query Match 100.0%; Score 943; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 ERENRRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOALOGIHSILKXSCI 180
DB 162 ERENRRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOALOGIHSILKXSCI 221
QY 181 E 181
DB 222 E 222

RESULT 14

US-10-201-292-32
Sequence 32, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-32

Query Match 100.0%; Score 943; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.9e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQ 101

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QY      61  IROGLEELQKVLPGGDTYMHGEPERASEOIYENRQGYRTASVIALTDGELHEDLFFYS 120
      102  IROGLEELQKVLPGGDTYMHGEPERASEOIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY      121  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHHSILKSCIT 180
      162  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHHSILKSCIT 221
QY      181  E 181
      222  E 222
Db

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RESULT 15
US-10-201-292-34
; Sequence 34, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 504
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-201-292-34

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Query Match      100.0%; Score 943; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.1e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GFDLYFTLDKSGSVLHMHNEIYFVEQLAKFTSPQLRMSFIVPSTRGTTLMKLTEDPREQ 60
      42  GFDLYFTLDKSGSVLHMHNEIYFVEQLAKFTSPQLRMSFIVPSTRGTTLMKLTEDPREQ 101
QY      61  IROGLEELQKVLPGGDTYMHGEPERASEOIYENRQGYRTASVIALTDGELHEDLFFYS 120
      102  IROGLEELQKVLPGGDTYMHGEPERASEOIYENRQGYRTASVIALTDGELHEDLFFYS 161
Db      121  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHHSILKSCIT 180
      162  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHHSILKSCIT 221
QY      181  E 181
      222  E 222
Db

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Search completed: December 14, 2005, 11:59:02
 Job time : 55.6964 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 2.65999 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Perfect score: 943
Sequence: 1 GFLYFLIDKSGSVLHMHNE.....DGFQALQGIHSLKKSCTE 181

Scoring table:

BLOSUM62

Searched: Gap0 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA New:
1: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB pep.*
2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB pep.*
3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB pep.*
4: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB pep.*
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6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB pep.*
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8: /cgn2_6/prodata/1/pubppa/US00_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1 | 943 | 100.0 | 564 | US-11-186-284-199 | Sequence 199, App |
| 2 | 132.5 | 14.1 | 1152 | US-11-080-026-4 | Sequence 4, Appl |
| 3 | 126.5 | 13.4 | 3063 | US-11-186-284-26 | Sequence 26, Appl |
| 4 | 109 | 11.6 | 915 | US-10-131-826A-294 | Sequence 294, Appl |
| 5 | 109 | 11.6 | 956 | US-11-113-424-39 | Sequence 39, Appl |
| 6 | 108 | 11.5 | 1141 | US-10-601-368-24 | Sequence 24, Appl |
| 7 | 108 | 11.5 | 1166 | US-10-601-368-22 | Sequence 22, Appl |
| 8 | 108 | 11.5 | 1188 | US-10-601-368-21 | Sequence 21, Appl |
| 9 | 105.5 | 11.2 | 739 | US-11-057-047-2 | Sequence 2, Appl |
| 10 | 105.5 | 11.2 | 764 | US-11-057-047-1 | Sequence 1, Appl |
| 11 | 105.5 | 11.2 | 798 | US-10-821-234-1034 | Sequence 1034, App |
| 12 | 104 | 11.0 | 1141 | US-10-601-368-6 | Sequence 6, Appl |
| 13 | 104 | 11.0 | 1166 | US-10-601-368-4 | Sequence 3, Appl |
| 14 | 104 | 11.0 | 1188 | US-10-601-368-3 | Sequence 3, Appl |
| 15 | 104 | 11.0 | 1188 | US-11-000-463-338 | Sequence 338, App |
| 16 | 104 | 11.0 | 1188 | US-11-000-463-810 | Sequence 810, App |
| 17 | 103.5 | 11.0 | 182 | US-10-601-368-25 | Sequence 25, Appl |
| 18 | 100.5 | 10.7 | 828 | US-10-995-561-983 | Sequence 983, App |
| 19 | 100.5 | 10.7 | 918 | US-10-995-561-981 | Sequence 981, App |
| 20 | 100.5 | 10.7 | 1019 | US-10-995-561-982 | Sequence 982, App |
| 21 | 99.5 | 10.6 | 182 | US-10-601-368-7 | Sequence 7, Appl |
| 22 | 97.5 | 10.3 | 761 | US-11-057-047-6 | Sequence 6, Appl |
| 23 | 95.5 | 10.1 | 1179 | US-11-057-125-1 | Sequence 921, App |
| 24 | 95.5 | 10.1 | 1196 | US-10-995-561-921 | Sequence 921, App |
| 25 | 94 | 10.0 | 678 | US-11-102-240-34 | Sequence 34, Appl |

| | | | | | |
|----|------|-----|------|--------------------|--------------------|
| 26 | 91.5 | 9.7 | 1167 | US-11-097-125-2 | Sequence 2, Appl |
| 27 | 90 | 9.5 | 1167 | US-10-601-368-18 | Sequence 18, Appl |
| 28 | 89.5 | 9.5 | 353 | US-11-137-465-44 | Sequence 44, Appl |
| 29 | 89.5 | 9.5 | 448 | US-11-137-465-45 | Sequence 45, Appl |
| 30 | 74 | 7.8 | 384 | US-10-510-386-158 | Sequence 158, App |
| 31 | 73.5 | 7.8 | 509 | US-10-793-626-2880 | Sequence 2880, App |
| 32 | 73 | 7.7 | 264 | US-10-793-626-388 | Sequence 388, App |
| 33 | 73 | 7.7 | 292 | US-10-793-626-2636 | Sequence 2636, App |
| 34 | 72 | 7.6 | 786 | US-10-467-657-103 | Sequence 103, App |
| 35 | 70 | 7.4 | 488 | US-10-467-657-5636 | Sequence 5636, App |
| 36 | 69.5 | 7.4 | 489 | US-10-467-657-7846 | Sequence 7846, App |
| 37 | 69.5 | 7.4 | 629 | US-10-467-657-250 | Sequence 250, App |
| 38 | 69.5 | 7.4 | 629 | US-10-467-657-3084 | Sequence 3084, App |
| 39 | 69 | 7.3 | 242 | US-10-467-657-7306 | Sequence 7306, App |
| 40 | 68.5 | 7.3 | 1734 | US-11-192-867-6 | Sequence 6, Appl |
| 41 | 68.5 | 7.3 | 1734 | US-11-193-715-6 | Sequence 6, Appl |
| 42 | 68 | 7.2 | 348 | US-10-674-767-4 | Sequence 4, Appl |
| 43 | 66.5 | 7.1 | 1538 | US-10-995-561-772 | Sequence 772, App |
| 44 | 66.5 | 7.1 | 1804 | US-10-513-786-2 | Sequence 2, Appl |
| 45 | 66.5 | 7.1 | 3704 | US-10-513-786-1 | Sequence 1, Appl |

ALIGNMENTS

| | | | | | |
|---|-----|--|-----|--|--|
| RESULT 1 | | | | | |
| US-11-186-284-199 | | | | | |
| Sequence 199, Application US/11186284 | | | | | |
| Publication No. US20050266493A1 | | | | | |
| GENERAL INFORMATION: | | | | | |
| APPLICANT: Millennium Pharmaceuticals, Inc. | | | | | |
| APPLICANT: Berger, Allison | | | | | |
| APPLICANT: Guillemette, Tracy L. | | | | | |
| APPLICANT: Kamatkar, Shubhangt | | | | | |
| APPLICANT: Schlegel, Robert | | | | | |
| APPLICANT: Monahan, John B. | | | | | |
| APPLICANT: Thibodeau, Stephen N. | | | | | |
| APPLICANT: Burgart, Lawrence J. | | | | | |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND | | | | | |
| TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND | | | | | |
| FILE REFERENCE: MEMO1-029P2RM | | | | | |
| CURRENT APPLICATION NUMBER: US/11/186,284 | | | | | |
| CURRENT FILING DATE: 2005-07-21 | | | | | |
| PRIOR APPLICATION NUMBER: US/10/301,822 | | | | | |
| PRIOR FILING DATE: 2002-11-21 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/339,971 | | | | | |
| PRIOR FILING DATE: 2001-12-10 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/361,978 | | | | | |
| PRIOR FILING DATE: 2002-03-05 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/381,988 | | | | | |
| PRIOR FILING DATE: 2002-05-20 | | | | | |
| NUMBER OF SEQ ID NOS: 228 | | | | | |
| SOFTWARE: FastSeq for Windows Version 4.0 | | | | | |
| SEQ ID NO 199 | | | | | |
| LENGTH: 564 | | | | | |
| TYPE: PRT | | | | | |
| ORGANISM: Homo Sapiens | | | | | |
| US-11-186-284-199 | | | | | |
| Query Match | | | | | |
| Best Local Similarity 100.0%; Pred. No. 1.3e-84; | | | | | |
| Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | |
| QY | 1 | GFLYFLIDKSGSVLHMHNEIYFVEQLAKFISPOLRMSFIVSTRGTTMLKLTEDREQ | 60 | | |
| DB | 42 | GFLYFLIDKSGSVLHMHNEIYFVEQLAKFISPOLRMSFIVSTRGTTMLKLTEDREQ | 101 | | |
| QY | 61 | IRGGLBELQVLPFGDPTVMEGPERASBOIYNNRCGYRTASVITLTDGELEDLFFVS | 120 | | |
| DB | 102 | IRGGLBELQVLPFGDPTVMEGPERASBOIYNNRCGYRTASVITLTDGELEDLFFVS | 161 | | |
| QY | 121 | ERANNSRDGALVYCVGVDFNETQLARIADSKDHVPVNDGFQALQGIHSLKKSCTE | 180 | | |


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? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/052263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/053352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/055588
? PRIOR FILING DATE: 1997-09-19
? Remaining seq ID Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 294
? LENGTH: 915
? TYPE: FRT
? ORGANISM: Homo Sapien
? OS-10-131-826A-294

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Query Match 11.6%; Score 109; DB 6; Length 915;
 Best Local Similarity 24.0%; Pred. No. 0.0045;
 Matches 46; Conservative 43; Mismatches 77; Indels 26; Gaps 10;

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QY      3 DLVFIIDLKSSV-LHHMNEYF-YEQLAHKFISPOL-RMSPIVSTGTGLT-----MKL 54
Db      57 DLVFIIDSSKSVTHDYAKKEFIYDILPFDIGPVYTRVGLLQY--GSTVKOEFSFKT 111
QY      55 TEDREQIROLLELOKYLPGCDTYMHGEFERASEQIYVENROGYR-----TASYIALTD 109
Db      114 FKKSSEYERAVKMRHLSTGTMTGLAIQY--ALNTASEAGANPLRENPVRYMTAYTD 170
QY      110 GELIHEDLFYFSREARNSRDIGAIYVCYV--KDFNETLARLADSKDHVFPVNDFOAL 167
Db      171 GRQQDSV---ASVAAKARDTGILIPAIQVGVDFNTLKSSISEPHEDHVELVAN-PSQI 222

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| | | | |
|----|-----|-------------|-----|
| Oy | 168 | OGIHSILKSC | 179 |
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| | : | : | |
| Db | 226 | ETLTSVFQKLC | 237 |

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RESULT 5
US-11-113-424-39
; Sequence 39, Application US/11113424
; Publication No. US200502600713A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113, 424

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PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,5500
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,3144
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,6133
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,6177
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/307,5066
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,3568
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,0755
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/288,1533
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 936
TYPE: PRT

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ORGANISM: Homo sapiens
US-11-113-424-39

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|-----------------------|------------------|-------------------|------------|-------------|
| Query Match | 11.6% | Score 109; | DB 7; | Length 956; |
| Best Local Similarity | 24.0% | Pred. No. 0.0047; | | |
| Matches 46; | Conservative 43; | Mismatches 77; | Indels 26; | Gaps 10; |

| | | | |
|----|-----|--|-----|
| QY | 3 | DLYEILDKSGGV--LHNNHEIYF--VEQJLHFKFSPOL-RMSFVFSRGTLL-----MKL | 54 |
| | | :: :: :: :: :: :: | |
| Db | 57 | DLVEIISSSSVNHDYAKVKEFIVDLIQFDLIDPDTVRGLIYQ---GSTVKKEFSIKT | 113 |
| QY | 55 | TEDEEOLROGLEELQKLPGGDTYMHGSPERASQIYYENROGR-----TASYIILATD | 109 |
| | | :: :: :: :: :: :: | |
| Db | 114 | PKRSEVERAKVRKRRHLSTGTMTGLAIQY--ALNIAFSKAGKAPLRANVPRIYMTVD | 170 |
| QY | 110 | GEIHEDLPFYSEREANRSDLGAIIVCGV--KDFNETQLARIADSKDHYFPVNDGFOAL | 167 |
| | | :: :: :: :: :: :: | |
| Db | 171 | GRPDQSV---AEVVAARDTGLIIFAIIGVQVDENLTKSIGSEPHNDHVELVAN--FSQI | 225 |

| | | | |
|----|-----|------------|-----|
| Qy | 168 | QGIHSLKKSC | 179 |
| | : | : | |
| | : | : | |
| | : | : | |
| Db | 226 | ETLTSEFKLC | 237 |

RESULT 6
US-10-601-368-24
Sequence 24, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368

```

: PRIOR APPLICATION NUMBER: US/09/561,263A
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: US 09/322,790
: PRIOR FILING DATE: 1999-05-28
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0.
: SEQ ID NO 24
: LENGTH: 1141
: TYPE: PRT
: ORGANISM: Mus musculus
: US-10-601-368-24

```

| | | | | |
|-----------------------|------------------|-------------------|------------|--------------|
| Query Match | 11.5% | Score 108; | DB 6; | Length 1141; |
| Best Local Similarity | 24.2%; | Pred. NO. 0.0074; | | |
| Matches 48; | Conservative 28; | Mismatches 84; | Indels 38; | Gaps 9; |

[illegible]

```

RESULT 7
US-10-601-368-22
; Sequence 22, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:

```

```

1  APPLICANT: Pan, Yang
2  APPLICANT: Lora, Jose M.
3  TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
4  FILE REFERENCE: 0734-275001
5  CURRENT APPLICATION NUMBER: US/10/601,368
6  CURRENT FILING DATE: 2003-06-23
7  PRIOR APPLICATION NUMBER: US/09/561,263A
8  PRIOR FILING DATE: 2000-04-27
9  PRIOR APPLICATION NUMBER: US 09/322,790
10 PRIOR FILING DATE: 1999-05-28
11 NUMBER OF SEQ ID NOS: 40
12 SOFTWARE: FastSeq for Windows Version 3.0
13 SEQ ID NO 22
14 LENGTH: 1166
15 TYPE: PRT
16 ORGANISM: Mus musculus
17 US-10-601-368-22

```

| | | | | |
|-----------------------|-------|--|------|----------------------------------|
| Query Match | 11.5% | Score 108 | DB 6 | Length 1166 |
| Best Local Similarity | 24.2% | Pred. No. 0.0077 | | |
| Matches | 46 | Conservative | 28 | Mismatches 84; Indels 38; Gaps 9 |
| QY | 3 | DLYFIIDKSGSVLHMHNEIYVEVQLAHKF-ISP-QLRMSFIVSTRGCTIMKLTEDREQ | 60 | |
| Db | 142 | DIIVILDEGSNSI-YPMVEVOHFLINILTKKFYIGPQIQVGAIQXGEDAVHEFHL--NRYRS | 199 | |
| QY | 61 | IRGQLELQKVLDEGSGTYMHEGFE---RASEQIYYENRGYRTASVILATLDSGLHSD-- | 115 | |
| Db | 200 | VKDVLEAASHTEORGGETRTAGTGAIEFPAASEAFQKGGKRGAA--KVMILVITDGSHPD | 257 | |
| QY | 116 | -----LFFYSREANRSDIGAIVYCVGVND-----ENETQLARIA | 151 | |
| Db | 258 | LEKVIHQSEKQDNTRYAVAVLGYGNRRGINPETFLINEIKYIASDPDDKGFENVTDEAAL- | 316 | |
| QY | 152 | DSKDNFPPVNDGFQALQG | 169 | |
| Db | 317 | --KQIVDALGRIRFSLEG | 332 | |

```

RESULT 8
US-10-601-368-21
/ Sequence 21, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Iora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 21
/ LENGTH: 1168
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-21

```

Query March 11.5%; Score 108; DB 6; Length 1188;
Best Local Similarity 24.2%; Pred. No. 0.0079;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 5

Oy 3 DLYITLDKSGVLTNNHNEITYFEVQLAKF-ISP-QLRMSFVSTRGTTMLKLTEDEEQ 60
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 164 DIVILDLGNSNI-PPWVEVGHFLINTLIKREYIIPGGIOIGVQYEDAVAEHFHL-NDRS 221
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

| | | | | | | |
|----|-----|--------------|----------------|------------------------|--------------------|-------|
| Qy | 61 | IRCGEELKCVLP | PGDGYVHGEFE--- | PASQIYYENRQGRYTSV | IATDGLTHMD-- | 115 |
| | | : | : | : | : | : |
| Db | 222 | VKQVVEAASHI | IRGQGTETRTAF | GIIEFPAISAFQIGKRGKAK-- | KXMIIVITDGSHPD | 279 |
| Qy | 116 | ----- | ----- | ----- | ----- | ----- |
| | | : | : | : | : | : |
| Db | 280 | LEKVIROSEKDN | TRKYAAVLTGY | NRKQINBETFLNEIKY | IASDPDDKHFNVTDEAL- | 338 |
| Qy | 152 | DSKQHVFPVNDG | FQALQG | 169 | | |
| | | : | : | : | : | : |
| Db | 339 | --KDIVDALGR | IFSLG | 354 | | |

```

RESULT 9
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OR INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-057-047-2

```

| | | | | |
|-----------------------|-------|--|------|-----------------------------------|
| Query Match | 11.2% | Score 105.5 | DB 7 | Length 739 |
| Best Local Similarity | 22.6% | Pred. No. 0.0074 | | |
| Matches | 46 | Conservative | 44 | Mismatches 75; Indels 45; Gaps 10 |
| Qy | 3 | DLYFIIDKGSV-----LHHMNEIYYEVEQLAHKIFISPOLRMSFVSTGRTTLMKLT- | 56 | |
| | : | : | : | : |
| Db | 245 | NIYVLVDGSPISIGASNFTGAKKCLVLLIEKVASYGVK--RYGLATVATYKRIWVAKSEA | 302 | |
| | : | : | : | : |
| Qy | 57 | ---DREGIRGDEL-----QKVLPGSDPTMHGSEFASQIYYENR-----OGY-RTA | 102 | |
| | : | : | : | : |
| Db | 303 | DSSNADVYTKQLNEIYVEDHKLSGNT-----KCALQAVYSMMSSWDDVPEEGMNR | 350 | |
| | : | : | : | : |
| Qy | 102 | SVIIATLDG-----ELHEDLFYFSEREANRSDLGAIVCVG--VKDFNETQ | 146 | |
| | : | : | : | : |
| Db | 357 | HVIILMTDGLHNNGGDPTIVIDEIRDLIYIGDKRKNPREDYLDVYFVGVLVQNVINA | 416 | |
| | : | : | : | : |
| Qy | 147 | LARIADSKDVPFVYNDGFQALGIIHSILKLS | 178 | |
| | : | : | : | : |
| Db | 417 | LASKRQDEQHVFKYK-MENLEBDEVFMQIDES | 447 | |
| | : | : | : | : |

```
RESULT 10
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Tabe, Christian
; APPLICANT: Gelfand, Eryn
; APPLICANT: Gilkeson, Gary
```

```

; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; PRIOR APPLICATION NUMBER: 2005-02-10
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-057-047-1

```

| | | | | | | |
|---------|--|--------------|-------------------|------------|-------------|----------|
| | Query Match | 11.2% | Score 105.5 | DB 7 | length 764; | |
| | Best Local Similarity | 22.6% | Pred. No. 0.0077; | | | |
| Matches | 48; | Conservative | 44; | Mismatches | 75; | Gaps 10; |
| Oy | 3 DLYITLDKSGV-----LHMNEIYYFVEQLAHKFISPOLRMSPIVFSTGTTLMKLT- | 56 | | | | |
| Db | 270 NIYVLGGSDSIGASNFTGAKCKLVNLIEKVASGVK--RYGLVTYATYEKIMWKVSEA | 327 | | | | |
| Oy | 57 ---DREGIRQGLEEL---OKVLPGGDIYVMHGFEPAEEOIYYENR-----OGY-RTA | 101 | | | | |
| Db | 328 DSSADAVYTKQLANEINYNEDHKLKSGTNT-----KKALQAVYSMMSSWDDVDYPPEGMNFR | 381 | | | | |
| Oy | 102 SVIIALTGDG-----EDHEDIIFYSEREANRSRLGAIVYCVG--VYDFNETQ | 146 | | | | |
| Db | 382 HVILMTDTGLNMGGDPITTVIDEIRDLILYICGRDRNPREDYLDVVFGVGPLNVQNINA | 441 | | | | |
| Oy | 147 LARIADSKDHVPYNDGFQALGIHSILTKKS | 178 | | | | |
| Db | 442 LASKKDEQHAFVKVD-MENLEDVFPYQIDDS | 472 | | | | |

```

RESULT 11
US-10-821-234-1034
/ Sequence 1034, Application US/10821234
/ Publication No. US200502551141
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmant, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1034
/ LENGTH: 798
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-821-234-1034

```

```

Query Match      11.2%  Score 105.5;  DB 6;  Length 798;
Best Local Similarity 22.6%;  Pred. No. 0.0082;
Matches 48;  Conservative 44;  Mismatches 75;  Indels 45;  Gaps 10

QY      3  DLYEILDKSGSV-----LHNNEIYIYVEQALHKEPISPOLMSFIVFSTGTTLMLKTE- 56
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      304  NIVLVLDQSDSISGASNFTGAKKCLVNLLEKVASGYKRP--RGLVLYALVYPRIMWVQSA 361
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      57  ---DREQIQTGLEL-----QKVLPGSGDTYMHGEGFERASQIYYENR-----QGT-RTA 101
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

Db      362  DSSNAWMYTKQALNEINVEDHKLKSGTNT-----KKALQAYVSNMWSWPDVPEEGNMRTR 415
Oy      102  SVTIALTDG-----ELHEDFPEFYSEAREANSRDGAIYCVG--VDFPNETQ 146
Db      416  HVIIITMTDGLHNMGGDPIVIDEIKDLYIKDKRKNRPEDVLVDYVGVGELVQNVQVINA 475
Oy      147  IARIADSKDHFVPPVNDGFGALOGIHTSLKKS 178
Db      476  LASKDNEQGVKVKD-MENLEDVYFQINDSS 506

```

```

RESULT 12
US-10-601-368-6
Sequence 6, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US/09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1141
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-6

```

[illegible]

RESULT 13
US-10-601-368-4
Sequence 4, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OR INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
PRIOR FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 11:11:02 ; Search time 215.58 Seconds
(without alignments)
1160.284 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Sequence: 943
1 GFDLYFILDKSGSVLHHMNE.....DGFQALQGIHSHKSKSCIE 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/prodata/1/paa/US0605 COMB .pep:*

2: /cgn2_6/prodata/1/paa/US0606 COMB .pep:*

3: /cgn2_6/prodata/1/paa/US0703 COMB .pep:*

4: /cgn2_6/prodata/1/paa/US0704 COMB .pep:*

5: /cgn2_6/prodata/1/paa/US0705 COMB .pep:*

6: /cgn2_6/prodata/1/paa/US0706 COMB .pep:*

7: /cgn2_6/prodata/1/paa/US0707 COMB .pep:*

8: /cgn2_6/prodata/1/paa/US0708 COMB .pep:*

9: /cgn2_6/prodata/1/paa/US0709 COMB .pep:*

10: /cgn2_6/prodata/1/paa/US0801 COMB .pep:*

11: /cgn2_6/prodata/1/paa/US0802 COMB .pep:*

12: /cgn2_6/prodata/1/paa/US0803 COMB .pep:*

13: /cgn2_6/prodata/1/paa/US0804 COMB .pep:*

14: /cgn2_6/prodata/1/paa/US0805 COMB .pep:*

15: /cgn2_6/prodata/1/paa/US0806 COMB .pep:*

16: /cgn2_6/prodata/1/paa/US0807 COMB .pep:*

17: /cgn2_6/prodata/1/paa/US0808 COMB .pep:*

18: /cgn2_6/prodata/1/paa/US0809 COMB .pep:*

19: /cgn2_6/prodata/1/paa/US0810 COMB .pep:*

20: /cgn2_6/prodata/1/paa/US0901 COMB .pep:*

21: /cgn2_6/prodata/1/paa/US0902 COMB .pep:*

22: /cgn2_6/prodata/1/paa/US0903 COMB .pep:*

23: /cgn2_6/prodata/1/paa/US0904 COMB .pep:*

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25: /cgn2_6/prodata/1/paa/US0906 COMB .pep:*

26: /cgn2_6/prodata/1/paa/US0907 COMB .pep:*

27: /cgn2_6/prodata/1/paa/US0908 COMB .pep:*

28: /cgn2_6/prodata/1/paa/US0909 COMB .pep:*

29: /cgn2_6/prodata/1/paa/US0910 COMB .pep:*

30: /cgn2_6/prodata/1/paa/US1001 COMB .pep:*

31: /cgn2_6/prodata/1/paa/US1002 COMB .pep:*

32: /cgn2_6/prodata/1/paa/US1003 COMB .pep:*

33: /cgn2_6/prodata/1/paa/US1004 COMB .pep:*

34: /cgn2_6/prodata/1/paa/US1005 COMB .pep:*

35: /cgn2_6/prodata/1/paa/US1006 COMB .pep:*

36: /cgn2_6/prodata/1/paa/US1007 COMB .pep:*

37: /cgn2_6/prodata/1/paa/US1008 COMB .pep:*

38: /cgn2_6/prodata/1/paa/US1009 COMB .pep:*

39: /cgn2_6/prodata/1/paa/US1010 COMB .pep:*

40: /cgn2_6/prodata/1/paa/US1101 COMB .pep:*

41: /cgn2_6/prodata/1/paa/US1102 COMB .pep:*

42: /cgn2_6/prodata/1/paa/US1103 COMB .pep:*

43: /cgn2_6/prodata/1/paa/US1104 COMB .pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------------|--------------------|
| 1 | 943 | 100.0 | 274 | 1 PCT-US99-31025-50 | Sequence 50, Appl |
| 2 | 943 | 100.0 | 274 | 24 US-09-471-179-50 | Sequence 16, Appl |
| 3 | 943 | 100.0 | 293 | 49 US-60-561-086-16 | Sequence 2121, Ap |
| 4 | 943 | 100.0 | 297 | 24 US-09-488-725A-2121 | Sequence 2121, Ap |
| 5 | 943 | 100.0 | 297 | 32 US-10-258-898A-2121 | Sequence 2121, Ap |
| 6 | 943 | 100.0 | 297 | 32 US-10-286-897-2121 | Sequence 132, App |
| 7 | 943 | 100.0 | 301 | 1 PCT-US99-31025-132 | Sequence 132, App |
| 8 | 943 | 100.0 | 301 | 24 US-09-471-179-132 | Sequence 30, Appl |
| 9 | 943 | 100.0 | 306 | 1 PCT-US99-31025-30 | Sequence 51, Appl |
| 10 | 943 | 100.0 | 306 | 1 PCT-US99-31025-51 | Sequence 30, Appl |
| 11 | 943 | 100.0 | 306 | 24 US-09-471-179-30 | Sequence 51, Appl |
| 12 | 943 | 100.0 | 306 | 24 US-09-471-179-51 | Sequence 26, Appl |
| 13 | 943 | 100.0 | 328 | 30 US-10-038-307-26 | Sequence 26, Appl |
| 14 | 943 | 100.0 | 328 | 32 US-10-201-229A-26 | Sequence 26, Appl |
| 15 | 943 | 100.0 | 328 | 32 US-10-201-229A-26 | Sequence 26, Appl |
| 16 | 943 | 100.0 | 333 | 1 PCT-US99-31025-9 | Sequence 9, Appl |
| 17 | 943 | 100.0 | 333 | 22 US-09-471-179-9 | Sequence 9, Appl |
| 18 | 943 | 100.0 | 333 | 24 US-09-471-179-9 | Sequence 9, Appl |
| 19 | 943 | 100.0 | 333 | 25 US-09-599-596-9 | Sequence 12, Appl |
| 20 | 943 | 100.0 | 333 | 27 US-09-796-753-12 | Sequence 8, Appl |
| 21 | 943 | 100.0 | 333 | 29 US-09-970-076-8 | Sequence 2, Appl |
| 22 | 943 | 100.0 | 333 | 30 US-10-038-307-2 | Sequence 2, Appl |
| 23 | 943 | 100.0 | 333 | 32 US-10-201-292A-2 | Sequence 2, Appl |
| 24 | 943 | 100.0 | 333 | 32 US-10-201-292A-2 | Sequence 2, Appl |
| 25 | 943 | 100.0 | 333 | 40 US-11-047-228-8 | Sequence 8, Appl |
| 26 | 943 | 100.0 | 333 | 40 US-11-047-228-8 | Sequence 8, Appl |
| 27 | 943 | 100.0 | 333 | 49 US-60-568-073-741 | Sequence 741, App |
| 28 | 943 | 100.0 | 342 | 30 US-10-038-307-22 | Sequence 22, Appl |
| 29 | 943 | 100.0 | 342 | 32 US-10-201-292-22 | Sequence 22, Appl |
| 30 | 943 | 100.0 | 342 | 32 US-10-201-292A-22 | Sequence 22, Appl |
| 31 | 943 | 100.0 | 345 | 30 US-10-038-307-24 | Sequence 24, Appl |
| 32 | 943 | 100.0 | 345 | 32 US-10-201-229A-24 | Sequence 24, Appl |
| 33 | 943 | 100.0 | 345 | 32 US-10-201-229A-24 | Sequence 24, Appl |
| 34 | 943 | 100.0 | 368 | 29 US-09-970-076-2 | Sequence 2, Appl |
| 35 | 943 | 100.0 | 368 | 36 US-10-602-702-3 | Sequence 3, Appl |
| 36 | 943 | 100.0 | 368 | 36 US-10-602-727-3 | Sequence 3, Appl |
| 37 | 943 | 100.0 | 368 | 40 US-11-047-228-2 | Sequence 2, Appl |
| 38 | 943 | 100.0 | 368 | 40 US-11-047-228-2 | Sequence 2, Appl |
| 39 | 943 | 100.0 | 368 | 49 US-60-548-281-8 | Sequence 8, Appl |
| 40 | 943 | 100.0 | 403 | 1 PCT-US00-30045-94 | Sequence 94, Appl |
| 41 | 943 | 100.0 | 403 | 1 PCT-US01-11988-621 | Sequence 621, App |
| 42 | 943 | 100.0 | 403 | 28 US-09-833-245A-621 | Sequence 621, App |
| 43 | 943 | 100.0 | 403 | 28 US-09-833-245A-621 | Sequence 621, App |
| 44 | 943 | 100.0 | 403 | 28 US-09-833-245B-621 | Sequence 621, App |
| 45 | 943 | 100.0 | 403 | 31 US-10-100-683-9107 | Sequence 9107, App |

ALIGNMENTS

RESULT 1
PCT-US99-31025-50
; Sequence 50, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; FILE OF INVENTION: ENCODING THEM
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; EARLIER FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US99-31025-50
```

```

Query Match          100.0%; Score 943; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.3e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
    |||
DB 15 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 74
    |||
QY 61 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
    |||
DB 75 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 134
    |||
QY 121 EREANRSRDGLAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 180
    |||
DB 135 EREANRSRDGLAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 194
    |||
QY 181 E 181
DB 195 E 195
```

RESULT 2

```

; US-09-471-179-50
; Sequence 50, Application US/09471179
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 7853-173
; CURRENT APPLICATION NUMBER: US/09/471,179
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-471-179-50
```

```

Query Match          100.0%; Score 943; DB 24; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.3e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
    |||
DB 15 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 74
    |||
QY 61 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
    |||
DB 75 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 134
    |||
QY 121 EREANRSRDGLAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 180
    |||
DB 135 EREANRSRDGLAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 194
    |||
QY 181 E 181
DB 195 E 195
```

DB 195 E 195

RESULT 3

```

; US-60-561-086-16
; Sequence 16, Application US/60561086
; GENERAL INFORMATION:
; APPLICANT: Emtage, Peter
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods of Therapy and Diagnosis Using Targeting of Cells that Ex-
; FILE REFERENCE: NUVO-18
; CURRENT APPLICATION NUMBER: US/60/561,086
; CURRENT FILING DATE: 2004-04-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-561-086-16
```

```

Query Match          100.0%; Score 943; DB 49; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.6e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
    |||
DB 15 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 74
    |||
QY 61 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
    |||
DB 75 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 134
    |||
QY 121 EREANRSRDGLAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 180
    |||
DB 135 EREANRSRDGLAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 194
    |||
QY 181 E 181
DB 195 E 195
```

RESULT 4

```

; US-09-488-725A-2121
; Sequence 2121, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCR
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_Fl_gene_b Versions 1.0
; SEQ ID NO 2121
; LENGTH: 298
; TYPE: PRT
```

```
/ ORGANISM: Homo sapiens
US-09-488-725A-2121

Query Match      100.0%; Score 943; DB 24; Length 297;
Best Local Similarity 100.0%; Pred. No. 3,7e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAKHFTSPOLRMSFIYSTRGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAKHFTSPOLRMSFIYSTRGTTLMKLTEDREQ 101

QY 61 IROGLELEQLVLPDGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLELEQLVLPDGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161

QY 121 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFOLQGIHSLKKSCI 180
DB 162 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFOLQGIHSLKKSCI 221

QY 181 E 181
DB 222 E 222
```

```
RESULT 5
US-10-258-898A-2121
/ Sequence 2121, Application US/10258898A
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq Inc
/ TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
/ FILE REFERENCE: 784PLPCT
/ CURRENT APPLICATION NUMBER: US/10/258,898A
/ PRIOR FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: US/09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: US09/598,042
/ PRIOR FILING DATE: 2000-06-20
/ PRIOR APPLICATION NUMBER: US09/620,312
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: US09/653,450
/ PRIOR FILING DATE: 2000-08-31
/ PRIOR APPLICATION NUMBER: US09/662,191
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: US09/693,036
/ PRIOR FILING DATE: 2000-10-19
/ PRIOR APPLICATION NUMBER: US09/727,344
/ PRIOR FILING DATE: 2000-11-29
/ NUMBER OF SEQ ID NOS: 7143
/ SOFTWARE: pc_fl_genes_b Versions 1.0
/ SEQ ID NO 2121
/ LENGTH: 297
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-258-898A-2121
```

```
Query Match      100.0%; Score 943; DB 32; Length 297;
Best Local Similarity 100.0%; Pred. No. 3,7e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAKHFTSPOLRMSFIYSTRGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAKHFTSPOLRMSFIYSTRGTTLMKLTEDREQ 101

QY 61 IROGLELEQLVLPDGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLELEQLVLPDGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161

QY 121 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFOLQGIHSLKKSCI 180
DB 162 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFOLQGIHSLKKSCI 221
```

```
QY 181 E 181
DB 222 E 222
```

```
RESULT 6
US-10-286-897-2121
/ Sequence 2121, Application US/10286897
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq Inc
/ TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
/ FILE REFERENCE: 784PLPCT
/ CURRENT APPLICATION NUMBER: US/10/286,897
/ PRIOR FILING DATE: 2002-11-01
/ PRIOR APPLICATION NUMBER: US/09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US/09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: US/09/598,042
/ PRIOR FILING DATE: 2000-06-20
/ PRIOR APPLICATION NUMBER: US/09/620,312
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: US/09/653,450
/ PRIOR FILING DATE: 2000-08-31
/ PRIOR APPLICATION NUMBER: US/09/662,191
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: US/09/693,036
/ PRIOR FILING DATE: 2000-10-19
/ PRIOR APPLICATION NUMBER: US/09/727,344
/ PRIOR FILING DATE: 2000-11-29
/ NUMBER OF SEQ ID NOS: 7143
/ SOFTWARE: pc_fl_genes_b Versions 1.0
/ SEQ ID NO 2121
/ LENGTH: 297
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-286-897-2121
```

```
Query Match      100.0%; Score 943; DB 32; Length 297;
Best Local Similarity 100.0%; Pred. No. 3,7e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAKHFTSPOLRMSFIYSTRGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAKHFTSPOLRMSFIYSTRGTTLMKLTEDREQ 101

QY 61 IROGLELEQLVLPDGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLELEQLVLPDGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161

QY 121 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFOLQGIHSLKKSCI 180
DB 162 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFOLQGIHSLKKSCI 221

QY 181 E 181
DB 222 E 222
```

```
RESULT 7
PCT-US99-31025-132
/ Sequence 132, Application PC/TUS9931025
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE: 7853-173-228
/ CURRENT APPLICATION NUMBER: PCT/US99/31025
/ PRIOR FILING DATE: 1999-12-23
/ EARLIER APPLICATION NUMBER: 09/223,546
/ PRIOR FILING DATE: 1998-12-30
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 132
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-132
```

```
Query Match          100.0%; Score 943; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.8e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB      42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101
QY      61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB      102 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161
QY      121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB      162 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 221
```

```
QY      181 E 181
DB      222 E 222
```

```
RESULT 8
US-09-471-179-132
; Sequence 132, Application US/09471179
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 7853-173
; CURRENT APPLICATION NUMBER: US/09/471.179
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-179-132
```

```
Query Match          100.0%; Score 943; DB 24; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.8e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB      42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101
QY      61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB      102 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161
QY      121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB      162 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 221
QY      181 E 181
DB      222 E 222
```

```
RESULT 9
PCT-US99-31025-30
; Sequence 30, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
```

```
; TITLE OF INVENTION: ENCODING THEM
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-30
```

```
Query Match          100.0%; Score 943; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 3.9e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB      15 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 74
QY      61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB      75 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 134
QY      121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB      135 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 194
```

```
QY      181 E 181
DB      195 E 195
```

```
RESULT 10
PCT-US99-31025-51
; Sequence 51, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-51
```

```
Query Match          100.0%; Score 943; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 3.9e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB      15 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 74
QY      61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB      75 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 134
QY      121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB      135 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 194
QY      181 E 181
```


Db 195 E 195

RESULT 11

```

US-09-471-179-30
; Sequence 30, Application US/09471179
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 7853-173
; CURRENT APPLICATION NUMBER: US/09/471,179
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/722,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-179-30

```

| | | | | |
|-----------------------|----------------|--------------|----------|------------|
| Query Match | 100.0% | Score 943 | DB 24 | length 306 |
| Best Local Similarity | 100.0% | Pred. No. 3 | 9e-92 | |
| Matches 181 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

Qy 1 GFDLFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSRGTLMKLTEDREQ 60
D5 15 GFDLFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIVFSRGTLMKLTEDREQ 74

Qy 61 I R G I E E L Q K V L P G S D T Y M H E G F E R A S E Q I Y E N R Q G V R T A S V I I A L T D G E L H E D L F P F Y S 120
Dy 75 I R G I E E L Q K V L P G S D T Y M H E G F E R A S E Q I Y E N R Q G V R T A S V I I A L T D G E L H E D L F P F Y S 134

[illegible]

| | |
|----|-----------|
| QY | 181 E 181 |
| Db | 195 E 195 |

RESULT 12
119-00-471

```

US-09-471-179-51
/ Sequence 51, Application US/09471179
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Holtzman, Douglas
/
/ TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
/
/ FILE REFERENCE: 7853-173
/
/ CURRENT APPLICATION NUMBER: US/09/471,179
/
/ CURRENT FILING DATE: 1999-12-23
/
/ PRIOR APPLICATION NUMBER: 09/723,546
/
/ PRIOR FILING DATE: 1998-12-30
/
/ NUMBER OF SEQ ID NOS: 135
/
/ SOFTWARE: FastSeq for Windows Version 4.0
/
/ SEQ ID NO 51
/
/ LENGTH: 306
/
/ TYPE: PRT
/
/ ORGANISM: Homo sapiens
/
US-09-471-179-51

```

| | | | | |
|---------------------------|---------|--------------------|-----------|-------------|
| Query Match | 100.0%; | Score 943; | DB 24; | Length 306; |
| Best Local Similarity | 100.0%; | Pred. No. 3.9e-92; | | |
| Matches 181, Conservative | 0; | Mismatches 0; | Indels 0; | Gaps 0 |

Qy 1 GFDVLFIIDKSGSVLHHMNEIYFVEQLAHKFIIPQLRMSFIVFSTRGTTLMKLTEDREQ 60
Db 15 GFDLFIIDKSGSVLHHMNEIYFVEQLAHKFIIPQLRMSFIVFSTRGTTLMKLTEDREQ 74

Qy 61 I R G G I E L Q K V L P G S D T Y M H G F E R A S E Q I Y Y E N R Q G Y R T A S I I A L T D G E L H E D L F F Y S
Dd 75 I R G G I E L Q K V L P G S D T Y M H G F E R A S E Q I Y Y E N R Q G Y R T A S I I A L T D G E L H E D L F F Y S 134

Dy 121 EREANRSRLGAIYCVGVDFNEIQLARLADSKOHVFPVNDGFQALQGIHSLKKSCI 180

Dd 135 EREANRSRLGAIYCVGVDFNEIQLARLADSKOHVFPVNDGFQALQGIHSLKKSCI 194

| | |
|----|-----------|
| Qy | 181 E 181 |
| Db | 195 E 195 |

RESULT 13

```

US-10-038-307-26
Sequence 26, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 338
TYPE: PR1
ORGANISM: Homo sapiens
US-10-038-307-26

```

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 100.0%; | Score 943; | DB 30; | Length 328; |
| Best Local Similarity | 100.0%; | Pred. No. 4,3e-92; | | |
| Matches 181; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

DQ- 1 GFDLYFLDCKSGVLAHHNNEIYYFFEQLANHKEISPOLRMSEIVFSTRGTTLMKLTEDREQ 60
|||
DB 42 GFDLYFLDCKSGVLAHHNNEIYYFAEQLAHKFISPOLRMSEIVFSTRGTTLMKLTEDREQ 101

QY 61 IRGLLEELQKVLPGSDTYMHGFEPASEQIYYENQGYRTASVIIALTDGELHEDLFFYS 120
DB 102 IRGLLEELQKVLPGSDTYMHGFEPASEQIYYENQGYRTASVIIALTDGELHEDLFFYS 161

Dy 121 ERENRSRDLGAIYCVGYD FNEQLARIADSKHVPVNDGFALGGIHSILKSCI 180
|||
|||
|||
|||
|||
|||
|||
|||
|||
|||
Db 162 ERENRSRDLGAIYCVGYD FNEQLARIADSKHVPVNDGFALGGIHSILKSCI 221

| | |
|----|-------|
| QY | 181 E |
| Db | 222 E |

RESULT 14

```

US-10-201-292-26
/ Sequence 26, Application US/10201292
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-201-292-26

```

| | | | | |
|-----------------------|---------|--------------------|--------|-------------|
| Query Match | 100.0%; | Score 943; | DB 32; | Length 338; |
| Best Local Similarity | 100.0%; | Pred. No. 4.3e-92; | | |

```
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 60
Db 42 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 101
QY 61 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVITALTDEGLHEDLFFYS 120
Db 102 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVITALTDEGLHEDLFFYS 161
QY 121 EREANRSRDLGAIYVCVGDVFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCI 180
Db 162 EREANRSRDLGAIYVCVGDVFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCI 221
QY 181 E 181
Db 222 E 222

RESULT 15
US-10-201-292A-26
; Sequence 26, Application US/10201292A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: James B. Rottman
; APPLICANT: Theresa L. O'Keefe
; APPLICANT: Engin Ozkaynak
; APPLICANT: Judith J. Healey
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: MP101-307CPLM
; CURRENT APPLICATION NUMBER: US/10/201,292A
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 10/038,307
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PR1
; ORGANISM: Homo Sapiens
; US-10-201-292A-26

Query Match 100.0%; Score 943; DB 32; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 60
Db 42 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 101
QY 61 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVITALTDEGLHEDLFFYS 120
Db 102 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVITALTDEGLHEDLFFYS 161
QY 121 EREANRSRDLGAIYVCVGDVFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCI 180
Db 162 EREANRSRDLGAIYVCVGDVFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCI 221
QY 181 E 181
Db 222 E 222
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Search completed: December 14, 2005, 11:50:58
Job time : 216.58 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: December 18, 2005, 07:35:12 / Search time 579.877 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Percent score: 943

Sequence: 1 GFDLYFLIDSGSVLHHMNE.....DGFQALQGIHSLKSKSCIE 181

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Command line parameters:
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-Q=/cg2_1/USPTO.spool/US0970076/runat_14122005_11852_21035/app_query.fasta_1.2410
-DB=Published Applications NA Main -QPMT=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCD=0 -LOOPEXT=0 -UNITS=bases -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.cds -LIST=45 -LOCAL=LOCAL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=p2n -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0970076 @CGN_1_1_2715 @runat_14122005_11852_21035
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main.*

1: /cg2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cg2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cg2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
4: /cg2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
5: /cg2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
6: /cg2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
7: /cg2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
8: /cg2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
9: /cg2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
10: /cg2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------|-------------------|
| 1 | 943 | 100.0 | 1008 | US-10-038-307-25 | Sequence 25, Appl |
| 2 | 943 | 100.0 | 1008 | US-10-201-292-25 | Sequence 25, Appl |
| 3 | 943 | 100.0 | 1047 | US-10-038-307-21 | Sequence 21, Appl |
| 4 | 943 | 100.0 | 1047 | US-10-201-292-21 | Sequence 21, Appl |
| 5 | 943 | 100.0 | 1056 | US-10-038-307-23 | Sequence 23, Appl |
| 6 | 943 | 100.0 | 1056 | US-10-201-292-23 | Sequence 23, Appl |
| 7 | 943 | 100.0 | 1401 | US-10-201-292-27 | Sequence 27, Appl |
| 8 | 943 | 100.0 | 1401 | US-10-201-292-29 | Sequence 29, Appl |

| | | | | | |
|----|-----|-------|------|---------------------|--------------------|
| 9 | 943 | 100.0 | 1414 | US-11-047-278-1 | Sequence 1, Appl1 |
| 10 | 943 | 100.0 | 1436 | US-11-047-278-9 | Sequence 9, Appl1 |
| 11 | 943 | 100.0 | 1454 | US-10-133-937-58 | Sequence 58, Appl1 |
| 12 | 943 | 100.0 | 1454 | US-10-159-563-58 | Sequence 58, Appl1 |
| 13 | 943 | 100.0 | 1464 | US-10-201-292-31 | Sequence 31, Appl1 |
| 14 | 943 | 100.0 | 1534 | US-10-201-292-33 | Sequence 33, Appl1 |
| 15 | 943 | 100.0 | 1608 | US-10-201-292-35 | Sequence 35, Appl1 |
| 16 | 943 | 100.0 | 1609 | US-10-037-270-8 | Sequence 8, Appl1 |
| 17 | 943 | 100.0 | 1609 | US-10-117-222-8 | Sequence 8, Appl1 |
| 18 | 943 | 100.0 | 1609 | US-10-122-851-8 | Sequence 8, Appl1 |
| 19 | 943 | 100.0 | 1623 | US-10-038-307-11 | Sequence 11, Appl1 |
| 20 | 943 | 100.0 | 1623 | US-10-201-292-11 | Sequence 11, Appl1 |
| 21 | 943 | 100.0 | 1650 | US-10-038-307-9 | Sequence 9, Appl1 |
| 22 | 943 | 100.0 | 1650 | US-10-038-307-13 | Sequence 13, Appl1 |
| 23 | 943 | 100.0 | 1650 | US-10-201-292-9 | Sequence 9, Appl1 |
| 24 | 943 | 100.0 | 1650 | US-10-201-292-13 | Sequence 13, Appl1 |
| 25 | 943 | 100.0 | 1650 | US-10-201-292-13 | Sequence 13, Appl1 |
| 26 | 943 | 100.0 | 1650 | US-10-201-292-15 | Sequence 15, Appl1 |
| 27 | 943 | 100.0 | 1674 | US-10-038-307-17 | Sequence 17, Appl1 |
| 28 | 943 | 100.0 | 1674 | US-10-201-292-17 | Sequence 17, Appl1 |
| 29 | 943 | 100.0 | 1713 | US-10-038-307-19 | Sequence 19, Appl1 |
| 30 | 943 | 100.0 | 1713 | US-10-201-292-19 | Sequence 19, Appl1 |
| 31 | 943 | 100.0 | 1718 | US-10-357-930-30300 | Sequence 30300, A |
| 32 | 943 | 100.0 | 2112 | US-11-047-278-7 | Sequence 7, Appl1 |
| 33 | 943 | 100.0 | 2272 | US-09-796-753-11 | Sequence 11, Appl1 |
| 34 | 943 | 100.0 | 2272 | US-10-038-307-1 | Sequence 1, Appl1 |
| 35 | 943 | 100.0 | 2272 | US-10-201-292-1 | Sequence 1, Appl1 |
| 36 | 943 | 100.0 | 2253 | US-10-198-846-9957 | Sequence 9957, Ap |
| 37 | 943 | 100.0 | 5540 | US-09-918-115-176 | Sequence 176, App |
| 38 | 943 | 100.0 | 5540 | US-09-918-115-231 | Sequence 231, App |
| 39 | 943 | 100.0 | 5540 | US-10-301-822-198 | Sequence 198, App |
| 40 | 943 | 100.0 | 5540 | US-10-474-794-176 | Sequence 176, App |
| 41 | 943 | 100.0 | 5540 | US-10-474-794-231 | Sequence 231, App |
| 42 | 943 | 100.0 | 5540 | US-10-979-159-176 | Sequence 176, App |
| 43 | 943 | 100.0 | 5540 | US-10-979-159-231 | Sequence 231, App |
| 44 | 943 | 100.0 | 5540 | US-11-047-278-5 | Sequence 5, Appl1 |
| 45 | 943 | 99.0 | 5220 | US-09-918-715-186 | Sequence 186, App |

ALIGNMENTS

RESULT 1
US-10-038-307-25
; Sequence 25, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:

Pred. No.: 1,71e-116 Length: 1008
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-038-307-25 (1-1008)

Qy 1 GlyPhAspLeuYrHeLeuAspLySSeGlySeValLeuHISHeTpaEnGlu 20

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Db 136 GGAATTGACCTGACTTCAATTTTGGACAAATCGAAGTGTGTCACCACTCGAATGAA 195
Qy 21 ILETyTYrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40
Db 196 ATCTATTACTTGTGTGGAAACAGTTGGCTCACAATAATCATCAGCCACAGTTGAGAAATGTC 255
Qy 41 PheIIValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArgGluGln 60
Db 256 TTTATTGTTTCTTCCACCCGAGAACACTTAATGAACTGCACAGAACACAGAAACAA 315
Qy 61 ILEARGGInGlyLeuGlnGluLeuGlnIysValLeuProGlyGlyAspThrTyrmethis 80
Db 316 ATCCGTCAAGGCTGAGAAAGAACTCCAGAAAGTTCTCCGACAGAGAGACACTTACATGCAT 375
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyTYrGluAsnArgGlnGlyTYrArgThr 100
Db 376 GAAAGATTGAAAGGGCCAGTGCAGACATTATTATGAAAACAGACAAAGGTACAGACACA 435
Qy 101 AlAserValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrsr 120
Db 436 GCCAGGCTCATCTGCTGTTGACTGATGAGAACTCCATGAAAGTCTTTTCTATTTCA 495
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTYrCySValGlyValys 140
Db 496 GAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATTTGTTACTGTGTGGTGGAA 555
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
Db 556 GATTTCATAGACACACAGCTGGCCCGATTGCGACAGTAAGATCATGTGTTCCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSerCySile 180
Db 616 AATGACGCTTTCAGGCTCTGCAAGGACATCCATCTCAATTTTGAAGAACTCTGCATC 675
Qy 181 Glu 181
Db 676 GAA 678
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RESULT 2
US-10-201-292-25
; Sequence 25, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-25

Alignment Scores:
Pred. No.: 1,716-116 Length: 1008
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-25 (1-1008)

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Qy 1 GlyPheAspLeuTyYPheIleLeuAspIysSerGlySerValLeuHisIleSTrPAAsnGlu 20
Db 136 GGAATTGACCTGACTTCAATTTTGGACAAATCGAAGTGTGTCACCACTCGAATGAA 195
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Qy 21 ILETyTYrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40
Db 196 ATCTATTACTTGTGTGGAAACAGTTGGCTCACAATAATCATCAGCCACAGTTGAGAAATGTC 255
Qy 41 PheIIValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArgGluGln 60
Db 256 TTTATTGTTTCTTCCACCCGAGAACACTTAATGAACTGCACAGAACACAGAAACAA 315
Qy 61 ILEARGGInGlyLeuGlnGluLeuGlnIysValLeuProGlyGlyAspThrTyrmethis 80
Db 316 ATCCGTCAAGGCTGAGAAAGAACTCCAGAAAGTTCTCCGACAGAGAGACACTTACATGCAT 375
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyTYrGluAsnArgGlnGlyTYrArgThr 100
Db 376 GAAAGATTGAAAGGGCCAGTGCAGACATTATTATGAAAACAGACAAAGGTACAGACACA 435
Qy 101 AlAserValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrsr 120
Db 436 GCCAGGCTCATCTGCTGTTGACTGATGAGAACTCCATGAAAGTCTTTTCTATTTCA 495
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTYrCySValGlyValys 140
Db 496 GAGAGGAGGCTAATAGTCTCGAGATCTTGATGCAATTTGTTACTGTGTGGTGGAA 555
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
Db 556 GATTTCATAGACACACAGCTGGCCCGATTGCGACAGTAAGATCATGTGTTCCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSerCySile 180
Db 616 AATGACGCTTTCAGGCTCTGCAAGGACATCCATCTCAATTTTGAAGAACTCTGCATC 675
Qy 181 Glu 181
Db 676 GAA 678
```

```
RESULT 3
US-10-038-307-21
; Sequence 21, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-21
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```
Alignment Scores:
Pred. No.: 1,826-116 Length: 1047
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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US-09-970-076-2_COPY_42_222 (1-181) x US-10-038-307-21 (1-1047)

```
Qy 1 GlyPheAspLeuTyYPheIleLeuAspIysSerGlySerValLeuHisIleSTrPAAsnGlu 20
Db 163 GGAATTGACCTGACTTCAATTTTGGACAAATCGAAGTGTGTCACCACTCGAATGAA 222
Qy 21 ILETyTYrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40
```

```
|||||
Db 223 ATCATTAATTGTTGGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATGTC 282
Qy 41 Phe11eValPheSerThrArg1yThrThleuMetLysLeuThrgluAspArgGluGln 60
Db 283 TTTATTGTTTCTCCACCCAGAAACACTTAATGAACACGACAGAAACAGAAACAA 342
Qy 61 11eArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyMetHis 80
Db 343 ATCCGTAAAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCAT 402
Qy 81 GluGlyPheGluArgAlaSerGluGln11eTyTyTyGluAsnArgGlnGlyTyArgThr 100
Db 403 GAAGGATTGMAAGGCGCAGTGAGACAGATTATTAAGAAACAGACAAAGGTTACAGACA 462
Qy 101 AlSerVal11e11eAlaLeuThrAspGlyGluLeuHisGlyAspLeuPhePheTySer 120
Db 463 GCCAGCTCATCATCTGCTTGGACTGATGAGACTCATGAAAGATCTTTTCTATTCA 522
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyVal11eValTyTyCysValGlyValLys 140
Db 523 GAGAGGAGGCTAATAGCTCTCGAGATCTGGTCAATGTTACTGTGTGGTGAA 582
Qy 141 AspPheAsnGluThrglnLeuAlaArg11eAlaAspSerLysAspHisValPheProVal 160
Db 583 GATTTCATGACAGACACAGCTGCGCCGATTCGACAGTAAGATCATGTGTTCCCGTG 642
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGly11e11eHisSer11eLeuLysLysSerCys11e 180
Db 643 AATGACCGCTTTCAGGCTTGACGACGATCATCATCAATTGGAAGAGTCTTGATC 702
Qy 181 Glu 181
Db 703 GAA 705

RESULT 4
US-10-201-292-21
; Sequence 21, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-21

Alignment Scores:
Pred. No.: 1,82e-116 Length: 1047
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-21 (1-1047)
Qy 1 G1yPheAspLeuTyTrPhe11eLeuAspLysSerGlySerValLeuHis1StrPaAnglu 20
Db 163 GGAATTGACCTGTAATCTTATTTGGACAATACGAAAGTGCTGCACTGGAAATGAA 222
Qy 21 11eTyTyTyPheValGluGlnLeuAlaHisLysPhe11eSerProGlnLeuArgMetSer 40
Db 223 ATCATTAATTGTTGGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATGTC 282
```

```
Qy 41 Phe11eValPheSerThrArg1yThrThleuMetLysLeuThrgluAspArgGluGln 60
Db 283 TTTATTGTTTCTCCACCCAGAAACACTTAATGAACACGACAGAAACAGAAACAA 342
Qy 61 11eArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyMetHis 80
Db 343 ATCCGTAAAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCAT 402
Qy 81 GluGlyPheGluArgAlaSerGluGln11eTyTyTyGluAsnArgGlnGlyTyArgThr 100
Db 403 GAAGGATTGMAAGGCGCAGTGAGACAGATTATTAAGAAACAGACAAAGGTTACAGACA 462
Qy 101 AlSerVal11e11eAlaLeuThrAspGlyGluLeuHisGlyAspLeuPhePheTySer 120
Db 463 GCCAGCTCATCATCTGCTTGGACTGATGAGACTCATGAAAGATCTTTTCTATTCA 522
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyVal11eValTyTyCysValGlyValLys 140
Db 523 GAGAGGAGGCTAATAGCTCTCGAGATCTGGTCAATGTTACTGTGTGGTGAA 582
Qy 141 AspPheAsnGluThrglnLeuAlaArg11eAlaAspSerLysAspHisValPheProVal 160
Db 583 GATTTCATGACAGACACAGCTGCGCCGATTCGACAGTAAGATCATGTGTTCCCGTG 642
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGly11e11eHisSer11eLeuLysLysSerCys11e 180
Db 643 AATGACCGCTTTCAGGCTTGACGACGATCATCATCAATTGGAAGAGTCTTGATC 702
Qy 181 Glu 181
Db 703 GAA 705

RESULT 5
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23

Alignment Scores:
Pred. No.: 1,84e-116 Length: 1056
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-038-307-23 (1-1056)
Qy 1 G1yPheAspLeuTyTrPhe11eLeuAspLysSerGlySerValLeuHis1StrPaAnglu 20
Db 136 GGAATTGACCTGTAATCTTATTTGGACAATACGAAAGTGCTGCACTGGAAATGAA 195
Qy 21 11eTyTyTyPheValGluGlnLeuAlaHisLysPhe11eSerProGlnLeuArgMetSer 40
Db 196 ATCATTAATTGTTGGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATGTC 255
Qy 41 Phe11eValPheSerThrArg1yThrThleuMetLysLeuThrgluAspArgGluGln 60
```

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Db      256 TTTATGTTTCTCCACCGAGAACACTTAATGAACAGAGAACAA 315
      |||
Qy      61 IleaRGInGlyLeuGluLeuGlnlyValLeuProGlyGlyAspThrTyrmehis 80
      |||
Db      316 ATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATGCAT 375
      |||
Qy      81 GluGlyPheGluArgAlaSerGluGlnIleTyrrTyrgluAsnArgGlnGlyTyraGthr 100
      |||
Db      376 GAAGGATTTGAAAGGGCCAGTGACAGATTATTATGAAGAACAGACAGGGATACAGACA 435
      |||
Qy      101 AlaSerValIleIleAlaLeuThrAspGlyGluLeuHisglnAspLeuPhePheTyrsr 120
      |||
Db      436 GCCAGCTCATCTGCTTGTGACTGATGAGAACTCCATGAGATCTCTTTTCTATTTCA 495
      |||
Qy      121 GluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrcysValGlyValIys 140
      |||
Db      496 GAGAGGAGGCTAATAGCTCTCGAGATCTTGCGCAATTGTTTACTGTGGTGGAA 555
      |||
Qy      141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
      |||
Db      556 GATTTCAATGAGACACAGCTGGCCGGATTGCGAGACGTAAGATCATGTGTTCCCGTG 615
      |||
Qy      161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysAspCysIle 180
      |||
Db      616 AATGACGGCTTTCAGGCTCTGCAAGGCATCATCACTCAATTTGAAAGATCTGCATC 675
      |||
Qy      181 Glu 181
      |||
Db      676 GAA 678
```

RESULT 6
US-10-201-292-23
; Sequence 23, Application US/10201292
; Publication No. US20030144193A1

```
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 1056  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-23
```

Alignment Scores:
Pred. No.: 1,84e-116 Length: 1056
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-23 (1-1056)

```
Qy      1 GlyPheAspLeuTyrrPheIleLeuAspIysSerGlySerValLeuHisIleTPraGln 20
      |||
Db      136 GGATTTGACCTGTACTTCATTTTGACAAATCAGAAAGTGTGCACTGGAATGAA 195
      |||
Qy      21 IleTyrrTyrrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40
      |||
Db      196 ATCTAATTACTTTGTGAAACAGTTGGCTCAAAATTCATCCACCACTTGAGAAATGTC 255
      |||
Qy      41 PheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArgGluGln 60
      |||
Db      256 TTTATGTTTCTCCACCGAGAACAACTTAATGAAGATGACAGAAACAGAGAACAA 315
```

```
Qy      61 IleaRGInGlyLeuGluLeuGlnlyValLeuProGlyGlyAspThrTyrmehis 80
      |||
Db      316 ATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATGCAT 375
      |||
Qy      81 GluGlyPheGluArgAlaSerGluGlnIleTyrrTyrgluAsnArgGlnGlyTyraGthr 100
      |||
Db      376 GAAGGATTTGAAAGGGCCAGTGACAGATTATTATGAAGAACAGACAGGGATACAGACA 435
      |||
Qy      101 AlaSerValIleIleAlaLeuThrAspGlyGluLeuHisglnAspLeuPhePheTyrsr 120
      |||
Db      436 GCCAGCTCATCTGCTTGTGACTGATGAGAACTCCATGAGATCTCTTTTCTATTTCA 495
      |||
Qy      121 GluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrcysValGlyValIys 140
      |||
Db      496 GAGAGGAGGCTAATAGCTCTCGAGATCTTGCGCAATTGTTTACTGTGGTGGAA 555
      |||
Qy      141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
      |||
Db      556 GATTTCAATGAGACACAGCTGGCCGGATTGCGAGACAGTAAGATCATGTGTTCCCGTG 615
      |||
Qy      161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysAspCysIle 180
      |||
Db      616 AATGACGGCTTTCAGGCTCTGCAAGGCATCATCACTCAATTTGAAAGATCTGCATC 675
      |||
Qy      181 Glu 181
      |||
Db      676 GAA 678
```

RESULT 7
US-10-201-292-27
; Sequence 27, Application US/10201292
; Publication No. US20030144193A1

```
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 1401  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-27
```

Alignment Scores:
Pred. No.: 2,84e-116 Length: 1401
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-27 (1-1401)

```
Qy      1 GlyPheAspLeuTyrrPheIleLeuAspIysSerGlySerValLeuHisIleTPraGln 20
      |||
Db      136 GGATTTGACCTGTACTTCATTTTGACAAATCAGAAAGTGTGCACTGGAATGAA 195
      |||
Qy      21 IleTyrrTyrrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40
      |||
Db      196 ATCTAATTACTTTGTGAAACAGTTGGCTCAAAATTCATCCACCACTTGAGAAATGTC 255
      |||
Qy      41 PheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArgGluGln 60
      |||
Db      256 TTTATGTTTCTCCACCGAGAACAACTTAATGAAGATGACAGAAACAGAGAACAA 315
      |||
Qy      61 IleaRGInGlyLeuGluLeuGlnlyValLeuProGlyGlyAspThrTyrmehis 80
```

```
Db 316 ATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATCAT 375
Qy 81 GUGUlyPheGluAaGAlaSerGluGlnIleTyTyTgUlnAaArgGlnGlyTyArgThr 100
Db 376 GAAGGATTGAAAGGGCCAGTGAACAGATTATATGAAACAGACAGAGGTACAGACA 435
Qy 101 AlaserValIleIleAlaLeuThrAspGlyGluLeuHisGluAaPhePheTySer 120
Db 436 GCCAGGCTCATCTTGGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCA 495
Qy 121 GUAArgGluAlaAaArgSerArgAspLeuGlyAlaIleValTyTgCysValGlyValLys 140
Db 496 GAGAGGAGGCTAAATAGCTCTCGAGATCTTGTCGAATTTGTTACTGTGTTGGTGAAA 555
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 556 GATTTCATATAGACACAGCTGGCCCGATTCGGACAGTAAAGATCATGTGTTCCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCysIle 180
Db 616 AATGACGGCTTTTCAGGCTCTGCAGAGCATCATCTCACTTATTTGAAGAGTCTGCATC 675
Qy 181 Glu 181
Db 676 GAA 678

RESULT 8
US-10-201-292-29
; Sequence 29, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; PRIORITY FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-201-292-29

Alignment Scores:
Pred. No.: 2,846-116 Length: 1401
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-29 (1-1401)
Qy 1 GlyPheAspLeuTyRrPheIleLeuAspLysSerGlySerValLeuHisIleSTrPaGln 20
Db 136 GGAATTGACCTGTACTTTCATTTTGGACAATCAGAAAGTGTGTGCACTGGAAATGAA 195
Qy 21 IleTyTyTgPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMetSer 40
Db 196 ATCTATTACTTGTGGAAAGTTGGCTCACAATAATTCAGCCCAAGTTGAGATGTCC 255
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAaArgGluGln 60
Db 256 TTTATTCTTTCTCCACCCAGAAACAACCTTATGAACTGACAGAAAGACAGAAACA 315
Qy 61 IleArgGlnIleLeuGlnIleLeuGlnLysValLeuProGlyIleAspThrTyMetHis 80
Db 316 ATCCGTCAAGGCTTAGAAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATCAT 375
```

```
Qy 81 GUGUlyPheGluAaGAlaSerGluGlnIleTyTyTgUlnAaArgGlnGlyTyArgThr 100
Db 376 GAAGGATTGAAAGGGCCAGTGAACAGATTATATGAAACAGACAGAGGTACAGACA 435
Qy 101 AlaserValIleIleAlaLeuThrAspGlyGluLeuHisGluAaPhePheTySer 120
Db 436 GCCAGGCTCATCTTGGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCA 495
Qy 121 GUAArgGluAlaAaArgSerArgAspLeuGlyAlaIleValTyTgCysValGlyValLys 140
Db 496 GAGAGGAGGCTAAATAGCTCTCGAGATCTTGTCGAATTTGTTACTGTGTTGGTGAAA 555
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 556 GATTTCATATAGACACAGCTGGCCCGATTCGGACAGTAAAGATCATGTGTTCCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCysIle 180
Db 616 AATGACGGCTTTTCAGGCTCTGCAGAGCATCATCTCACTTATTTGAAGAGTCTGCATC 675
Qy 181 Glu 181
Db 676 GAA 678

RESULT 9
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047.278
; PRIORITY FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970.076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251.481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
; US-11-047-278-1

Alignment Scores:
Pred. No.: 2,886-116 Length: 1414
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-11-047-278-1 (1-1414)
Qy 1 GlyPheAspLeuTyRrPheIleLeuAspLysSerGlySerValLeuHisIleSTrPaGln 20
Db 227 GGAATTGACCTGTACTTTCATTTTGGACAATCAGAAAGTGTGTGCACTGGAAATGAA 286
Qy 21 IleTyTyTgPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMetSer 40
Db 287 ATCTATTACTTGTGGAAAGTTGGCTCACAATAATTCAGCCCAAGTTGAGAAATGTCC 346
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAaArgGluGln 60
```

Db 347 TTTATTGTTTCTCCACCCGAGAGACACTTAATGAACTGACAGAGACAGAGAACAA 406
Qy 61 TLeArgGlnGlyLeuGlnGlyLeuGlnGlyValLeuProGlyGlyAspThrTyrMetHis 80
Db 407 ATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGCAAT 466
Qy 81 GlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGlnuAsnArgGlnGlyTyrArgThr 100
Db 467 GAAGATTTCAGAAAGCCGACAGAGATTTATTAAGAAACAGACAGAGGTACAGAGAC 526
Qy 101 AlaSerValIleIleAlaLeuThrAspGlyGlnuLeuHisGlnuAspLeuPhePheTyrSer 120
Db 527 GCCAGGCTCATCTTGGCTTTCATGATGAGAACTCCATGAAATCTCTTTTCTTATCA 586
Qy 121 GlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLys 140
Db 587 GAGAGGAGGCTTAATAGGTCTCGAGATCTTGAGCAATTTTACGTGTGTGTGAAA 646
Qy 141 AspPheAsnGlnuThrGlnuLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 647 GATTTCATAGACACACAGCTGCCCGGATTCGGGACAGTAAGATCATGTGTTCCCGTG 706
Qy 161 AsnAspGlyPheGlnuAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 707 AATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAAAGTCTGCATC 766
Qy 181 Gln 181
Db 767 GAA 769

RESULT 10

US-11-047-278-9
; Sequence 9, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047, 278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970, 076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251, 481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-11-047-278-9

Alignment Scores:
Pred. No.: 2,95e-116 Length: 1436
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-11-047-278-9 (1-1436)

Qy 1 GlnPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTPaAnglu 20
Db 266 GGATTTCAGCTGTACTTCATTTTGGACAAATCAGAAAGTGTGTCACCACTGGAAATGAA 325
Qy 21 TLeTyrTyrPheValGlnGlnuLeuAlaHisLysPheIleSerProGlnuLeuArgMetSer 40

Db 326 ATCTATTCTTGTGTGGAACAGTTGGCTCACAATTCATCAGGCCACAGTTGGAATGTC 385
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnuAspArgGlnu 60
Db 386 TTTATTGTTTCTCCACCCGAGAAACACTTAATGAACTGACAGAAACAGAGAACAA 445
Qy 61 TLeArgGlnGlyLeuGlnuLeuGlnuLysValLeuProGlyGlyAspThrTyrMetHis 80
Db 446 ATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGCAAT 505
Qy 81 GlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGlnuAsnArgGlnGlyTyrArgThr 100
Db 506 GAAGATTTCAGAAAGCCGACAGAGCAATTTATTTGAAACAGCAAGGATACAGAGAA 565
Qy 101 AlaSerValIleIleAlaLeuThrAspGlyGlnuLeuHisGlnuAspLeuPhePheTyrSer 120
Db 566 GCTAGGCTCATCTTGGCTTTCATGATGAGAACTCCATGAAATCTCTTTTCTTATTC 625
Qy 121 GlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLys 140
Db 626 GAGAGGAGGCTTAATAGGTCTCGAGATCTTGTCAAATTTTACTGTGTGTGAAA 685
Qy 141 AspPheAsnGlnuThrGlnuLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 686 GATTTCATAGACACACAGCTGCCCGGATTCGGGACAGTAAGATCATGTGTTCCCGTG 745
Qy 161 AsnAspGlyPheGlnuAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 746 AATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAAAGTCTGCATC 805
Qy 181 Gln 181
Db 806 GAA 808

RESULT 11

US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Petersen, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133, 937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 3e-116 Length: 1454
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-133-937-58 (1-1454)

Qy 1 GlnPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTPaAnglu 20
Db 267 GGATTTCAGCTGTACTTCATTTTGGACAAATCAGAAAGTGTGTCACCACTGGAAATGAA 326
Qy 21 TLeTyrTyrPheValGlnGlnuLeuAlaHisLysPheIleSerProGlnuLeuArgMetSer 40

DB 327 ATCTATTACTTGTGGAAACAGTTGGCTCACAATTCATCAGCCACAGTTGAGATGTCC 386
QY PheIleValPheSerThrArgGlyThrThreumetylserLeuThrGluAspArgGluGln 60
DB 387 TTTATGTTTCTTCACCCGAGAACAACTTAATGAAGTGAACAGACAGAACAA 446
QY IleArgGlnGlyLeuGluGluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHis 80
DB 447 ATCCGTACAGGCTCAGAAAGAACTCCAGAACTTCAGAGAGAGACACTTACATCAT 506
QY GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
DB 507 GAAGGATTGGAAGGCGCAGTGAAGCATTTATGAAACAGACAGAGGTTACAGACA 566
QY AlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
DB 567 GCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTTATTTCA 626
QY GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValIys 140
DB 627 GAGAGGAGGCTAATAGCTCTCGAGATCTTGTCATTTGTTCTGTGGTGTA 686
QY AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
DB 687 GATTTCATGAGACACAGCTGGCCGAGATTCCGACAGTAAGATCATGTGTTCCCGTG 746
QY 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysSerCysIle 180
DB 747 AATGACGGCTTTCAGGCTCTGCAAGGATCATTCACATTTTGAAGAGTCTCGATC 806
QY 181 Glu 181
DB 807 GAA 809

RESULT 12

US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Metzger, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:

Pred. No.: 3e-116
Score: 943.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

Length: 1454
Matches: 181
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-159-563-58 (1-1454)

QY 1 GTPheAspLeuTyrPheIleValLeuAspIysSerGlySerValLeuHisThrPheGln 20
DB 267 GGAATTGACCTGACTTCACTTATTTGGACAAATCAGAAAGTGTGTGACACACGGAATGAA 326

QY 21 IleTyrTyrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40
DB 327 ATCTATTACTTGTGGAAACAGTTGGCTCACAATTCATCAGCCACAGTTGAGATGTCC 386
QY PheIleValPheSerThrArgGlyThrThreumetylserLeuThrGluAspArgGluGln 60
DB 387 TTTATGTTTCTTCACCCGAGAACAACTTAATGAAGTGAACAGACAGAACAA 446
QY IleArgGlnGlyLeuGluGluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHis 80
DB 447 ATCCGTACAGGCTCAGAAAGAACTCCAGAACTTCAGAGAGAGACACTTACATCAT 506
QY GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
DB 507 GAAGGATTGGAAGGCGCAGTGAAGCATTTATGAAACAGACAGAGGTTACAGACA 566
QY AlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
DB 567 GCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTTATTTCA 626
QY GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValIys 140
DB 627 GAGAGGAGGCTAATAGCTCTCGAGATCTTGTCATTTGTTCTGTGGTGTA 686
QY AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
DB 687 GATTTCATGAGACACAGCTGGCCGAGATTCCGACAGTAAGATCATGTGTTCCCGTG 746
QY 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysSerCysIle 180
DB 747 AATGACGGCTTTCAGGCTCTGCAAGGATCATTCACATTTTGAAGAGTCTCGATC 806
QY 181 Glu 181
DB 807 GAA 809

RESULT 13

US-10-201-292-31
; Sequence 31, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALRY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-31

Alignment Scores:

Pred. No.: 3.04e-116
Score: 943.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

Length: 1464
Matches: 181
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-31 (1-1464)

QY 1 GTPheAspLeuTyrPheIleValLeuAspIysSerGlySerValLeuHisThrPheGln 20
DB 136 GGAATTGACCTGACTTCACTTATTTGGACAAATCAGAAAGTGTGTGACACACGGAATGAA 195
QY 21 IleTyrTyrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40

Db 196 ATCTATTACTTTGTGGAAACAGTTGGCTCAAAATTCATACGCCACAGTTGAGAAATGTCC 255
Qy 41 PheIIeValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArgGluGln 60
Db 256 TTTATTGTTTCTTCACCCGAGAAACAACCTTAATGAACCTGACAGAAACAGAGAACAA 315
Qy 61 IleArgGlnGlyLeuGlnGluLeuGlnIleValIleuProGlyGlyAspThrTyrmethis 80
Db 316 ATCCGTCAAGGCTTAAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATGCAT 375
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsnArgGlnGlyTyArgThr 100
Db 376 GAAGAGATTGAAAAGGCGCAGTGAAGATTTATATGAAAACAGACAGGGGTACAGACAC 435
Qy 101 AlAserValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTySer 120
Db 436 GCCAGGCTCATCTGCTTGTGACATGATGAGAACTCCATGAATCTCTTTCTCATATCA 495
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyTyCysValGlyValIys 140
Db 496 GAAGAGAGGCTTAATAGCTCTCCAGATCTTGCGCAATTTGTTACTGTGTGGTGGAAA 555
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
Db 556 GATTCAATGACACACAGCTGCGCCGATTCGCGACAGTAAGATCATCTGTTCCTCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSerCysIle 180
Db 616 AATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAAAGTCTGCAATC 675
Qy 181 Glu 181
Db 676 GAA 678

RESULT 14
US-10-201-292-33
/ Sequence 33, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 1534
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-33

Alignment Scores:
Pred. No.: 3,26e-116 Length: 1534
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-33 (1-1534)

Qy 1 GlyPheAspLeuTyrrPheIleLeuAspIysSerGlySerValIleuHisHisIleTPAsnGlu 20
Db 136 GGATTGACCTGTACTTCAATTTGGACAATAACAGAAATGTGCTGCACCACTGGAATGAA 195
Qy 21 IleTyTyrrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuAspMetSer 40
Db 196 ATCTATTACTTTGTGGAAACAGTTGGCTCAAAATTCATCAAGCCACAGTTGAGATGTCC 255

Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArgGluGln 60
Db 256 TTTATTGTTTCTTCACCCGAGAAACAACCTTAATGAACCTGACAGAAACAGAGAACAA 315
Qy 61 IleArgGlnGlyLeuGlnGluLeuGlnIleValIleuProGlyGlyAspThrTyrmethis 80
Db 316 ATCCGTCAAGGCTTAAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATGCAT 375
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsnArgGlnGlyTyArgThr 100
Db 376 GAAGAGATTGAAAAGGCGCAGTGAAGATTTATATGAAAACAGACAGGGGTACAGACAC 435
Qy 101 AlAserValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTySer 120
Db 436 GCCAGGCTCATCTGCTTGTGACATGATGAGAACTCCATGAAGATCTCTTTCTCATATCA 495
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyTyCysValGlyValIys 140
Db 496 GAAGAGAGGCTTAATAGCTCTCCAGATCTTGCGCAATTTGTTACTGTGTGGTGGAAA 555
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
Db 556 GATTCAATGACACACAGCTGCGCCGATTCGCGACAGTAAGATCATCTGTTCCTCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSerCysIle 180
Db 616 AATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAAAGTCTGCAATC 675
Qy 181 Glu 181
Db 676 GAA 678

RESULT 15
US-10-201-292-35
/ Sequence 35, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 1608
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-35

Alignment Scores:
Pred. No.: 3,51e-116 Length: 1608
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-35 (1-1608)

Qy 1 GlyPheAspLeuTyrrPheIleLeuAspIysSerGlySerValIleuHisHisIleTPAsnGlu 20
Db 136 GGATTGACCTGTACTTCAATTTGGACAATAACAGAAATGTGCTGCACCACTGGAATGAA 195
Qy 21 IleTyTyrrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuAspMetSer 40
Db 196 ATCTATTACTTTGTGGAAACAGTTGGCTCAAAATTCATCAAGCCACAGTTGAGATGTCC 255
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArgGluGln 60

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Db      256 TTTATTGTTTCTCCACCCGAGAACAACTTAATGAAGTACAGAGAACAGAACAA 315
Qy      61  |||
Db      316 ATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCA 375
Qy      81  |||
Db      376 GAAGGATTTGAAAGGCCACAGTACAGCAATTTATTTGAAACAGACAAAGGTACAGACA 435
Qy      101 AlaserValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
Db      436 GCCAGCGTCATCATTTGCTTGACTGATGAGAACTCCATGAAGATCTCTTTCTCATTCA 495
Qy      121 GluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValIys 140
Db      496 GAGAGGAGGCTTAATAGGTCCTGAGATCTTGTCMAATTTGTTACTGTGTGTGAGAA 555
Qy      141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db      556 GATTTCATAGACACACAGCTGCGCCGATTCGAGACAGTANAGATCATGTGTTCCCGTG 615
Qy      161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db      616 AATGACGGCTTTTCAGGCTCTGCAAGGCATCATCCAAATTTTGAAGAAAGTCTGCATC 675
Qy      181 Glu 181
Db      676 GAA 678
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Search completed: December 19, 2005, 02:10:36
Job time : 586.877 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 146.057 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Perfect score: 943
Sequence: 1 GFDLYFLDKSGSVLHMNE.....DGFQALQGIHSILKKSCTE 181

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human4.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076.cgn.1.675_rnuc.14122005.11853.21065
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

Published Applications NA New:
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2: /cgn2_6/ptodata/1/pubphn/US06_NEW_PUB.seq:
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5: /cgn2_6/ptodata/1/pubphn/PCT_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubphn/US10_NEW_PUB.seq:
7: /cgn2_6/ptodata/1/pubphn/US11_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubphn/US11_NEW_PUB.seq2:
9: /cgn2_6/ptodata/1/pubphn/US11_NEW_PUB.seq3:
10: /cgn2_6/ptodata/1/pubphn/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1 | 943 | 100.0 | 5540 | 7 US-11-186-284-198 | Sequence 198, App |
| 2 | 132.5 | 14.1 | 4740 | 7 US-11-080-026-3 | Sequence 3, Appl |
| 3 | 126.5 | 13.4 | 11447 | 7 US-11-186-284-25 | Sequence 25, Appl |
| 4 | 122 | 12.9 | 2834 | 6 US-10-750-185-39040 | Sequence 39040, A |
| 5 | 109 | 11.6 | 3449 | 6 US-10-131-826A-293 | Sequence 293, App |
| 6 | 108 | 11.5 | 3564 | 6 US-10-601-368-20 | Sequence 20, Appl |
| 7 | 108 | 11.5 | 4858 | 6 US-10-601-368-19 | Sequence 19, Appl |
| 8 | 107 | 11.3 | 1325 | 6 US-10-750-185-56394 | Sequence 56394, A |

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|---|----|-------|------|-------|-----------------------|--------------------|
| C | 9 | 105.5 | 11.2 | 2501 | 6 US-10-821-234-182 | Sequence 182, App |
| | 10 | 104 | 11.0 | 3564 | 6 US-10-601-368-2 | Sequence 2, Appl |
| | 11 | 104 | 11.0 | 3967 | 7 US-11-000-463-574 | Sequence 574, App |
| | 12 | 104 | 11.0 | 3969 | 7 US-11-000-463-102 | Sequence 102, App |
| | 13 | 104 | 11.0 | 5042 | 6 US-10-601-368-1 | Sequence 1, Appl |
| | 14 | 103.5 | 11.0 | 3175 | 6 US-10-995-561-464 | Sequence 464, App |
| | 15 | 103.5 | 11.0 | 3464 | 6 US-10-995-561-465 | Sequence 465, App |
| | 16 | 103.5 | 11.0 | 3468 | 6 US-10-995-561-466 | Sequence 466, App |
| | 17 | 101.5 | 10.8 | 47572 | 6 US-10-995-561-13356 | Sequence 13356, A |
| | 18 | 95.5 | 10.1 | 3868 | 6 US-10-995-561-404 | Sequence 404, App |
| | 19 | 95 | 10.1 | 3884 | 6 US-10-601-368-17 | Sequence 17, Appl |
| | 20 | 94 | 10.0 | 2773 | 7 US-11-102-240-33 | Sequence 33, Appl |
| | 21 | 89.5 | 9.5 | 1062 | 7 US-11-137-465-11 | Sequence 11, Appl |
| | 22 | 89.5 | 9.5 | 1347 | 7 US-11-137-465-12 | Sequence 12, Appl |
| C | 23 | 79.5 | 8.4 | 3366 | 6 US-10-467-657-6111 | Sequence 6111, App |
| | 24 | 75 | 8.0 | 3435 | 6 US-10-793-626-3648 | Sequence 3648, App |
| | 25 | 74 | 7.8 | 1688 | 6 US-10-510-186-157 | Sequence 157, App |
| C | 26 | 73.5 | 7.8 | 1530 | 6 US-10-793-626-2879 | Sequence 2879, App |
| | 27 | 73.5 | 7.8 | 2996 | 6 US-10-793-626-3563 | Sequence 3563, App |
| C | 28 | 73.5 | 7.8 | 3092 | 6 US-10-793-626-3559 | Sequence 3559, App |
| | 29 | 73.5 | 7.8 | 3900 | 6 US-10-793-626-4177 | Sequence 4177, App |
| | 30 | 73 | 7.7 | 795 | 6 US-10-793-626-387 | Sequence 387, App |
| | 31 | 73 | 7.7 | 876 | 6 US-10-793-626-2635 | Sequence 2635, App |
| | 32 | 73 | 7.7 | 2657 | 6 US-10-793-626-3472 | Sequence 3472, App |
| C | 33 | 73 | 7.7 | 3281 | 6 US-10-793-626-4324 | Sequence 4324, App |
| | 34 | 73 | 7.7 | 3290 | 6 US-10-793-626-3960 | Sequence 3960, App |
| C | 35 | 73 | 7.7 | 3633 | 6 US-10-793-626-4307 | Sequence 4307, App |
| | 36 | 72 | 7.6 | 2361 | 6 US-10-467-626-102 | Sequence 102, App |
| | 37 | 70 | 7.4 | 1305 | 6 US-10-467-657-5693 | Sequence 5693, App |
| C | 38 | 70 | 7.4 | 1404 | 6 US-10-467-657-5695 | Sequence 5695, App |
| | 39 | 70 | 7.4 | 96988 | 7 US-11-117-187-196 | Sequence 196, App |
| | 40 | 69.5 | 7.4 | 730 | 6 US-10-750-185-61019 | Sequence 61019, A |
| | 41 | 69.5 | 7.4 | 1467 | 6 US-10-467-657-7845 | Sequence 7845, App |
| | 42 | 69.5 | 7.4 | 1887 | 6 US-10-467-657-249 | Sequence 249, App |
| | 43 | 69.5 | 7.4 | 1887 | 6 US-10-467-657-3083 | Sequence 3083, App |
| | 44 | 69 | 7.3 | 726 | 6 US-10-467-657-7305 | Sequence 7305, App |
| C | 45 | 69 | 7.3 | 786 | 6 US-10-467-657-7299 | Sequence 7299, App |

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Sequence 198, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgett, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RM
; CURRENT APPLICATION NUMBER: US/11186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA


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; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
; US-11-186-284-25

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Alignment Scores:
Pred. No.: 7,18e-05 Length: 11447
Score: 126.50 Matches: 55
Percent Similarity: 48.95% Conservative: 38
Best Local Similarity: 28.95% Mismatches: 74
Query Match: 13.41% Indels: 23
Gaps: 12

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US-09-970-076-2_COPY_42_222 (1-181) x US-11-186-284-25 (1-11447)
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QY 3 AspleuTyRheleuAerlySeSerGlySeVal---leuHsiStrPaenglu 21
DB 1318 GATATCTGTTTGGTGTGATGCTCTATAGCATTCGAGTTCGAACTTTGTTAAAGTT 1377
QY 22 TyTyTyRheValGluGluInleuAaHsiLePhe---lleSePro---GlnleuAerGmet 39
DB 1378 AGAGCCCTTTTGGAGTCTCTGTAAAGTTTGAATTTTCAACCAATTAAGGCTTCAGATT 1437
QY 40 SerPheleValPheSerThr-----ArgGlyThrRheuMeLysLeuThrGlu 56
DB 1438 AGCTTGTGCAATACAGCCCGGATCTCATACAGTTCCTTTGAAAAAATTCACCAAA 1497
QY 57 AsparGluGluInleuArgGluGlyLeuGluGluLeuGluInleuValleuPro-----Gly 74
DB 1498 GTTGAAGATATAATT-----GAAGCAATAAACAACCTTCCTTACAGAGA 1542
QY 75 GlyAspThrTyRheHsiGluGlyPheGluArgAlaSerGluGluInleuTyTyTyGluAa 94
DB 1543 GGATCTTCAAAATCTGGCAAGCAATGATTATGTCAAGAAATAATTTGTGCTTAC 1602
QY 95 ArgGlnGlyTyRArgThr-----AlaSerValleleleuThrAspGlyGluLeu 112
DB 1603 AAG---GGATCAAGCAATGATGCGCAAGATCATGATTTCTTATACAGGATGGAAA--- 1656
QY 113 HsiGluAspLeuPhePheTyRSerGluArgGluAlaAspArgSerArgAspLeuGlyAla 132
DB 1657 TCATCGATGCTTTTC-----AGAGATCTGCGATAAATCAAGGAATTCAGATGTT 1707
QY 133 lleValTyRcyValGlyValleuAspPheAsnGluThrGlnleuAlaArglleAlaAsp 152
DB 1708 GAATCTTTTGCAGTGTGTGAGAGATGCGCTTGCAGATTTGGAAGCTTATTTGCTCT 1767
QY 153 -----SerTyAspHsiValPheProValAspAspGlyPheGlnAlaLeuGlnGlylle 170
DB 1768 CTCCTGCAAGACCAATGCTTTCACAGTGAAGAT---TTTATGCTTTTTCAGAGATA 1824
QY 171 lleHsiSerlleuLeuTyblySerCyslle 180
DB 1825 TCTTTGAACTCACACAGTCTATCTGCTT 1854

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RESULT 4

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US-10-750-185-39040/c
; Sequence 39040, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39040
; LENGTH: 2834
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-39040

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Alignment Scores:
Pred. No.: 3.66e-05 Length: 2834
Score: 122.00 Matches: 54
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 29.03% Mismatches: 71
Query Match: 12.94% Indels: 24
Gaps: 10

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US-09-970-076-2_COPY_42_222 (1-181) x US-10-750-185-39040 (1-2834)
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DB 2115 GACATTTACTCTTTTGTGAGGGGCTTGGCAGTACC-----CACCAAGCAGCTTCTC 2062
QY 21 ---lleTyTyRheValGluGluInleuAaHsiLePhe---lleSeProGlnleuAerG 38
DB 2061 GCAGTGAAGGTGTTTCAATGATAGATGATTAAGATGTTCCAGCTTGGACCGAAC---AGA 2005
QY 39 MetSerPheleValPheSerThrArgGlyThrRheuMeLysLeuThrGluAsp 58
DB 2004 GTCCAGTTTGGAGTCTCTGATCTGCGATGGAAGTCACTCCAGATTACCTCAGCCAG 1945
QY 58 GlnGluInleuArgGlnGlyLeuGlu-----GlnleuGlnleuValleuProG 74
DB 1944 CACTCCAGTGTGCGACGGCTTGGAGTACCGCTTACAGCATCCAGCAG-----AAGGG 1891
QY 74 YGlyAspThrTyRheHsiGluGlyPheGluArgAlaSerGluGluInleuTyTyTyGluAa 94
DB 1890 AGGGGACCAACAAATGAGGAGGCGCTG---GGCAGATGATCCAGGTTTCCAGACTC 1834
QY 94 nArgGlnGlyTyRArgThrAlaSerValleleleuThrAspGlyGluLeuHsiG 114
DB 1833 TGCTCCAGCAA---CGTGCCCTT---GGTATCTCATTTGTTGTACATCGAGCGCAATCTATGGA 1776
QY 114 uAspLeuPhePheTyRSerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleVa 134
DB 1775 CCGGGTG-----GCTGATCTGCAAGGCGCTGAGGGGCGCATGAGATCACCAT 1728
QY 134 lTyRcyValGlyValleuAspPheAsnGluThrGlnleuAlaArglleAlaAspSerly 154
DB 1727 TTATGCAAGTTGAGTGAAGATCTAATATGCTGAGCTTCAAGAGATTGCTGAA----- 1673
QY 154 AspHsiValPheProValAspAspGlyPheGlnAlaLeuGlnGlylleHsiSer1 174
DB 1672 -GACAGAAATGTTTGTGTCATGAT---TTTATGCTCTTGAAGACCATCCACACAGAAAT 1617
QY 174 eleuTyblySerCys 179

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Db 490 GACATCGTCATTGCTTAGATGCTCCAGACAGCATC---TACCCCTGGGTGGAGGTCAA 546
Qy 23 TyrPheValGluGlnLeuAlaHisIlePhe---IleSerPro---GlnLeuArgMetSer 40
Db 547 CACTTCTCTCATATCTCTCAAAAAGTTCTACATCTGAGCCCGCCAGATCCAGGTGGA 606
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIleValLeuArgGluGln 60
Db 607 ATAGTCCAGATGAGAAAGATGCCGTCATGATTCACCTT---AATGACTACAGGTCT 663
Qy 61 IleArgGlnGlyLeuGluGlnLeuGlnIleValLeuProGlyGlyAspThrTyrMetHis 80
Db 664 GTAAAGATGTGTGGAGAGCCGACGACCATTTGAGAGAGAGGAGGACAGACCCGC 723
Qy 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 97
Db 724 ACCGCAATTTGGCATTTGAATTTGACGCGCTGGAGGCTTTCCAGAAAGGTGAGAAAGGG 783
Qy 98 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 115
Db 784 GCCAAG-----AAAGTGAATGATTTGTCATCGAGCGGGAATCCACAGACGCCAGAC 837
Qy 115 ----- 115
Db 838 CTGGAGAAAGGTGATCCGGCAGAGCGAGAAAGGACAACTGACACAGATACGCTGTGCCGTT 897
Qy 116 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 135
Db 898 TTGGGCTACTACAAACCGCAGGGGATCATACAGACCTTTCTAAATGAATCAAAATAC 957
Qy 136 CyeValGlyValIlyAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
Db 958 ATGCCACGACACCTTGACAGCAACACACTTCTTCAACGTCAAGATGAGCGGCCCTG--- 1014
Qy 152 AspSerIlyAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 169
Db 1015 -----AAGGACATTTGTTGATGCCCTTGGGAGCAGATCTTCAGCTTGAAAGGC 1062

RESULT 7

US-10-601-368-19
; Sequence 19, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lota, Jose M.
; FILE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; TITLE REFERENCE: 07334-27501
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28)...(3591)
; US-10-601-368-19

Alignment Scores:

Pred. No.: 0.00581 Length: 4858
Score: 108.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.45% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-2_COPY_42_222 (1-181) x US-10-601-368-19 (1-4858)

Qy 3 AspLeuTyrPheIleLeuAspIlySerGlySerValLeuHisHisTPanGluIleTyr 22
Db 517 GACATCGTCATTGCTTAGATGCTCCAAACAGATC---TACCCCTGGGTGGAGGTCAA 573
Qy 23 TyrPheValGluGlnLeuAlaHisIlePhe---IleSerPro---GlnLeuArgMetSer 40
Db 574 CACTTCTCTCATATCTCTCAAAAAGTTCTACATCTGAGCCCGCCAGATCCAGGTGGA 633
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIleValLeuArgGluGln 60
Db 634 ATAGTCCAGATGAGAAAGATGCCGTCATGATTCACCTT---AATGACTACAGGTCT 690
Qy 61 IleArgGlnGlyLeuGluGlnLeuGlnIleValLeuProGlyGlyAspThrTyrMetHis 80
Db 691 GTAAAGATGTGTGGAGAGCCGACGACCATTTGAGAGAGAGGAGGACAGACCCGC 750
Qy 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 97
Db 751 ACCGCAATTTGGCATTTGAATTTGACGCGCTGGAGGCTTTCCAGAAAGGTGAGAAAGGG 810
Qy 98 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 115
Db 811 GCCAAG-----AAAGTGAATGATTTGTCATCGAGCGGGAATCCACAGACGCCAGAC 864
Qy 115 ----- 115
Db 865 CTGGAGAAAGGTGATCCGGCAGAGCGAGAAAGGACAACTGACACAGATACGCTGTGCCGTT 924
Qy 116 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 135
Db 925 TTGGGCTACTACAAACCGCAGGGGATCATACAGACCTTTCTAAATGAATCAAAATAC 984
Qy 136 CyeValGlyValIlyAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
Db 985 ATGCCACGACACCTTGACAGCAACACACTTCTTCAACGTCAAGATGAGCGGCCCTG--- 1041
Qy 152 AspSerIlyAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 169
Db 1042 -----AAGGACATTTGTTGATGCCCTTGGGAGCAGATCTTCAGCTTGAAAGGC 1089

RESULT 8

US-10-750-185-56394
; Sequence 56394, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56394
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-56394

Alignment Scores:

Pred. No.: 0.00117 Length: 1325
Score: 107.00 Matches: 45
Percent Similarity: 46.35% Conservative: 44
Best Local Similarity: 23.44% Mismatches: 77
Query Match: 11.35% Indels: 26

DB: 6 Gaps: 10
US-09-970-076-2_COPY_42_222 (1-181) x US-10-750-185-56394 (1-1325)
QY 3 ApeleuTyRheIleuAaplySerGlySerVal-----LeuHisStrpAanGluIle 21
DB 483 GAGGTGGTCTTTATCATATTCAGACATCCAGCGGTCAACCCAGCATCAAGCAAGGTC 542
QY 22 TyTyrPhe---ValGluGlnLeuAlaIlePheIleSerProGlnLeu---ArgMet 39
DB 543 AAGAGATTCATTGTGACATCTTCAGACTTTTGACATTGGCCCTGACGTACCCGTGTG 602
QY 40 SerPheIleValPheSerThrArgGlyThrThrLeu-----MetLysLeu 54
DB 603 GGTGTCTCCAGTAT-----GGCAGCAGCGGTCAAGACAGATTCTCCCTCAAGACC 653
QY 55 ThrGluAapArgGluGlnIleArgGlnGlyLeuGluGlnLeuValIleProGly 74
DB 654 TTCAGAGGAAGTCCGAGGTGAGCGGTGAGCGGTCAAGAGATGCGGCACTGTCCAGCGGC 713
QY 75 GlyAapThrTyRheHisGluGlyPheGluArgAlaSerGluGlnIleTyTyrGluAan 94
DB 714 ACCATGCGGGGCTGGCCATCCAGTAC-----GCCCTGAACATCGCTTCTGGAA 764
QY 95 ArgGlnGlyTyArg-----ThrAlaSerValIleIleAlaLeuThrAap 109
DB 765 GCAAGAGGGGCGCCGCTGAGGAGAGATGTGCTGGGTCAATGATCGTACGTGAT 824
QY 110 GlyGluLeuHisGluAapLeuPhePheTyRSerGluArgGluAlaAanGlySerAArg 129
DB 825 GGAAGGCCCCAGGAGCTGGTG-----GCCAGAGTGGCCGCAAAAGCCCGGAG 872
QY 130 LeuGlyAlaIleValTyRcyValGlyVal-----LysAapPheAanGluThrGlnLeu 147
DB 873 ACAGGCACTCTGATCTTTCGATCGTGTGGGCCAGGTGACATTCAACAGCTGAAGGCC 932
QY 148 AlaArgIleAlaAapSerLysAapHisValPheProValAanAapGlyPheGlnAlaLeu 167
DB 933 ATGGAGGAGGAGCCCCAGAGAGACACGTCTTCTGTGGCCAAAC---TTCAGCCAGATT 989
QY 168 GlnGlyIleIleHisSerIleLeuLysSerGly 179
DB 990 GAGAGCTGACCTCAGTGTTCAGAGAAAGTTGTGC 1025
RESULT 9
US-10-821-234-182/C
; Sequence 182, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Steache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 182
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-821-234-182
Alignment Scores:
Pred. No.: 0.00471 Length: 2501
Score: 105.50 Matches: 48
Percent Similarity: 43.40% Conservative: 44
Best Local Similarity: 22.64% Mismatches: 75
Query Match: 11.19% Indels: 45

DB: 6 Gaps: 10
US-09-970-076-2_COPY_42_222 (1-181) x US-10-821-234-182 (1-2501)
QY 3 ApeleuTyRheIleuAaplySerGlySerVal-----LeuHisHis 17
DB 1550 AACATCTACTGTGTGATGATGATGACACATTTGGGGCCAGCACTTCAGAGAGCC 1491
QY 18 TrpAanGluTyTyrTyRheValGluGlnLeuAlaIleLysPheIleSerProGlnLeu 37
DB 1490 AAAAGTCTAGTACATACTAATTAGAAAGTGGCAAGTAAAGTGAAGCA----- 1437
QY 38 ArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlu--- 56
DB 1436 AGATATGTCTGTAGTACATATGCCATATCCACATCCCAAAATTTGGGTCAAAATGCTGAAGCA 1377
QY 57 -----AapArgGluGlnIleArgGlnGlyLeuGluGlnLeu-----Gln 69
DB 1376 GACAGCAGTAAAGCAGACTGGGTCAAGAGACTCAATGAATTCATTATGAAGCAC 1317
QY 70 LysValIleuProGlyGlyAapThrTyRheHisGluGlyPheGluArgAlaSerGluGln 89
DB 1316 AAGTTGAAGTCAAGGACATAACAC-----AAGAAGCCCTCCAGGCA 1275
QY 90 IleTyTyrGluAanArg-----GlnGlyTyR---ArgThrAla 101
DB 1274 GTGTACAGCATGATGAGCTGGCCAGATGACGTCTCTGTAAGGCTGAACCGCACCCGC 1215
QY 102 SerValIleIleAlaLeuThrAapGly----- 110
DB 1214 CATGTATCATCTCTCATGTACTGATTTGCCAACATATGGCGGAGCCCAATTACTGTC 1155
QY 111 -----GluLeuHisGluAapLeuPhePheTyRSerGluArgGluAlaAanGlySerAArg 128
DB 1154 ATTGAGAGATCCGGGACTTGCTATACATTGGCAAGATCGCAAAACCAAGAGAGAT 1095
QY 129 ApeleuGlyAlaIleValTyRcyValGly-----ValLysAapPheAanGluThrGln 146
DB 1094 TATCTGATGTCTATATGTTTGGGTGGCGCTTTGGTGAACCAAGTGAACATCAATGCT 1035
QY 147 LeuAlaArgIleAlaAapSerLysAapHisValPheProValAanAapGlyPheGlnAla 166
DB 1034 TTGGCTTCAAGAAAGACATAGCAACATGTGTTCAAAAGTCAAGAT---ATGAAAC 978
QY 167 LeuGlnGlyIleIleHisSerIleLeuLysSer 178
DB 977 CTGGAAGATGTTTCTACCAATGATGATGAAGC 942
RESULT 10
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2

Alignment Scores:

| Pred. No.: | 0.0125 | Length: | 3564 |
|------------------------|--------|---------------|------|
| Score: | 104.00 | Matches: | 48 |
| Percent Similarity: | 38.38% | Conservative: | 28 |
| Best Local Similarity: | 24.24% | Mismatches: | 84 |
| Query Match: | 11.03% | Indels: | 38 |
| DB: | 6 | Gaps: | 9 |

US-09-970-076-2_COPY_42_222 (1-181) x US-10-601-368-2 (1-3564)

QY 3 AspLeuTyrPheIleValLeuAAspLysSerGlySerValLeuH18IleTyrPaengIuIleTyr 22
490 GACATGCTCATTTGCTCGATGAGTGGCTCCACAGCATC---TACCCCTGGGGAGGTTTCAG 546
DB 23 TyrPheValGluLeuAlaHisIlePhe---IleSerPro---GlnLeuAArgMetSer 40
547 CACTTCTCATTCACACCTCTGMAAAGTTTACATTGGCCAGGCGCATCGGTTGGA 606
QY 41 PheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAArgGluGln 60
607 GTTGTGACATGATGCGCAAGATGCTGTCATGATTCACCTC---AACGACTACAGTCT 663
QY 61 IleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyIleAspThrTyrMetHis 80
664 GTAAAGATGTGGTGGAGAGTGGCCAGCCACATTGACAGAGAGAGAGAGAACAGACCCGG 723
QY 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAAspArgGlnGly 97
724 ACGGCACTTTCATTCATTAATTTGCACGCTCAGAGGCTTTCCAGAAAGGTGGAGAAAGGA 783
QY 98 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuH18IleValTyr 115
784 GCCAAG-----AAGGTGATGATTTGTATCATCAGATGGGAGTCCACAGACCCAGAC 837
QY 115 ----- 115
DB 838 CTGAGAGAGGTGATCCAGCAAGAGAAAGAGACAGTAACAAGATATGGCGTGGCCGTC 897
QY 116 LeuPhePheTyrSerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyr 135
DB 898 CTGGGCTACTACAAACCGCAGGGGATCAATCCAGAAACCTTTCTTAATGAATCAATAC 957
QY 136 CysValGlyValLysAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
958 ATGCCACATGACCCCTGATGACAAAGCACTTCTTCAATGTCACTGATGAGGCTGCTTG--- 1014
QY 152 AspSerLysAspHisValPheProValAspAspGlyPheGlnAlaLeuGlnGly 169
DB 1015 -----AAGGACATTTGTTCATGCGCTGGGGGACAGATCTTCAAGCTCGAAGGC 1062

RESULT 11
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aouni, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhilwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dimauc, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 574
; LENGTH: 3967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-574

Alignment Scores:

| Pred. No.: | 0.0147 | Length: | 3967 |
|------------------------|--------|---------------|------|
| Score: | 104.00 | Matches: | 48 |
| Percent Similarity: | 38.38% | Conservative: | 28 |
| Best Local Similarity: | 24.24% | Mismatches: | 84 |
| Query Match: | 11.03% | Indels: | 38 |
| DB: | 7 | Gaps: | 9 |

US-09-970-076-2_COPY_42_222 (1-181) x US-11-000-463-574 (1-3967)

QY 3 AspLeuTyrPheIleValLeuAAspLysSerGlySerValLeuH18IleTyrPaengIuIleTyr 22
539 GACATGCTCATTTGCTCGATGAGTGGCTCCACAGCATC---TACCCCTGGGGAGGTTTCAG 595
DB 23 TyrPheValGluLeuAlaHisIlePhe---IleSerPro---GlnLeuAArgMetSer 40
596 CACTTCTCATTCACACCTCTGMAAAGTTTACATTGGCCAGGCGCATCGGTTGGA 655
QY 41 PheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAArgGluGln 60
656 GTTGTGACATGATGCGCAAGATGCTGTCATGATTCACCTC---AACGACTACAGTCT 712
QY 61 IleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyIleAspThrTyrMetHis 80
713 GTAAAGATGTGGTGGAGAGTGGCCAGCCACATTGACAGAGAGAGAGAACAGACCCGG 772
QY 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAAspArgGlnGly 97
773 ACGGCACTTTCATTCATTAATTTGCACGCTCAGAGGCTTTCCAGAAAGGTGGAGAAAGGA 832
QY 98 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuH18IleValTyr 115
833 GCCAAG-----AAGGTGATGATTTGTATCATCAGATGGGAGTCCACAGACCCAGAC 886
QY 115 ----- 115
DB 887 CTGAGAGAGGTGATCCAGCAAGCCGAAAGAGACAGTAACAAGATATGGCGTGGCCGTC 946
QY 116 LeuPhePheTyrSerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyr 135
DB 947 CTGGGCTACTACAAACCGCAGGGGATCAATCCAGAAACCTTTCTTAATGAATCAATAC 1006
QY 136 CysValGlyValLysAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
1007 ATGCCACATGACCCCTGATGACAAAGCACTTCTTCAATGTCACTGATGAGGCTGCTTG--- 1063
QY 152 AspSerLysAspHisValPheProValAspAspGlyPheGlnAlaLeuGlnGly 169
DB 1064 -----AAGGACATTTGTTCATGCGCTGGGGGACAGATCTTCAAGCTCGAAGGC 1111

RESULT 12
US-11-000-463-102
; Sequence 102, Application US/11000463


```
Db      850  ACCGCAATTGGCATTGTAATTGCAGCTTCAGAGGCTTTCCAGAAAGGTGGAGAAAGGA 909
Qy      98  TyArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 115
      910  GCCAAG-----AAGGTGATGTTGTCATCAGATGGGAGTCCACGACAGCCAGAC 963
Qy      115  ----- 115
Db      964  CTGGAGAGGTGATCCAGAAAGGAAGACACCTAACAAGATATGCGGTGGCCGTC 1023
Qy      116  LeuPhePheTySerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 135
      1024  CTGGGCTACTACCAACCGCGGGGATCATCCAGAACTTTCTTAATGAATCAATCATAC 1083
Qy      136  CyValaGlyValIlyAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
      1084  ATGCCCAAGTACCCCTGATGACAAAGACACTTCTCAATCTCACTGATGAGCTGCGCTTG-- 1140
Qy      152  AspSerIyAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 169
      1141  -----AAGCACTATGTCATGCGCTGGGGACAGATCTTCAGCCCTGAAGGC 1188
Db
RESULT 14
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464
Alignment Scores:
Pred. No.: 0.0123 Length: 3175
Score: 103.50 Matches: 49
Percent Similarity: 40.00% Conservative: 37
Best Local Similarity: 22.79% Mismatches: 84
Query Match: 10.98% Indels: 45
DB: Gaps: 9
US-09-970-076-2_COPY_42_222 (1-181) x US-10-995-561-464 (1-3175)
Qy      4  LeuTyRheIleLeuAspIySerGlySerVal----- 14
      243  GTGTACTCTGCTGCTGACACCTCGAAGAGGTACCATGACATGCCCCACGACATCTG 302
Db      15  LeuHisIleTrrAsnGlu---IleTyTyRheValGlnGluLeuAlaHisIyPheIle 33
      303  CTCTTCCACATGAAGCAGTTGTCGCGCAGCTTCATCAGCCAGCTGCAGAAAGAGTTCTAC 362
Qy      34  SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 49
      363  CTGACACCAAGTGGCGCTGAGCTGGCGCTTAVGCGCGCTGCATTTCTGACCAAGTGGAG 422
Db      50  ThrLeuMetIyLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGln 69
      423  GTGTTCAGCCCAACCGGCGACGACCGGCGCTCTTATCAAGAACTGCGAGGGCATCAGC 482
Qy      70  LysValaLeuProGlyIyAspThrTyRMetHisGluGlyPheGluArgAlaSerGluGln 89
      483  TCCTTCGCGCGCGG-----ACCTTCACCGAAGTGGCGCGTGCACATGACGAGGACG 536
Db      90  IleTyTyRGlunAsnArgGlnGlyTyArgThrAlaSerValIleIleAlaLeuThrAsp 109
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Db      537  ATCCGCAAGACCGCAGCAAGGCG-----ACCGTCACCTTCCCGCGTGCATCACCGAC 590
Qy      110  GlyIyLeuHisIyGluAspLeuPhePheTySerGluArgGluAlaAsnArgSerArgAsp 129
      591  GCGCAGTCAACCGCGCAGCCCTGCGGGGCGATCAAGCTGAGCGGCGAGCGCGGAG 650
Qy      130  LeuGlyAlaIleValTyRcyVal-----GlyValIys 140
      651  GAGGCAATCCGCGCTTTCGCGCTGGCCCGCCCAACCAAGACCTGAAGAGCAGGCGCTGCGG 710
Qy      141  AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerIyAspHisValPhe 158
      711  GACATGCGCAGCAGCGCGCGCAGAGCTTACCGC-----AAGCACTACGCGCAC 758
Qy      159  ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 175
      759  ATGCTGCTGACCTCCACCGAGATTCACAGACCATCAACCGCATCATCAAGTCAAGTCAATG 818
Db      176  -----LysIySerCysIleGlu 181
      819  AAACAGAAAGCTTACGAGAGAGTGTACAGAGTGAAGTGTGCTGGA 863
Db
RESULT 15
US-10-995-561-465
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 3464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-465
Alignment Scores:
Pred. No.: 0.014 Length: 3464
Score: 103.50 Matches: 49
Percent Similarity: 40.00% Conservative: 37
Best Local Similarity: 22.79% Mismatches: 84
Query Match: 10.98% Indels: 45
DB: Gaps: 9
US-09-970-076-2_COPY_42_222 (1-181) x US-10-995-561-465 (1-3464)
Qy      4  LeuTyRheIleLeuAspIySerGlySerVal----- 14
      243  GTGTACTCTGCTGCTGACACCTCGAAGAGGTACCATGACATGCCCCACGACATCTG 302
Db      15  LeuHisIleTrrAsnGlu---IleTyTyRheValGlnGluLeuAlaHisIyPheIle 33
      303  CTCTTCCACATGAAGCAGTTGTCGCGCAGCTTCATCAGCCAGCTGCAGAAAGAGTTCTAC 362
Qy      34  SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 49
      363  CTGACACCAAGTGGCGCTGAGCTGGCGCTTAVGCGCGCTGCATTTCTGACCAAGTGGAG 422
Db      50  ThrLeuMetIyLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGln 69
      423  GTGTTCAGCCCAACCGGCGACGACCGGCGCTCTTATCAAGAACTGCGAGGGCATCAGC 482
Qy      70  LysValaLeuProGlyIyAspThrTyRMetHisGluGlyPheGluArgAlaSerGluGln 89
      483  TCCTTCGCGCGCGG-----ACCTTCACCGAAGTGGCGCGTGCACATGACGAGGACG 536
Db
```

```
Qy 90 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAsp 109
    |||  ::|  ::|  |||  |||  ::|  ::|  |||  |||  ::|  ::|  |||  |||
Db 537 ATCCGGCAGGACCGCGCAGCAAGGCG-----ACCGTCGACTTCGCGGTGGTCATCACCGAC 590
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 110 GlyGluLeuHisGluAsnLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 129
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 591 GGCACAGTCACCGCGCAGCCCGCTGCGGGGCGATCAAGCTGCAGCGCGCGCGCGAG 650
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 130 LeuGlyAlaIleValTyrCysVal-----GlyValLys 140
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 651 GAGGGCATTCGGGCTCTTCGCCGCTGGCCCCCACCAGACCTGAAGAGCAGGGGCTGCGG 710
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 141 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 158
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 711 GACATCGCCGCGCAGCGCGCGCAGAGCTCTACCGC-----AACGACTAGCGCACCC 758
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 159 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 175
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 759 ATGCTGCGCYGACTCCACCGAGATCRAACGAGACACCATCAACCGCATCATCAAGTCATG 818
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 176 -----LysLysSerCysIleGlu 181
    |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 819 AAACACGAGCCTACGAGAGAGTGCTACAGAGTGAGTGCTGGAA 863
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Search completed: December 19, 2005, 02:30:57
Job time : 162.057 secs


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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-37

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Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFLIDKGSV-LHMHNEIYFVEQLAHKFI SPQLMSFIVSTGTMTKLTE----- 54
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 142 DIAFLIDGSGSINQRFQAKMDPVKALMGEPASTSTFLSMQVSNLIKHTFTTEPKNIL 201
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 55 DREQIRQGLEELQKVLPGSDTYMHGFERASEQIYENRQGYRTA-SVIALTDGELHED 113
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 202 DPQSLVDPIVQLQ-----GLTYTATGIRVMEELFHSKNGSRSAKKIILVITDQKYPD 256
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 114 LFFYSE--REANSRDLGAIYVCVGYKD-FNE-TQLART-----ADSKHVPFVNDGFOA 164
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 257 PLEYSDVIPAADKA--GIIRYALGVDAFOEPTALKELNTIGSAPPODHVFVGN-FAA 312
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 165 LQGI 168
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 313 LRSI 316

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RESULT 3
US-08-485-618-37
Sequence 37, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunitc
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-37

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Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFLIDKGSV-LHMHNEIYFVEQLAHKFI SPQLMSFIVSTGTMTKLTE----- 54
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 142 DIAFLIDGSGSINQRFQAKMDPVKALMGEPASTSTFLSMQVSNLIKHTFTTEPKNIL 201
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 55 DREQIRQGLEELQKVLPGSDTYMHGFERASEQIYENRQGYRTA-SVIALTDGELHED 113
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 202 DPQSLVDPIVQLQ-----GLTYTATGIRVMEELFHSKNGSRSAKKIILVITDQKYPD 256
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 114 LFFYSE--REANSRDLGAIYVCVGYKD-FNE-TQLART-----ADSKHVPFVNDGFOA 164
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 257 PLEYSDVIPAADKA--GIIRYALGVDAFOEPTALKELNTIGSAPPODHVFVGN-FAA 312
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 165 LQGI 168
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 313 LRSI 316

```

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RESULT 4
US-08-362-652-37
Sequence 37, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunitc
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652

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/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-362-652-37
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Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;
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QY 1 DLYFILDKSGSV-LHHMNEIYFVEQLAHKFIQPMKSFIVSTRCTIMKLT-----54
DB 142 DIAFLIDSGSINORDPAQMKDFKALMGEPASTSTLFSIMQYSNLIKHTFTFEFNIL 201
QY 55 DRQIQIGLELQKVLPGSDTYMHEGFERASQIYYENRGYRTA-SVIALTDGELHED 113
DB 202 DPOSVDPIVQLQ-----GLTYTATGIRTYMBELFHSKNSRKSAAKILLVITDGOQYRD 256
QY 114 LFFYSE--REANSRDLGAIYVCVYKD-FNE--TQIARI-----ADSKDHVPYNDGFOA 164
DB 257 PLEYSDVTPADRA---GIIRVAIGVDARFQEPFLAKELNTIGSAPPDHVFVKGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316
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RESULT 5
US-08-605-672-37
/ Sequence 37, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/605,672
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-605-672-37
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Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;
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QY 1 DLYFILDKSGSV-LHHMNEIYFVEQLAHKFIQPMKSFIVSTRCTIMKLT-----54
DB 142 DIAFLIDSGSINORDPAQMKDFKALMGEPASTSTLFSIMQYSNLIKHTFTFEFNIL 201
QY 55 DRQIQIGLELQKVLPGSDTYMHEGFERASQIYYENRGYRTA-SVIALTDGELHED 113
DB 202 DPOSVDPIVQLQ-----GLTYTATGIRTYMBELFHSKNSRKSAAKILLVITDGOQYRD 256
QY 114 LFFYSE--REANSRDLGAIYVCVYKD-FNE--TQIARI-----ADSKDHVPYNDGFOA 164
DB 257 PLEYSDVTPADRA---GIIRVAIGVDARFQEPFLAKELNTIGSAPPDHVFVKGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316
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RESULT 6
US-08-482-293A-37
/ Sequence 37, Application US/08482293A
/ Patent No. 5831029
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ APPLICATION NUMBER: US 08/286,889
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; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-293A-37

Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFLDKSGSV-LHHNNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLT----- 54
DB 142 DIAFLIDSGSINORDFAQMKDFV KALMGFASTSTLFSLMQYSNILKTHFTTFEKNIL 201
QY 55 DREQIRQGLEELQKVLPGSDTYMHGEFERASEQIYYENNQGYRTA-SVIALTDGELHED 113
DB 202 DPQSLVDPIVQLQ-----GLTYATGIRTYMELFHSKNGSRKSAKKILLVITDQKRYD 256
QY 114 LFFYSE--REANSRDLGAIYVCVGYD-FNE-TQLARI-----ADSKDHVPVNDGFQA 164
DB 257 PLEYSDVIPADAKA---GIIRYAIQVGDAFOEPTALKELNTIGSAPPODHVFVGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316

RESULT 7
US-08-943-363-37
; Sequence 37, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-363-37

Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFLDKSGSV-LHHNNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLT----- 54
DB 142 DIAFLIDSGSINORDFAQMKDFV KALMGFASTSTLFSLMQYSNILKTHFTTFEKNIL 201
QY 55 DREQIRQGLEELQKVLPGSDTYMHGEFERASEQIYYENNQGYRTA-SVIALTDGELHED 113
DB 202 DPQSLVDPIVQLQ-----GLTYATGIRTYMELFHSKNGSRKSAKKILLVITDQKRYD 256
QY 114 LFFYSE--REANSRDLGAIYVCVGYD-FNE-TQLARI-----ADSKDHVPVNDGFQA 164
DB 257 PLEYSDVIPADAKA---GIIRYAIQVGDAFOEPTALKELNTIGSAPPODHVFVGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316

RESULT 8
US-09-193-043-37
; Sequence 37, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 37
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Rattus rattus
; US-09-193-043-37

Query Match      15.4%; Score 138.5; DB 2; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFLDKSGSV-LHHNNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLT----- 54
DB 142 DIAFLIDSGSINORDFAQMKDFV KALMGFASTSTLFSLMQYSNILKTHFTTFEKNIL 201
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OY      55 REQDROGJEBELQKVLPGGDVTMHEGFERASEQIYYENRQGVRTA-SVIALTDGEIHED 113
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      202 DPOSIVDPVQLQ-----GLITTAGIRTWMEBELFSKNGRSKSAKKILLVITDGOKTR 256
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      114 LFPEYE--REANRSRLDLGAIVYCVGVKD-FNE-TOLARI-----ADSKDHVEPVNDGFOA 164
        || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      257 PLEYSDVLPAAADKA---GIIRYAIGVGDAFQEPETALKEINTIGSAPPDHHVFKNV-FAA 312
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Db      313 LRST 316

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RESULT 9
US-09-688-307A-37
Sequence 37, Application US/09688307A
Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6432404e1 Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03
NUMBER OR SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 1151
TYPE: PRT
ORGANISM: Rattus rattus
FEATURES:
NAME/KEY: misc_feature
LOCATION: 361
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 486
OTHER INFORMATION: Xaa = any or unknown amino acid
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OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1117
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-688-307A-37

Query Match      15.4%; Score 138.5; DB 2; Length 1151;
Beet Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10

Qy      1 DLYPLIDSGSV-LHHMNEIYFVEQLAHKFISPOLRMSFIYSTRGTTLMKLT----- 54
|:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      142 DIAFLIDSGSGINGNDPAQMMDPVKALMGEFASTLPFLMDGYSNLTKHFTPTFKNTL 201
55 DRDGRQGLBELQKVLRGGDTYMHGFEFASQIYYENFGYRTA-SVIALTDGEHMED 113

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| Db | 202 | DPSGLVDPIVQ | ---- | GLTYTARGIRTMELPHSKNGSKRSKAKILLVITDQKYRD | 256 |
| QY | 114 | LFYFSE--REANRSDDLGAIVYCVGKD--FNE--TQLARI----- | ADSKOHVFPVNDGFOA | 164 | |
| Db | 257 | PLEYSDVPIPADKA---GIIRYAGVGAFQEPALKEINTIGSAPPDHFVCGN--FAA | 312 | | |
| QY | 165 | LGQI | 168 | | |
| Db | 313 | LRSI | 316 | | |

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10 RESULT 10
11 US-09-350-259-37
12 ; Sequence 37, Application US/09350259
13 ; Patent No. 6620915
14 ; GENERAL INFORMATION:
15 ; APPLICANT: Gallatin, Michael W.
16 ; APPLICANT: Van der Vieren, Monica
17 ; TITLE OF INVENTION: No. 6620915el Human 2
18 ; FILE REFERENCE: 27866/35004
19 ; CURRENT APPLICATION NUMBER: US/09/350,259
20 ; CURRENT FILING DATE: 1999-07-08
21 ; EARLIER APPLICATION NUMBER: 09/193,043
22 ; EARLIER FILING DATE: 1998-11-16
23 ; EARLIER APPLICATION NUMBER: 08/173,497
24 ; EARLIER FILING DATE: 1993-12-23
25 ; EARLIER APPLICATION NUMBER: 08/286,889
26 ; EARLIER FILING DATE: 1994-08-05
27 ; EARLIER APPLICATION NUMBER: 08/362,652
28 ; EARLIER FILING DATE: 1994-12-21
29 ; EARLIER APPLICATION NUMBER: 08/943,363
30 ; EARLIER FILING DATE: 1997-10-03
31 ; NUMBER OF SEQ ID NOS: 114
32 ; SOFTWARE: Patentin Ver. 2.0
33 ; SEQ ID NO 37
34 ; LENGTH: 1151
35 ; TYPE: prt
36 ; ORGANISM: Rattus rattus
37 US-09-350-259-37

```

```

Query Match          15.4%; Score 138.5; DB 2; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches      52; Conservative 36; Mismatches 71; Indels 25; Gaps 10

QY      1 DLYFLDKSGSV-LHHNMEIYFVEQLAKFISPOLRMSPIVFSTRGTTLNKLT-----54
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB     142 DIAFLIDGSSINGRDFAQMDPFKALMGEPASSTLFSLMQYSNLKTHPTFEFKNIL 201
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      55 DREQIROGLELQKYLPEGDTYMEGEFRASSEQIYENRQGYRTA-SYIALTLTGELHED 113
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB     202 DPOSIVDPYVOLQ-----GLTYTATGIRTWEEBELFHSNKGSRKSAKILLVITTOGQKRD 256
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY     114 LFPFSE--REANRSRDIGAIYYCQVND-FME-TQLARI-----ADSKDHFPVNDGFOA 164
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB     257 PLEYSIVDPADAKA--GIIRYAIQVGDAFQEPALXELNTIGSAPPDQHVFKVGN-FAA 312
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      165 LQGI 168
      ||::||
DB     313 LRSI 316

RESULT 11
US-08-485-618-55
; Sequence 55, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
; ADDRESSSE: Marshall, O'Toole, Getzstein, Murray & Borun
;

```



```
/
/  COMPUTER:  IBM PC compatible
/  OPERATING SYSTEM:  PC-DOS/MS-DOS
/  SOFTWARE:  Patent In Release #1.0, Version #1.25
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER:  US/08/605,672
/  FILING DATE:
/  CLASSIFICATION:  530
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER:  US 08/173,497
/  FILING DATE:  23-DEC-1993
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER:  US 08/286,889
/  FILING DATE:  5-AUG-1994
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER:  US 08/362,652
/  FILING DATE:  21-DEC-1994
/  ATTORNEY/AGENT INFORMATION:
/  NAME:  Williams Jr., Joseph A.
/  REGISTRATION NUMBER:  38,659
/  REFERENCE/DOCKET NUMBER:  27866/32684
/  TELECOMMUNICATION INFORMATION:
/  TELEPHONE:  312-474-6300
/  TELEFAX:  312-474-0448
/  TELEX:  25-3856
/  INFORMATION FOR SEQ ID NO:  55:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH:  1161 amino acids
/  TYPE:  amino acid
/  TOPOLOGY:  linear
/  MOLECULE TYPE:  protein
/
US-08-605-672-55
```

```
Query Match      15.4%; Score 138.5; DB 1; Length 1161;
Best Local Similarity 28.3%; Pred. No. 7.6e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY      1  DLVFIIDKSGSV-LHMHNEIYFVEQLAHKFIISPOLMSFIVSTGCTTLMKLT----- 54
      152  DIAFLIDSGSINQRDPAQKDFKALMGEPASTSTLFSIMQYSNILKHTFTFEPNLT 211
      55  DRQIQGLELEOKVLPFGDTYHGEFERASEQIYYENRGYRTA-SVIALTDGELHED 113
      212  DPQSLVDPIVQLQ-----GLTYATGIRTYMBELFHSKNGSRKSAKILLVITDQKCYRD 266
QY      114  LPEYSE--REANSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKHVPVNDGFOA 164
      267  PLEYSVDIIPADKA---GIIRYAIYGVDAPQEPFALKELNTIGSAPPQDHVFYGN-FAA 322
      165  LQGI 168
      323  LRSI 326
DB
```

```
RESULT 14
US-08-482-293A-55
; Sequence 55, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT:  Gallatin, W. Michael
; TITLE OF INVENTION:  No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES:  103
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
; STREET:  233 South Wacker Drive, 6300 Sear Tower
; CITY:  Chicago
; STATE:  Illinois
; COUNTRY:  United States
; ZIP:  60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
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```
/
/  SOFTWARE:  Patent In Release #1.0, Version #1.25
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER:  US/08/482,293A
/  FILING DATE:
/  CLASSIFICATION:  530
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER:  US 08/173,497
/  FILING DATE:  23-DEC-1993
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER:  US 08/286,889
/  FILING DATE:  5-AUG-1994
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER:  US 08/362,652
/  FILING DATE:  21-DEC-1994
/  ATTORNEY/AGENT INFORMATION:
/  NAME:  Williams Jr., Joseph A.
/  REGISTRATION NUMBER:  38,659
/  REFERENCE/DOCKET NUMBER:  27866/32684
/  TELECOMMUNICATION INFORMATION:
/  TELEPHONE:  312-474-6300
/  TELEFAX:  312-474-0448
/  TELEX:  25-3856
/  INFORMATION FOR SEQ ID NO:  55:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH:  1161 amino acids
/  TYPE:  amino acid
/  TOPOLOGY:  linear
/  MOLECULE TYPE:  protein
/
US-08-482-293A-55
```

```
Query Match      15.4%; Score 138.5; DB 1; Length 1161;
Best Local Similarity 28.3%; Pred. No. 7.6e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY      1  DLVFIIDKSGSV-LHMHNEIYFVEQLAHKFIISPOLMSFIVSTGCTTLMKLT----- 54
      152  DIAFLIDSGSINQRDPAQKDFKALMGEPASTSTLFSIMQYSNILKHTFTFEPNLT 211
      55  DRQIQGLELEOKVLPFGDTYHGEFERASEQIYYENRGYRTA-SVIALTDGELHED 113
      212  DPQSLVDPIVQLQ-----GLTYATGIRTYMBELFHSKNGSRKSAKILLVITDQKCYRD 266
QY      114  LPEYSE--REANSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKHVPVNDGFOA 164
      267  PLEYSVDIIPADKA---GIIRYAIYGVDAPQEPFALKELNTIGSAPPQDHVFYGN-FAA 322
      165  LQGI 168
      323  LRSI 326
DB
```

```
RESULT 15
US-08-943-363-55
; Sequence 55, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT:  Gallatin, W. Michael
; TITLE OF INVENTION:  No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES:  114
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
; STREET:  233 South Wacker Drive, 6300 Sear Tower
; CITY:  Chicago
; STATE:  Illinois
; COUNTRY:  United States
; ZIP:  60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ. ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-363-55

```

```

Query Match 15.4%; Score 138.5; DB 1; Length 1161;
Best Local Similarity 28.3%; Pred. No. 7.6e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

```

```

QY 1 DLYFIIDKSGSV-LHMHNEIYFVEQIAHKEISPOLMSFIVSTRTGLMKLTE----- 54
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 152 DIAFLIDSGSINORDPAQMKDFKALMGEPASTSTFSLMOYSNLIKTHFTFRGNIL 211
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 DREQIRQGLEBELQKVLPGCDTYMHGFERASEQIYYENRQGYRTA-SVIALTDGELHED 113
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 212 DPQSLVDPIVQLQ-----GLTYTATGIRITVMEBELFHSKNSRKSAKKILLVITDGQKYRD 266
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 LFPYSE--REANRSRDIGAIVYCVGKD-FNE-TQLARI-----ADSKDHVPVNDGFOA 164
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 PLEYSDVIPAADKA---GIIRVAIGVDAPQEPALKEINTIGSAPPQDHVFKVGN-FAA 322
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 LOGI 168
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 323 LRSI 326
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: December 14, 2005, 11:21:08
 Job time : 16.6012 secs


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; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PaSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-26

Query Match      100.0%; Score 899; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 60
    |||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 103
    |||

QY 61 QGLEELQKVLPGGDTYMHGFEFASBOIYYENRGYRTASVIALTDGELHEDLFFYSER 120
    |||
DB 104 QGLEELQKVLPGGDTYMHGFEFASBOIYYENRGYRTASVIALTDGELHEDLFFYSER 163
    |||

QY 121 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 173
    |||
DB 164 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 216
    |||

RESULT 3
US-09-796-753-12
; Sequence 12, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
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; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12

Query Match      100.0%; Score 899; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 60
    |||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 103
    |||

QY 61 QGLEELQKVLPGGDTYMHGFEFASBOIYYENRGYRTASVIALTDGELHEDLFFYSER 120
    |||
DB 104 QGLEELQKVLPGGDTYMHGFEFASBOIYYENRGYRTASVIALTDGELHEDLFFYSER 163
    |||

QY 121 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 173
    |||
DB 164 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 216
    |||

RESULT 4
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PaSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-2

Query Match      100.0%; Score 899; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 60
    |||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 103
    |||

QY 61 QGLEELQKVLPGGDTYMHGFEFASBOIYYENRGYRTASVIALTDGELHEDLFFYSER 120
    |||
DB 104 QGLEELQKVLPGGDTYMHGFEFASBOIYYENRGYRTASVIALTDGELHEDLFFYSER 163
    |||

QY 121 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 173
    |||
```


Db 164 EANSRDLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 216

RESULT 5
US-10-201-292-2

Sequence 2, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-2

Query Match 100.0%; Score 899; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
Db 44 DLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
Qy 61 OGLEELQKVLPGGDTYHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 120
Db 104 OGLEELQKVLPGGDTYHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 163
Qy 121 EANSRDLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 173
Db 164 EANSRDLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 216

RESULT 6
US-11-047-278-8

Sequence 8, Application US/11047278
Publication No. US20050196407A1
GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: US/11/047,278
CURRENT FILING DATE: 2005-01-31
PRIOR APPLICATION NUMBER: US/09/970,076
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-11-047-278-8

Query Match 100.0%; Score 899; DB 6; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60

Db 44 DLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103

Qy 61 OGLEELQKVLPGGDTYHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 120
Db 104 OGLEELQKVLPGGDTYHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 163

Qy 121 EANSRDLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 173
Db 164 EANSRDLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 216

RESULT 7
US-10-038-307-22

Sequence 22, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-22

Query Match 100.0%; Score 899; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,2e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
Db 53 DLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 112
Qy 61 OGLEELQKVLPGGDTYHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 120
Db 113 OGLEELQKVLPGGDTYHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 172
Qy 121 EANSRDLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 173
Db 173 EANSRDLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 225

RESULT 8

US-10-201-292-22
Sequence 22, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-22

Query Match 100.0%; Score 899; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,2e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 60
|||
DB 53 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 112
|||
QY 61 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
|||
DB 113 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 172
|||
QY 121 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
|||
DB 173 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 225
|||

RESULT 9
US-10-038-307-24
; Sequence 24, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-038-307-24

Query Match 100.0%; Score 899; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 60
|||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 103
|||
QY 61 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
|||
DB 104 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
|||
QY 121 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
|||
DB 164 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 216
|||

RESULT 10
US-10-201-292-24
; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-201-292-24

Query Match 100.0%; Score 899; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 60
|||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 103
|||
QY 61 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
|||
DB 104 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
|||
QY 121 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
|||
DB 164 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 216
|||

RESULT 11
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-047-278-2

Query Match 100.0%; Score 899; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 60
|||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISPOLMSFIVFSTRGTTLMKLTEDREQIR 103
|||
QY 61 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
|||
DB 104 OGLEELQKVLPGGDTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
|||
QY 121 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
|||
DB 164 EANRSRLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 216
|||

RESULT 12
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21

PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-621

Query Match 100.0%; Score 899; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.5e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 216

RESULT 13

US-10-201-292-28
Sequence 28, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2003-02-14
CURRENT APPLICATION NUMBER: US/10/201,292
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-28

Query Match 100.0%; Score 899; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 216

RESULT 14

US-10-201-292-30
Sequence 30, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-30

Query Match 100.0%; Score 899; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 216

RESULT 15

US-10-201-292-32
Sequence 32, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2003-02-14
CURRENT APPLICATION NUMBER: US/10/201,292
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-32

Query Match 100.0%; Score 899; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.9e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEELQKVLPGGDTYMHGFEFPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALQGIHSIL 216

Search completed: December 14, 2005, 11:59:01
Job time : 53.2862 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 2.54242 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_44_216

Perfect score: 899
Sequence: 1 DLVFILDKSGSVLHNNNEIY.....HVFVNDGFGALGIIHSIL 173

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1 | 899 | 100.0 | 564 | 7 US-11-186-284-199 | Sequence 199, App |
| 2 | 128.5 | 14.3 | 1152 | 7 US-11-080-026-4 | Sequence 26, App |
| 3 | 118.5 | 13.2 | 3063 | 7 US-11-186-284-26 | Sequence 24, App |
| 4 | 108 | 12.0 | 1141 | 6 US-10-601-368-24 | Sequence 22, App |
| 5 | 108 | 12.0 | 1166 | 6 US-10-601-368-22 | Sequence 21, App |
| 6 | 108 | 12.0 | 1188 | 6 US-10-601-368-21 | Sequence 6, App |
| 7 | 104 | 11.6 | 1141 | 6 US-10-601-368-6 | Sequence 4, App |
| 8 | 104 | 11.6 | 1166 | 6 US-10-601-368-4 | Sequence 3, App |
| 9 | 104 | 11.6 | 1188 | 6 US-10-601-368-3 | Sequence 38, App |
| 10 | 104 | 11.6 | 1188 | 7 US-11-000-463-338 | Sequence 810, App |
| 11 | 104 | 11.6 | 1188 | 7 US-11-000-463-810 | Sequence 25, App |
| 12 | 103.5 | 11.3 | 182 | 6 US-10-601-368-25 | Sequence 2, App |
| 13 | 101.5 | 11.3 | 739 | 7 US-11-057-047-2 | Sequence 1, App |
| 14 | 101.5 | 11.3 | 764 | 7 US-11-057-047-1 | Sequence 1034, App |
| 15 | 101.5 | 11.3 | 798 | 7 US-10-821-234-1034 | Sequence 294, App |
| 16 | 100.5 | 11.2 | 915 | 6 US-10-131-8264-294 | Sequence 7, App |
| 17 | 100.5 | 11.2 | 956 | 7 US-11-113-424-39 | Sequence 3, App |
| 18 | 99.5 | 11.1 | 182 | 6 US-10-601-368-7 | Sequence 981, App |
| 19 | 96.5 | 10.7 | 761 | 7 US-11-057-047-6 | Sequence 982, App |
| 20 | 93.5 | 10.4 | 828 | 6 US-10-995-561-983 | Sequence 921, App |
| 21 | 93.5 | 10.4 | 918 | 6 US-10-995-561-981 | Sequence 16, App |
| 22 | 93.5 | 10.4 | 1019 | 6 US-10-995-561-982 | |
| 23 | 91.5 | 10.2 | 1179 | 7 US-11-097-125-1 | |
| 24 | 91.5 | 10.2 | 1196 | 6 US-10-995-561-921 | |
| 25 | 90 | 10.0 | 1167 | 6 US-10-601-368-18 | |

| | | | | | |
|----|------|-----|------|----------------------|--------------------|
| 26 | 86.5 | 9.6 | 1167 | 7 US-11-097-125-2 | Sequence 2, App |
| 27 | 82 | 9.1 | 678 | 7 US-11-102-240-34 | Sequence 34, App |
| 28 | 81.5 | 9.1 | 353 | 7 US-11-137-465-44 | Sequence 44, App |
| 29 | 81.5 | 9.1 | 448 | 7 US-11-137-465-45 | Sequence 45, App |
| 30 | 73.5 | 8.2 | 359 | 6 US-10-510-386-158 | Sequence 158, App |
| 31 | 72 | 8.0 | 264 | 6 US-10-793-626-2880 | Sequence 2880, App |
| 32 | 72 | 8.0 | 264 | 6 US-10-793-626-388 | Sequence 103, App |
| 33 | 72 | 8.0 | 766 | 6 US-10-467-6628-103 | Sequence 2636, App |
| 34 | 70 | 7.8 | 292 | 6 US-10-793-626-2636 | Sequence 5696, App |
| 35 | 70 | 7.8 | 468 | 6 US-10-467-657-5696 | Sequence 7846, App |
| 36 | 69.5 | 7.7 | 489 | 6 US-10-467-657-7846 | Sequence 7306, App |
| 37 | 69 | 7.7 | 242 | 6 US-10-467-657-7306 | Sequence 6, App |
| 38 | 68.5 | 7.6 | 1734 | 7 US-11-192-967-6 | Sequence 4, App |
| 39 | 68.5 | 7.6 | 1734 | 7 US-11-193-715-6 | Sequence 4, App |
| 40 | 68 | 7.6 | 348 | 6 US-10-674-767-4 | Sequence 7066, App |
| 41 | 66 | 7.3 | 403 | 6 US-10-467-657-7066 | Sequence 70, App |
| 42 | 66 | 7.3 | 919 | 7 US-11-102-240-70 | Sequence 1145, App |
| 43 | 65.5 | 7.3 | 1299 | 6 US-10-821-234-1145 | Sequence 7272, App |
| 44 | 65 | 7.2 | 167 | 6 US-10-467-657-7272 | Sequence 250, App |
| 45 | 64.5 | 7.2 | 629 | 6 US-10-467-657-250 | |

ALIGNMENTS

RESULT 1
US-11-186-284-199
Sequence 199, Application US/11186284
Publication No. US2005026493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangt
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
FILE REFERENCE: MEMO-029P22NM
CURRENT APPLICATION NUMBER: US/11/186,284
PRIOR FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-199

Query Match 100.0%; Score 899; DB 7; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.6e-81;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLVFILDKSGSVLHNNNEIYFVEQLAKHKEISPOLMSPFVSTRTGTLMLKLTEDRQIR 60
DB 44 DLVFILDKSGSVLHNNNEIYFVEQLAKHKEISPOLMSPFVSTRTGTLMLKLTEDRQIR 103
QY 61 QGIEELQKVLPGDDTYTHGSEFERASBOIYYENQGRITASVIALTDGEIHEDLFFPSER 120
DB 104 QGIEELQKVLPGDDTYTHGSEFERASBOIYYENQGRITASVIALTDGEIHEDLFFPSER 163
QY 121 EAKRSRLGAIYCVGVKVDNENETOLARIADSKDHVFVNDGFGALGIIHSIL 173

Db 164 EANRSRDIGAIVYCVGVDFNETQLARIADSKDHVPVNDGFQALOGIHSIL 216

RESULT 2
US-11-080-026-4
Sequence 4, Application US/11080026
Publication No. US20050260192A1
GENERAL INFORMATION:

APPLICANT: Springer, Timothy A.
APPLICANT: Shimooka, Motomu
APPLICANT: Lu, Chafen

TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
FILE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
FILE REFERENCE: CFBP-P02-021
CURRENT APPLICATION NUMBER: US/11/080,026
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 09/945,265
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,700
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1152
TYPE: PRT
ORGANISM: Homo sapiens
US-11-080-026-4

Query Match 14.3%; Score 128.5; DB 7; Length 1152;
Best Local Similarity 26.7%; Pred. No. 5.6e-05;
Matches 51; Conservative 38; Mismatches 63; Indels 39; Gaps 11;

Db 150 DIAFLIDSGSIIIPHDRKKEFVST---VMEQLKSKTLPs---LMQVSEFRRIH 199
QY 56 -----REQIROLGELQKLVPGDVTYHGEFERASEQIYYENRQGYRTA-SVIALT 106
Db 200 FTREKPNPNRRLVPIQL--GRTHATGIRKTVRELFINTRAGAKRLIVIT 257
QY 107 DGEIHEDLFYYS--REANRSRDIGAIVYCVGVDFNETQLAR----IADS--KDHVP 157
Db 258 DGEKFGDPLGVEDVTPADRE---GVIRYVIGVDADFRSEKSGELNTLIASKPRDHVQ 314

QY 158 VNDGFQALOGI 168
Db 315 VNN-FEALKTI 324

RESULT 3
US-11-186-284-26
Sequence 26, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MEMO1-029P2RMM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10

Db 150 DSKDHVPVNDGFQALOG 167
QY 339 --KDIYDALGDRIFSLG 354

PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-26

Query Match 13.2%; Score 118.5; DB 7; Length 3063;
Best Local Similarity 30.0%; Pred. No. 0.0019;
Matches 54; Conservative 35; Mismatches 68; Indels 23; Gaps 12;

QY 1 DLYFLIDSGSV-LHNNETIYFVEQLAHKF-ISP-QLRMSFTVST---RRTTLMLKTE 54
Db 440 DIVFLVDGSYSIGIANFVRAFLVLVKSFEISPNRVOISLVQSRDPHTFTLKKFTK 499
QY 55 DREQIROLGELQKLVPGDVTYHGEFERASEQIYYENRQGYRT--ASVIALTDGEL 110
Db 500 VEDIT-----EAINTPYRGSTNTGKAMTYREKIFVPSK-GSRSNVPMKMIILTDGK- 552

QY 111 HEDLFFYSERREANRSRDIGAIVYCVGVDFNETQLARIAD--SKDHVPVNDGFQALOGI 168
Db 553 SSDAF---RDPAIKLRNSDVEIFAVGVKDAVSELEAIASPPAETHVTEVD-FDAFCRI 608

RESULT 4
US-10-601-368-24
Sequence 24, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:

APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 0734-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1141
TYPE: PRT
ORGANISM: Mus musculus
US-10-601-368-24

Query Match 12.0%; Score 108; DB 6; Length 1141;
Best Local Similarity 24.2%; Pred. No. 0.0058;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY 1 DLYFLIDSGSV-LHNNETIYFVEQLAHKF-ISP-QLRMSFTVSTRTTLMLKLTEDREQ 58
Db 164 DIVFLVDGSNST-YPMVEVQHPLINLTKFTYIGPGIOVGIYOGSDAHEPHL-NDYNS 221

QY 59 IROGLELOKVLPGDVTYHGEFE--RASEQIYYENRQGYRTASVIALTDGELHED-- 113
Db 222 VKQVNEASHIEBQGTETRTAFGIEFARSEAFQKGRGAK--KVMIVITDGSHESDSPD 279

QY 114 -----LFFYSERREANRSRDIGAIVYCVGVND----FNETQLARIA 149
Db 280 LKRVIRQSEKDNVTRVAVALGYNNRGINPETFLNEIYIASDPDKHFPVNTDEAL- 338

QY 150 DSKDHVPVNDGFQALOG 167
Db 339 --KDIYDALGDRIFSLG 354

```
RESULT 5
US-10-601-368-22
; Sequence 22, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-601-368-22
```

```
Query Match      12.0%; Score 108; DB 6; Length 1166;
Best Local Similarity 24.2%; Pred. No. 0.006;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY      1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKF-ISP-QLRMSFIYFSTRTGLTKLTEDREQ 58
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      142 DIVIVLDGNSI-YPWVEVOHFLINILKKFYIGPGQIVGVGEDVAHEFHL-NDYRS 199
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      59 IROGLELQKVLPGDGYMEHGEF---RASEQIYENRQGYRTASVIALTDGELHED-- 113
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      200 VKQVEAASHIEBGRGTETRTAGIEFARSEARQKGRKAK--KMIVITDGSHPD 257
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      114 -----LFFYSERANRSDLGAIYCVGVK-----FNETOLARIA 149
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      258 LEKVIQSEKDNTRYAVAVLGYNNRGINPETFLEIKYIASDPDDKHFFNTDEAL- 316
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      150 DSKDHVFPVNDGFQALOG 167
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      317 --KDIVDALGDRIFSLG 332
```

```
RESULT 6
US-10-601-368-21
; Sequence 21, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(122)
US-10-601-368-21
```

```
Query Match      12.0%; Score 108; DB 6; Length 1188;
Best Local Similarity 24.2%; Pred. No. 0.0061;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;
```

```
QY      1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKF-ISP-QLRMSFIYFSTRTGLTKLTEDREQ 58
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      164 DIVIVLDGNSI-YPWVEVOHFLINILKKFYIGPGQIVGVGEDVAHEFHL-NDYRS 221
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      59 IROGLELQKVLPGDGYMEHGEF---RASEQIYENRQGYRTASVIALTDGELHED-- 113
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      222 VKQVEAASHIEBGRGTETRTAGIEFARSEARQKGRKAK--KMIVITDGSHPD 279
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      114 -----LFFYSERANRSDLGAIYCVGVK-----FNETOLARIA 149
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      280 LEKVIQSEKDNTRYAVAVLGYNNRGINPETFLEIKYIASDPDDKHFFNTDEAL- 338
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      150 DSKDHVFPVNDGFQALOG 167
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      339 --KDIVDALGDRIFSLG 354
```

```
RESULT 7
US-10-601-368-6
; Sequence 6, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(122)
US-10-601-368-6
```

```
Query Match      11.6%; Score 104; DB 6; Length 1141;
Best Local Similarity 24.2%; Pred. No. 0.014;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;
```

```
QY      1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKF-ISP-QLRMSFIYFSTRTGLTKLTEDREQ 58
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      164 DIVIVLDGNSI-YPWVEVOHFLINILKKFYIGPGQIVGVGEDVAHEFHL-NDYRS 221
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      59 IROGLELQKVLPGDGYMEHGEF---RASEQIYENRQGYRTASVIALTDGELHED-- 113
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      222 VKQVEAASHIEBGRGTETRTAGIEFARSEARQKGRKAK--KMIVITDGSHPD 279
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      114 -----LFFYSERANRSDLGAIYCVGVK-----FNETOLARIA 149
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      280 LEKVIQSEKDNTRYAVAVLGYNNRGINPETFLEIKYIASDPDDKHFFNTDEAL- 338
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      150 DSKDHVFPVNDGFQALOG 167
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      339 --KDIVDALGDRIFSLG 354
```

```
RESULT 8
US-10-601-368-4
; Sequence 4, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
```


Db 303 DSSNADWYTKQLEINVEDHKLKSGTNT-----KKALQAVYSMMSPDDVPEGMNRR 356
Qy 100 SVIITLTDG-----ELHEDLFFYSERANRRDGAIVYCYG--VKDFNETQ 144
Db 357 HVIILMTDGLHNMGGDPITVIDEIRDLVYIGDKRKNRPEDYLDVYVGVGPLVNOVNINA 416
Qy 145 LARIADSKDHPVPVNDGFOALQGIHSIL 173
Db 417 LASKKDNEQHVFKVD-MENLEDVIFYOMI 444

RESULT 14
US-11-057-047-1
Sequence 1, Application US/11057047
Publication No. US20050260198A1
GENERAL INFORMATION:
APPLICANT: Holers, Vernon
APPLICANT: Thurman, Joshua
APPLICANT: Taube, Christian
APPLICANT: Gelfand, Erwin
APPLICANT: Gilkeson, Gary
TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
FILE REFERENCE: 2848-66
CURRENT APPLICATION NUMBER: US/11/057,047
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,594
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/536,239
PRIOR FILING DATE: 2004-12-14
PRIOR APPLICATION NUMBER: US04/015040
PRIOR FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 764
TYPE: PRT
ORGANISM: Homo sapiens
US-11-057-047-1

Query Match 11.3%; Score 101.5; DB 7; Length 764;
Best Local Similarity 22.5%; Pred. No. 0.015;
Matches 47; Conservative 43; Mismatches 74; Indels 45; Gaps 10;

Qy 1 DLYFIIDKSGSV-----LHNMNEIYFVEQLAHKFIISPOLRMSFVFSRGTTLMLTE- 54
Db 270 NIYVLDDSDSISGASNFTGAKKCLVNLIEKVASGVKP--RYGLVTYATYPKIWKVSE 327
Qy 55 ---DREQIRQGLEBL-----QKVLPGGDTYMHGFEFASQIYYENR-----QGY-RTA 99
Db 328 DSSNADWYTKQLEINVEDHKLKSGTNT-----KKALQAVYSMMSPDDVPEGMNRR 381
Qy 100 SVIITLTDG-----ELHEDLFFYSERANRRDGAIVYCYG--VKDFNETQ 144
Db 382 HVIILMTDGLHNMGGDPITVIDEIRDLVYIGDKRKNRPEDYLDVYVGVGPLVNOVNINA 441
Qy 145 LARIADSKDHPVPVNDGFOALQGIHSIL 173
Db 442 LASKKDNEQHVFKVD-MENLEDVIFYOMI 469

RESULT 15
US-10-821-234-1034
Sequence 1034, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Steach-Crain, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234

/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: PC_SEQ_genes Version 1.0
/ SEQ ID NO 1034
/ LENGTH: 798
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1034

Query Match 11.3%; Score 101.5; DB 6; Length 798;
Best Local Similarity 22.5%; Pred. No. 0.016;
Matches 47; Conservative 43; Mismatches 74; Indels 45; Gaps 10;

Qy 1 DLYFIIDKSGSV-----LHNMNEIYFVEQLAHKFIISPOLRMSFVFSRGTTLMLTE- 54
Db 304 NIYVLDDSDSISGASNFTGAKKCLVNLIEKVASGVKP--RYGLVTYATYPKIWKVSE 361
Qy 55 ---DREQIRQGLEBL-----QKVLPGGDTYMHGFEFASQIYYENR-----QGY-RTA 99
Db 362 DSSNADWYTKQLEINVEDHKLKSGTNT-----KKALQAVYSMMSPDDVPEGMNRR 415
Qy 100 SVIITLTDG-----ELHEDLFFYSERANRRDGAIVYCYG--VKDFNETQ 144
Db 416 HVIILMTDGLHNMGGDPITVIDEIRDLVYIGDKRKNRPEDYLDVYVGVGPLVNOVNINA 475
Qy 145 LARIADSKDHPVPVNDGFOALQGIHSIL 173
Db 476 LASKKDNEQHVFKVD-MENLEDVIFYOMI 503

Search completed: December 14, 2005, 11:59:29
Job time : 2.54242 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:35:12 : Search time 554.247 Seconds
(without alignments)
2581.163 million cell updates/sec

Title: US-09-970-076-2_COPY_44_216

Perfect score: 899

Sequence: 1 DLYFIDKSGSVLHNNHNIY.....HVPVNDGFOALQGIHSIL 173

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q=/cg2_1/USPTO.epool/US09970076/runat_14122005_111852_21035/app_query.fasta_1.2410
-DB=Published Applications NA_Main -QPM=faetap -SUFFIX=rnphm -MINMATCH=0.1
-LOPCU=0 -LOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.cgi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 -CGN_1_1_2715 -runat_14122005_111852_21035
-NCPU=6 -ICPU=3 -NO_MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA_Main.*

1: /cg2_6/ptodaca/1/pubpna/US07_PUBCOMB.seq:*
2: /cg2_6/ptodaca/1/pubpna/US08_PUBCOMB.seq:*
3: /cg2_6/ptodaca/1/pubpna/US09_PUBCOMB.seq:*
4: /cg2_6/ptodaca/1/pubpna/US09A_PUBCOMB.seq:*
5: /cg2_6/ptodaca/1/pubpna/US10A_PUBCOMB.seq:*
6: /cg2_6/ptodaca/1/pubpna/US10B_PUBCOMB.seq:*
7: /cg2_6/ptodaca/1/pubpna/US10C_PUBCOMB.seq:*
8: /cg2_6/ptodaca/1/pubpna/US10D_PUBCOMB.seq:*
9: /cg2_6/ptodaca/1/pubpna/US10E_PUBCOMB.seq:*
10: /cg2_6/ptodaca/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 899 | 100.0 | 1008 | 6 | US-10-038-307-25 |
| 2 | 899 | 100.0 | 1008 | 6 | US-10-201-292-25 |
| 3 | 899 | 100.0 | 1047 | 6 | US-10-038-307-21 |
| 4 | 899 | 100.0 | 1047 | 6 | US-10-201-292-21 |
| 5 | 899 | 100.0 | 1056 | 6 | US-10-038-307-23 |
| 6 | 899 | 100.0 | 1056 | 6 | US-10-201-292-23 |
| 7 | 899 | 100.0 | 1401 | 6 | US-10-201-292-27 |
| 8 | 899 | 100.0 | 1401 | 6 | US-10-201-292-29 |

| | | | | | | |
|----|-----|-------|------|----|---------------------|--------------------|
| 9 | 899 | 100.0 | 1414 | 10 | US-11-047-278-1 | Sequence 1, Appl1 |
| 10 | 899 | 100.0 | 1436 | 10 | US-11-047-278-9 | Sequence 9, Appl1 |
| 11 | 899 | 100.0 | 1454 | 6 | US-10-133-937-58 | Sequence 58, Appl1 |
| 12 | 899 | 100.0 | 1454 | 6 | US-10-159-563-58 | Sequence 58, Appl1 |
| 13 | 899 | 100.0 | 1464 | 6 | US-10-201-292-31 | Sequence 31, Appl1 |
| 14 | 899 | 100.0 | 1534 | 6 | US-10-201-292-33 | Sequence 33, Appl1 |
| 15 | 899 | 100.0 | 1608 | 6 | US-10-037-292-35 | Sequence 35, Appl1 |
| 16 | 899 | 100.0 | 1609 | 5 | US-10-037-270-8 | Sequence 8, Appl1 |
| 17 | 899 | 100.0 | 1609 | 6 | US-10-117-122-8 | Sequence 8, Appl1 |
| 18 | 899 | 100.0 | 1609 | 9 | US-10-122-651-8 | Sequence 8, Appl1 |
| 19 | 899 | 100.0 | 1623 | 6 | US-10-038-307-11 | Sequence 11, Appl1 |
| 20 | 899 | 100.0 | 1623 | 6 | US-10-201-292-11 | Sequence 11, Appl1 |
| 21 | 899 | 100.0 | 1650 | 5 | US-10-047-542-98 | Sequence 98, Appl1 |
| 22 | 899 | 100.0 | 1650 | 6 | US-10-038-307-13 | Sequence 9, Appl1 |
| 23 | 899 | 100.0 | 1650 | 6 | US-10-038-307-13 | Sequence 13, Appl1 |
| 24 | 899 | 100.0 | 1650 | 6 | US-10-038-307-15 | Sequence 15, Appl1 |
| 25 | 899 | 100.0 | 1650 | 6 | US-10-201-292-9 | Sequence 9, Appl1 |
| 26 | 899 | 100.0 | 1650 | 6 | US-10-201-292-13 | Sequence 13, Appl1 |
| 27 | 899 | 100.0 | 1650 | 6 | US-10-201-292-15 | Sequence 15, Appl1 |
| 28 | 899 | 100.0 | 1674 | 6 | US-10-038-307-17 | Sequence 17, Appl1 |
| 29 | 899 | 100.0 | 1674 | 6 | US-10-201-292-17 | Sequence 17, Appl1 |
| 30 | 899 | 100.0 | 1713 | 6 | US-10-038-307-19 | Sequence 19, Appl1 |
| 31 | 899 | 100.0 | 1713 | 6 | US-10-201-292-19 | Sequence 19, Appl1 |
| 32 | 899 | 100.0 | 1718 | 8 | US-10-357-930-30300 | Sequence 30300, A |
| 33 | 899 | 100.0 | 2112 | 10 | US-11-047-278-7 | Sequence 7, Appl1 |
| 34 | 899 | 100.0 | 2272 | 3 | US-09-796-753-11 | Sequence 11, Appl1 |
| 35 | 899 | 100.0 | 2272 | 6 | US-10-038-307-1 | Sequence 1, Appl1 |
| 36 | 899 | 100.0 | 2272 | 6 | US-10-201-292-1 | Sequence 1, Appl1 |
| 37 | 899 | 100.0 | 2353 | 5 | US-10-198-846-9957 | Sequence 9957, Ap |
| 38 | 899 | 100.0 | 5540 | 3 | US-09-918-715-176 | Sequence 176, App |
| 39 | 899 | 100.0 | 5540 | 3 | US-09-918-715-231 | Sequence 231, App |
| 40 | 899 | 100.0 | 5540 | 6 | US-10-301-822-198 | Sequence 198, App |
| 41 | 899 | 100.0 | 5540 | 8 | US-10-474-794-176 | Sequence 176, App |
| 42 | 899 | 100.0 | 5540 | 8 | US-10-474-794-231 | Sequence 231, App |
| 43 | 899 | 100.0 | 5540 | 9 | US-10-979-159-176 | Sequence 176, App |
| 44 | 899 | 100.0 | 5540 | 9 | US-10-979-159-231 | Sequence 231, App |
| 45 | 899 | 100.0 | 5540 | 10 | US-11-047-278-5 | Sequence 5, Appl1 |

ALIGNMENTS

RESULT 1
US-10-038-307-25 Application US/10038307
Sequence 25, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 1008
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:

Pred. No.: 3.58e-111
Score: 899.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
Length: 1008
Matches: 173
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-038-307-25 (1-1008)

QY 1 AsplenTyrrhetleuAplySerGlySerValLeuHisHisrTpAengIuIetyr 20

```
Db 142 GACCTTACTTCACTTTTGGACAATACAGAAAGCTGTCTCCACACCTGGAATGAATCTAT 201
Qy 21 TyrPheValGluGlnLeuAlaHisIleValSerPheIleSerProGlnLeuArgMetSerPheIle 40
Db 202 TACTTTGTGGACAAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGTCCTTATT 261
Qy 41 ValPheSerThrArgGlyThrThrLeuMetIleValLeuThrGluAspArgGluGlnIleArg 60
Db 262 GTTTTCTCCACCCGAGAGAACACCTTAATGAACCTACAGAAAGACAGAAACAATCCGT 321
Qy 61 GlnGlyLeuGluGlnIleValLeuProGlyGlyAspThrTyrMetHisGluGly 80
Db 322 CAAAGCCTACAGAAACTCCAGAAAGTCTCCAGAGAGACACTTACATGCATGAAGA 381
Qy 81 PheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSer 100
Db 382 TTGGAAGGGCCAGTGAGCAGATTATTAATGAAGAACAGAACAGGTAACAGACCCAGC 441
Qy 101 ValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheThrTyrSerGluArg 120
Db 442 GTCATCATTCCTTTGACTGATGAGAACTCCATGAAGATCTTTTTCATATTCAGAGAG 501
Qy 121 GluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValIleAspPhe 140
Db 502 GAGGCTAATAGCTCTCGAAGATCTTGCGCAATGTTTACTGCTGTGGTGAAGATTC 561
Qy 141 AsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPheProValAsnArg 160
Db 562 AATGAGACACAGCTGCGCCGATGCGGACAGTAAGATCATGTTCCTCCGTGAATGAC 621
Qy 161 GlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
Db 622 GCCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660

RESULT 2
US-10-201-292-25
; Sequence 25, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-25

Alignment Scores:
Pred. No.: 3,586-111 Length: 1008
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-25 (1-1008)
Qy 1 AspLeuTyrPheIleLeuAspIleValSerGlySerValLeuHisIleTrpAsnGluIleTyr 20
Db 142 GACCTGTAATTCATTTTGGACAATACAGAAAGTGTGTCAGCCCACTGGAATGAATCTAT 201
Qy 21 TyrPheValGluGlnLeuAlaHisIleValSerPheIleSerProGlnLeuArgMetSerPheIle 40
Db 202 TACTTTGTGGACAAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGTCCTTATT 261
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Qy 41 ValPheSerThrArgGlyThrThrLeuMetIleValLeuThrGluAspArgGluGlnIleArg 60
Db 262 GTTTTCTCCACCCGAGAGAACACCTTAATGAACCTACAGAAAGACAGAAACAATCCGT 321
Qy 61 GlnGlyLeuGluGlnIleValLeuProGlyGlyAspThrTyrMetHisGluGly 80
Db 322 CAAAGCCTACAGAAACTCCAGAAAGTCTCCAGAGAGACACTTACATGCATGAAGA 381
Qy 81 PheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSer 100
Db 382 TTGGAAGGGCCAGTGAGCAGATTATTAATGAAGAACAGCAAGGTAACAGACCCAGC 441
Qy 101 ValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheThrTyrSerGluArg 120
Db 442 GTCATCATTCCTTTGACTGATGAGAACTCCATGAAGATCTTTTTCATATTCAGAGAG 501
Qy 121 GluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValIleAspPhe 140
Db 502 GAGGCTAATAGCTCTCGAAGATCTTGCGCAATGTTTACTGCTGTGGTGAAGATTC 561
Qy 141 AsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPheProValAsnArg 160
Db 562 AATGAGACACAGCTGCGCCGATGCGGACAGTAAGATCATGTTCCTCCGTGAATGAC 621
Qy 161 GlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
Db 622 GCCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660

RESULT 3
US-10-038-307-21
; Sequence 21, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-21

Alignment Scores:
Pred. No.: 3,796-111 Length: 1047
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-038-307-21 (1-1047)
Qy 1 AspLeuTyrPheIleLeuAspIleValSerGlySerValLeuHisIleTrpAsnGluIleTyr 20
Db 169 GACCTTACTTCACTTTTGGACAATACAGAAAGTGTCTCCACACCTGGAATGAATCTAT 228
Qy 21 TyrPheValGluGlnLeuAlaHisIleValSerPheIleSerProGlnLeuArgMetSerPheIle 40
Db 229 TACTTTGTGGACAAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGTCCTTATT 288
Qy 41 ValPheSerThrArgGlyThrThrLeuMetIleValLeuThrGluAspArgGluGlnIleArg 60
Db 289 GTTTTCTCCACCCGAGAGAACACCTTAATGAACCTACAGAAAGACAGAAACAATCCGT 348
Qy 61 GlnGlyLeuGluGlnIleValLeuProGlyGlyAspThrTyrMetHisGluGly 80
```

```
Db 349 CAAGGCGCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCATGAAGGA 408
|||
Qy 81 PheGluArgHisSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSer 100
|||
Db 409 TTGGAAGGGCGCACTGAGCAGATTATATATGAAAACAGACAGGGTTCACAGACGCCAGC 468
|||
Qy 101 ValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArg 120
|||
Db 469 GTCATCTTGTGCTGACTGATGAGAACTCCATGAAGTCTCTTTTCTATTCCAGAGAG 528
|||
Qy 121 GluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValAspPhe 140
|||
Db 529 GAGGCTAATAGTCTCGAGATCTTGTCGCAATGCTTACTGTGTGGTGGAAGATTTC 588
|||
Qy 141 AsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAsp 160
|||
Db 589 AATGAGACACAGCTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCTCGTAATGAC 648
|||
Qy 161 GlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
|||
Db 649 GGCCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 687
|||
RESULT 4
US-10-201-292-21
; Sequence 21, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; CURRENT FILING DATE: 2003-12-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-21
Alignment Scores:
Pred. No.: 3,796-111 Length: 1047
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-21 (1-1047)
Qy 1 AspleuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTPAangIuIleTyr 20
|||
Db 169 GACCTGACTTCAATTTTGGACAAATCGAAGATGTCTGCCACCTCGAATGAATCTTAT 228
|||
Qy 21 TyrPheValGluGlnLeuAlaHisIlyPheIleSerProGlnLeuArgMetSerPheIle 40
|||
Db 229 TACTTGTGGAAAGTGTGGCTCACAAAATTCATGACCCACAGTTGAGAAAGTCTTTAT 288
|||
Qy 41 ValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArg 60
|||
Db 289 GTTTTCTCCACCCAGAGAACAACTTAATGAACTGACAGAAACAGAGAACAAATCCGT 348
|||
Qy 61 GlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGluGly 80
|||
Db 349 CAAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATCATGAAGGA 408
|||
Qy 81 PheGluArgHisSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSer 100
|||
Db 409 TTGGAAGGGCGCACTGAGCAGATTATATATGAAAACAGACAGGGTTCACAGACGCCAGC 468
|||
```

```
Qy 101 ValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArg 120
|||
Db 469 GTCATCTTGTGCTGACTGATGAGAACTCCATGAAGTCTCTTTTCTATTCCAGAGAG 528
|||
Qy 121 GluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValAspPhe 140
|||
Db 529 GAGGCTAATAGTCTCGAGATCTTGTCGCAATGCTTACTGTGTGGTGGAAGATTTC 588
|||
Qy 141 AsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAsp 160
|||
Db 589 AATGAGACACAGCTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCTCGTAATGAC 648
|||
Qy 161 GlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
|||
Db 649 GGCCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 687
|||
RESULT 5
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23
Alignment Scores:
Pred. No.: 3,846-111 Length: 1056
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-09-970-076-2_COPY_44_216 (1-173) x US-10-038-307-23 (1-1056)
Qy 1 AspleuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTPAangIuIleTyr 20
|||
Db 142 GACCTGACTTCAATTTTGGACAAATCGAAGATGTCTGCCACCTCGAATGAATCTTAT 201
|||
Qy 21 TyrPheValGluGlnLeuAlaHisIlyPheIleSerProGlnLeuArgMetSerPheIle 40
|||
Db 202 TACTTGTGGAAAGTGTGGCTCACAAAATTCATGACCCACAGTTGAGAAATGCTTTAT 261
|||
Qy 41 ValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArg 60
|||
Db 262 GTTTTCTCCACCCAGAGAACAACTTAATGAACTGACAGAAACAGAGAACAAATCCGT 321
|||
Qy 61 GlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGluGly 80
|||
Db 322 CAAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATCATGAAGGA 381
|||
Qy 81 PheGluArgHisSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSer 100
|||
Db 382 TTGGAAGGGCGCACTGAGCAGATTATATGAAAACAGACAGGGTTCACAGACGCCAGC 441
|||
Qy 101 ValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArg 120
|||
Db 442 GTCATCTTGTGCTGACTGATGAGAACTCCAGAAAGTCTCTTTTCTATTCCAGAGAG 501
|||
Qy 121 GluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValAspPhe 140
|||
```

```
Db 502 GAGGCTAATGAGCTCGAATCTTGGGCAATGTTACTGTGTGTGGTGAAGATTC 561
Qy 141 AaenGluThGluLeuAlaArgIleAlaAspSerLyAspHisValPheProValAsnAsp 160
Db 562 AATGAGACACAGCTGGCCCGGATTCGGGACAGTAAGATCAATGTTTCCCGTAATGAC 621
Qy 161 GtPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
Db 622 GGCTTTCAGGCTCTGCAGGACATCATCTCAATTTTG 660

RESULT 6
US-10-201-292-23
; Sequence 23, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-23
```

```
Alignment Scores:
Pred. No.: 3,846-111 Length: 1056
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
```

US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-23 (1-1056)

```
Qy 1 AaPLeuTyRpheIleuAlaArgIleAlaAspSerLyAspHisValPheProValAsnAsp 20
Db 142 GACCTGATCTCAATTTTGGCAAAATCGAAGTGTGTGCACCACTGGAATGAATCTAT 201
Qy 21 TyRpheValGluGlnLeuAlaHisValPheIleSerProGlnLeuArgMetSerPheIle 40
Db 202 TACTTGTGGAACAGTGGCTCCAAATTCATCGACCCACAGTTGAGAAATGTCCTTAT 261
Qy 41 ValPheSerThrArgGlyThrThrIleuMetIleuThrGluAspArgGlnIleArg 60
Db 262 GTTTTCCACCCGAGAACACCTTAATGAAATGACAGAGACAGAAACAAATCCGT 321
Qy 61 GlnGlyLeuGlnGluLeuGlnValIleuProGlyGlyAspThrTyRmeHisGlnGly 80
Db 322 CAAGGCTTAAGAACTCCAGAAAGTCTGCCAGAGAGACACTTACATGAAAGAGA 381
Qy 81 PheGlnArgAlaSerGlnGlnIleTyRtyrGluAsnArgGlnGlyTyRargThrAlaSer 100
Db 382 TTGGAAGGGCCAGTGAAGATTTATTAAGAAACAGACAGGGTACAGAGACGCCAGC 441
Qy 101 ValIleIleAlaLeuThrAspGlyGluLeuHisGlnIleuAspIlePheTyRserGlnArg 120
Db 442 GTCATCATTCCTTTGATGAGAGAACTCCATGAATATCTCTTTTCTATTCAGAGAG 501
Qy 121 GlnAlaAsnArgSerArgAspLeuGlyAlaIleValTyRtyrCysValGlyValIleAspPhe 140
Db 502 GAGGCTAATAGGCTCGAATCTTGGTGCATATCTTACTGTGTGTGGTGAAGATTC 561
Qy 141 AaenGluThGlnLeuAlaArgIleAlaAspSerLyAspHisValPheProValAsnAsp 160
Db 562 AATGAGACACAGCTGGCCCGGATTCGGGACAGTAAGATCAATGTTTCCCGTAATGAC 621
```

```
Qy 161 GtPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
Db 622 GGCTTTCAGGCTCTGCAGGACATCATCTCAATTTTG 660
```

RESULT 7

```
US-10-201-292-27
; Sequence 27, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-27
```

```
Alignment Scores:
Pred. No.: 5,96-111 Length: 1401
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
```

US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-27 (1-1401)

```
Qy 1 AaPLeuTyRpheIleuAlaArgIleAlaAspSerLyAspHisValPheProValAsnAsp 20
Db 142 GACCTGATCTCAATTTTGGCAAAATCGAAGTGTGTGCACCACTGGAATGAATCTAT 201
Qy 21 TyRpheValGluGlnLeuAlaHisValPheIleSerProGlnLeuArgMetSerPheIle 40
Db 202 TACTTGTGGAACAGTGGCTCCAAATTCATCGACCCACAGTTGAGAAATGTCCTTAT 261
Qy 41 ValPheSerThrArgGlyThrThrIleuMetIleuThrGluAspArgGlnIleArg 60
Db 262 GTTTTCCACCCGAGAACACCTTAATGAAATGACAGAGACAGAAACAAATCCGT 321
Qy 61 GlnGlyLeuGlnGluLeuGlnValIleuProGlyGlyAspThrTyRmeHisGlnGly 80
Db 322 CAAGGCTTAAGAACTCCAGAAAGTCTGCCAGAGAGACACTTACATGAAAGAGA 381
Qy 81 PheGlnArgAlaSerGlnGlnIleTyRtyrGluAsnArgGlnGlyTyRargThrAlaSer 100
Db 382 TTGGAAGGGCCAGTGAAGATTTATTAAGAAACAGACAGGGTACAGAGACGCCAGC 441
Qy 101 ValIleIleAlaLeuThrAspGlyGluLeuHisGlnIleuAspIlePheTyRserGlnArg 120
Db 442 GTCATCATTCCTTTGATGAGAGAACTCCATGAATATCTCTTTTCTATTCAGAGAG 501
Qy 121 GlnAlaAsnArgSerArgAspLeuGlyAlaIleValTyRtyrCysValGlyValIleAspPhe 140
Db 502 GAGGCTAATAGGCTCGAATCTTGGTGCATATCTTACTGTGTGTGGTGAAGATTC 561
Qy 141 AaenGluThGlnLeuAlaArgIleAlaAspSerLyAspHisValPheProValAsnAsp 160
Db 562 AATGAGACACAGCTGGCCCGGATTCGGGACAGTAAGATCAATGTTTCCCGTAATGAC 621
Qy 161 GtPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
Db 622 GGCTTTCAGGCTCTGCAGGACATCATCTCAATTTTG 660
```

RESULT 8

```
US-10-201-292-29
; Sequence 29, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-29

Alignment Scores:
Pred. No.: 5.99e-111      Length: 1401
Score: 899.00           Matches: 173
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 6                      Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-29 (1-1401)
QY 1 AspleuTyrrPheilleuAaplySerglySerValIleuHishIstrPaengluIleTyr 20
DB 142 GACCTGACTTCAATTTTGGACAATTCAGAAAGTGTGTCACCACTGGAAATGAATCTAT 201
QY 21 TyrPheValgluInleuAahlslyPheIleSergProglInleuAargMetSerpheile 40
DB 202 TACTTGTGGACAGTGGTCCCAAAATTCATCAGCCACAGTTGAGAAATGCTCTTATT 261
QY 41 ValPheSerThrArglyThrThleuMetlyleuThrgluAparArggluInllearg 60
DB 262 GTTTTCTCCACCCGAGAACCACTTAATGAAACTGACAGAAACAGAAACAATCCGT 321
QY 61 GlnglyleuGlulueugInlyValIleuProgllyIlyAparThryrMetHsgluGly 80
DB 322 CAAGGCTTAAGAAGCTCCAGAAAGTTCTGCCAGAGAGAGACACTTCATGCAAGAGA 381
QY 81 PhegluArglaSergluInlleTyrTyrgluAparArgglnglyTyrrArgThraIaSer 100
DB 382 TTGAAAGGCGCAGTAGAGATTATTATGAAACAGACAGAGGTACAGAGACGCCAGC 441
QY 101 ValIlelleuAleuThraArglygluIleuHishgluAparleuPheThryrSergluArg 120
DB 442 GTCATCATTCCTTGGATGAGAACTCCATGAAAGATCTCTTTTCTATTCCAGAGAG 501
QY 121 GluAlaAparSergserArgAparleuGlyAlaIleValTyrcysValglValIlyAparPhe 140
DB 502 GAAGCTAATAGGCTGCAAGATCTTGGTGCATATGTTTACTGTGTGGTGGAAAGATTTC 561
QY 141 AasngluThrgInleuAalargIleAaPserlyAparHishValPheProValAasnApar 160
DB 562 AATGAGACACAGCTGGCCGGATGGCGAGACAGTAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGlnAlaIleuGlnnglyIlelleHishSerIleleu 173
DB 622 GGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660

RESULT 9
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
```

```
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1

Alignment Scores:
Pred. No.: 5.99e-111      Length: 1414
Score: 899.00           Matches: 173
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 10                      Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-11-047-278-1 (1-1414)
QY 1 AspleuTyrrPheilleuAaplySerglySerValIleuHishIstrPaengluIleTyr 20
DB 233 GACCTGACTTCAATTTTGGACAATTCAGAAAGTGTGTCACCACTGGAAATGAATCTAT 232
QY 21 TyrPheValgluInleuAahlslyPheIleSergProglInleuAargMetSerpheile 40
DB 293 TACTTGTGGACAGTGGTCCCAAAATTCATCAGCCACAGTTGAGAAATGCTCTTATT 352
QY 41 ValPheSerThrArglyThrThleuMetlyleuThrgluAparArggluInllearg 60
DB 353 GTTTTCTCCACCCGAGAACCACTTAATGAAACTGACAGAAACAGAAACAATCCGT 412
QY 61 GlnglyleuGlulueugInlyValIleuProgllyIlyAparThryrMetHsgluGly 80
DB 413 CAAGGCTTAAGAAGCTCCAGAAAGTTCTGCCAGAGAGAGACACTTCATGCAAGAGA 472
QY 81 PhegluArglaSergluInlleTyrTyrgluAparArgglnglyTyrrArgThraIaSer 100
DB 473 TTGAAAGGCGCAGTAGAGATTATTATGAAACAGACAGAGGTACAGAGACGCCAGC 532
QY 101 ValIlelleuAleuThraArglygluIleuHishgluAparleuPheThryrSergluArg 120
DB 533 GTCATCATTCCTTGGATGAGAACTCCATGAAAGATCTCTTTTCTATTCCAGAGAG 592
QY 121 GluAlaAparSergserArgAparleuGlyAlaIleValTyrcysValglValIlyAparPhe 140
DB 593 GAAGCTAATAGGCTGCAAGATCTTGGTGCATATGTTTACTGTGTGGTGGAAAGATTTC 652
QY 141 AasngluThrgInleuAalargIleAaPserlyAparHishValPheProValAasnApar 160
DB 653 AATGAGACACAGCTGGCCGGATGGCGAGACAGTAAGATCATGTGTTCCCGTAATGAC 712
QY 161 GlyPheGlnAlaIleuGlnnglyIlelleHishSerIleleu 173
DB 713 GGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 751

RESULT 10
US-11-047-278-9
; Sequence 9, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
```

```

; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-11-047-278-9

Alignment Scores:
Pred. No.: 6,136-111 Length: 1436
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-11-047-278-9 (1-1436)

QY 1 AapleuTyrrPheHleleuAaplySerGlySerValleuHleHleSTraPangluIleTyrr 20
DB 272 GACCTGTGACCTTCAATTTGGACAATTCAGAAAGTGTGTGACCACTGGAAATGAATCTAT 331

QY 21 TyrrPheValGluGluInleuAlaHlelyPheHleSerProGluInleuArgMetSerPheHle 40
DB 332 TACTTTGTGAAACAGTGGCTCACAATTCATCCAGCCCAAGTTGAGAAATGCTCTTATT 391

QY 41 ValPheSerThrArgGlyThrThrLeuMetIySleuThrGluAapArgGluGluInleArg 60
DB 392 GTTTTCTCCACCAGGAAACAACTTAATGAATCTGACAGAGACAGAGAAACAATCCGT 451

QY 61 GlnGlyLeuGluGluInleuGluInlyValleuProGlyGlyAapThrTyrrMetHleGluGly 80
DB 452 CAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGGA 511

QY 81 PheGluArgAlaSerGluGluInleTyrrTyrrGluAapArgGluGlyTyrrArgThrAlaSer 100
DB 512 TTTGAAAGGCCCACTGAGCAATTTATTTGAAACAGACAGAGGTTACAGACAGCTAGC 571

QY 101 ValIleIleAlaLeuThrAapGlyGluInleuHleGluAapLeuPheTyrrSerGluArg 120
DB 572 GTATCATTTGCTTGATGATGAGAACTCATGAAGATCTTTTCTATTCAGAGAGG 631

QY 121 GluAlaAapArgSerArgAapLeuGlyValIleValTyrrCysValGlyValIlyAapPhe 140
DB 632 GAGCTAATAGGTCTCGAGATCTTGAGTCAATTTGTTTAACTGTGTGGTGAAGAAATTC 691

QY 141 AapGluThrGluInleuAlaArgIleAlaAapSerIyAapPheIleValPheProValAapAap 160
DB 692 AATGAGACACAGCTGGCCCGGATGGGACAGTAAGATCATGTGTTCCCGTAATGAC 751

QY 161 GlyPheGluAlaLeuGluGlyIleIleHleSerIleleu 173
DB 752 GGCTTTCAAGCTCTGCAAGGATCATTCATCAATTTTG 790

RESULT 11
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
```

```

; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: OTHER BIOLOGICAL STATES
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 6,246-111 Length: 1454
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-133-937-58 (1-1454)

QY 1 AapleuTyrrPheHleleuAaplySerGlySerValleuHleHleSTraPangluIleTyrr 20
DB 273 GACCTGTGACCTTCAATTTGGACAATTCAGAAAGTGTGTGACCACTGGAAATGAATCTAT 332

QY 21 TyrrPheValGluGluInleuAlaHlelyPheHleSerProGluInleuArgMetSerPheHle 40
DB 333 TACTTTGTGAAACAGTGGCTCACAATTCATCCAGCCCAAGTTGAGAAATGCTCTTATT 392

QY 41 ValPheSerThrArgGlyThrThrLeuMetIySleuThrGluAapArgGluGluInleArg 60
DB 393 GTTTTCTCCACCAGGAAACAACCTTAATGAATCTGACAGAGACAGAGAAACAATCCGT 452

QY 61 GlnGlyLeuGluGluInleuGluInlyValleuProGlyGlyAapThrTyrrMetHleGluGly 80
DB 453 CAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGGA 512

QY 81 PheGluArgAlaSerGluGluInleTyrrTyrrGluAapArgGluGlyTyrrArgThrAlaSer 100
DB 513 TTTGAAAGGCCCACTGAGCAATTTATTTGAAACAGACAGAGGTTACAGACAGCTAGC 572

QY 101 ValIleIleAlaLeuThrAapGlyGluInleuHleGluAapLeuPheTyrrSerGluArg 120
DB 573 GTATCATTTGCTTGATGATGAGAACTCATGAAGATCTTTTCTATTCAGAGAGG 632

QY 121 GluAlaAapArgSerArgAapLeuGlyValIleValTyrrCysValGlyValIlyAapPhe 140
DB 633 GAGCTAATAGGTCTCGAGATCTTGAGTCAATTTGTTTAACTGTGTGGTGAAGAAATTC 692

QY 141 AapGluThrGluInleuAlaArgIleAlaAapSerIyAapPheIleValPheProValAapAap 160
DB 693 AATGAGACACAGCTGGCCCGGATGGGACAGTAAGATCATGTGTTCCCGTAATGAC 752

QY 161 GlyPheGluAlaLeuGluGlyIleIleHleSerIleleu 173
DB 753 GGCTTTCAAGCTCTGCAAGGATCATTCATCAATTTTG 791

RESULT 12
US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
```



```
/ TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
/ FILE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
/ FILE REFERENCE: 11613.56US11
/ CURRENT APPLICATION NUMBER: US/10/159,563
/ CURRENT FILING DATE: 2002-12-09
/ PRIOR APPLICATION NUMBER: US 10/133,937
/ PRIOR FILING DATE: 2002-04-25
/ NUMBER OF SEQ ID NOS: 444
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 58
/ LENGTH: 1454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:
Pred. No.: 6,24e-111 Length: 1454
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-159-563-58 (1-1454)
QY 1 AspleuTyRpheIleuAaplySergISeRValIeuHshIeTPaengIuIleTyR 20
Db 273 GACCTGACTTCTATTGGCAAAATTCAGAAAGTGCTGCAACCTGAATGAATCTAT 332
QY 21 TyRpheValGluInleuAlahIstlyPheIleSeRProGInleuAargMeSerpheIle 40
Db 333 TACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGAATGCTTTATT 392
QY 41 ValPheSeRThraRgIyThrThleuMeIlyleuThrgIuAapRagIuGInIleArg 60
Db 393 GTTTTCTCCACCCGAGAACAACTTAATGAAGTGCAGAGACAGAACAAATCCGT 452
QY 61 GluGluYleuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db 453 CAAGGCTTAAAGAACTCCGAAAGTTCTCCAGAGAGACACTTACATGATGAAGGA 512
QY 81 PheGluAargIaSeRgIuGInIleTyRyRgIuAaRgGInGlyTyRatgThraIaSeR 100
Db 513 TTTGAAAGGCCCACTGACGAGATTATTAAGAAACAGCAAGGTTACAGAGCCAGC 572
QY 101 ValIleIleAlaIeuThraRgIyGluLeuHshIuAapleuPheTyRSeRgIuAarg 120
Db 573 GTCATCATTCCTTTGATGAGAACTCATGAAGATCTCTTTTCTATTCAAGAGAG 632
QY 121 GluAlaAaRgSeRraRgaRpleuGlyAlaIleValTyRyRyRyRyRyRyRyRyRyRy 140
Db 633 GAGGCTTAATAGGCTTCAGAGATCTTGTCGCAATGTTACTGTGTGTGTAAGAAATTC 692
QY 141 AsnGluThrgInleuAlaRgIleAlaAapSeRlySaRphIstValPheProValaAasp 160
Db 693 AATGAGACACAGCTGGCCGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGAC 752
QY 161 GlyPheGInAlaIeuGInGlyIleIleHshIeSerIleIeu 173
Db 753 GGCCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 791

RESULT 13
US-10-201-292-31
/ Sequence 31, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZAYINAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
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/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 31
/ LENGTH: 1464
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-31

Alignment Scores:
Pred. No.: 6,31e-111 Length: 1464
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-31 (1-1464)
QY 1 AspleuTyRpheIleuAaplySergISeRValIeuHshIeTPaengIuIleTyR 20
Db 142 GACCTGACTTCTATTGGCAAAATTCAGAAAGTGCTGCAACCTGAATGAATCTAT 201
QY 21 TyRpheValGluInleuAlahIstlyPheIleSeRProGInleuAargMeSerpheIle 40
Db 202 TACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGAATGCTTTATT 261
QY 41 ValPheSeRThraRgIyThrThleuMeIlyleuThrgIuAapRagIuGInIleArg 60
Db 262 GTTTTCTCCACCCGAGAACAACTTAATGAAGTGCAGAGACAGAACAAATCCGT 321
QY 61 GluGluYleuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db 322 CAAGGCTTAAAGAACTCCGAAAGTTCTCCAGAGAGACACTTACATGATGAAGGA 381
QY 81 PheGluAargIaSeRgIuGInIleTyRyRgIuAaRgGInGlyTyRatgThraIaSeR 100
Db 382 TTTGAAAGGCCCACTGACGAGATTATTAAGAAACAGCAAGGTTACAGAGCCAGC 441
QY 101 ValIleIleAlaIeuThraRgIyGluLeuHshIuAapleuPheTyRSeRgIuAarg 120
Db 442 GTCATCATTCCTTTGATGAGAACTCATGAAGATCTCTTTTCTATTCAAGAGAG 501
QY 121 GluAlaAaRgSeRraRgaRpleuGlyAlaIleValTyRyRyRyRyRyRyRyRyRyRy 140
Db 502 GAGGCTTAATAGGCTTCAGAGATCTTGTCGCAATGTTACTGTGTGTGTAAGAAATTC 561
QY 141 AsnGluThrgInleuAlaRgIleAlaAapSeRlySaRphIstValPheProValaAasp 160
Db 562 AATGAGACACAGCTGGCCGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGInAlaIeuGInGlyIleIleHshIeSerIleIeu 173
Db 622 GGCCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660

RESULT 14
US-10-201-292-33
/ Sequence 33, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZAYINAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 1534
/ TYPE: DNA
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ORGANISM: Homo sapiens
US-10-201-292-33

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 6.77e-111 | Length: | 1534 |
| Score: | 899.00 | Matches: | 173 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-970-076-2_copy_44_216 (1-173) x US-10-201-292-33 (1-1534)

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QY 1 AspleuTyPheIleuAapLySerGlySerValIleuHsiSTPaengIuIeTy 20
DB 142 GACCTGACTTCATTGGACAATCCAGAAAGTGTGTCACCACTGGAAATGCTTATT 201
QY 21 TyPheValGluGluLeuAaHsiLyPheIleSerProGluLeuArgMetSerPheIle 40
DB 202 TACTTGTGGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAAGATGCTTATT 261
QY 41 ValPheSerThrArgGlyThrThrLeuMetLyLeuThrGluAapArgGluGluIleArg 60
DB 262 GTTTCTCCACCCGAGAGAACACTTAATGAAACTGACAGAAACAAATCCGT 321
QY 61 GlnGlyLeuGluGluLeuGluIleValIleuProGlyGlyAspThrTyrmethIsgIuGly 80
DB 322 CAAGGCTTAGAAGAACTCCAGAAAGTTCTGCAAGAGAGACACTTACATGCAAGGA 381
QY 81 PheGluArgAlaSerGluGluIleTyTyTyGluAaArgGlnGlyTyraArgThrAlaSer 100
DB 382 TTGAAAGGGCCAGTGAGAGATTATTATGAAAGCAAGAGGTACAGACAGCCAGC 441
QY 101 ValIleIleAlaLeuThrAapGlyGluLeuHsiGluAapLeuPhePheTySerGluArg 120
DB 442 GTCATCATTCCTTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTGAGAGAG 501
QY 121 GluAlaAaArgSerArgAapLeuGlyAlaIleValTyCyValGlyValIleAapPhe 140
DB 502 GAGGCTTAATAGGCTTCAGAACTTGTGCAATGTTTACTGTGTGTGTAAGATTTC 561
QY 141 AaArgIuThrGluLeuAaArgIleAlaAapSerLyAaPheIleValPheProValAaAap 160
DB 562 AATGAGACACAGCTGCCGAGATTGGGACAGTAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGlnAlaLeuGlnGlyIleIleHsiSerIleLeu 173
DB 622 GGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660
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RESULT 15

US-10-201-292-35
; Sequence 35, Application US/10201292
; Publication No. US20030141193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-35

Alignment Scores:

| | | | |
|------------|-----------|----------|------|
| Pred. No.: | 7.28e-111 | Length: | 1608 |
| Score: | 899.00 | Matches: | 173 |

| | | | |
|------------------------|---------|---------------|---|
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-970-076-2_copy_44_216 (1-173) x US-10-201-292-35 (1-1608)

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QY 1 AspleuTyPheIleuAapLySerGlySerValIleuHsiSTPaengIuIeTy 20
DB 142 GACCTGACTTCATTGGACAATCCAGAAAGTGTGTCACCACTGGAAATGCTTATT 201
QY 21 TyPheValGluGluLeuAaHsiLyPheIleSerProGluLeuArgMetSerPheIle 40
DB 202 TACTTGTGGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAAGATGCTTATT 261
QY 41 ValPheSerThrArgGlyThrThrLeuMetLyLeuThrGluAapArgGluGluIleArg 60
DB 262 GTTTCTCCACCCGAGAGAACACTTAATGAAACTGACAGAAACAAATCCGT 321
QY 61 GlnGlyLeuGluGluLeuGluIleValIleuProGlyGlyAspThrTyrmethIsgIuGly 80
DB 322 CAAGGCTTAGAAGAACTCCAGAAAGTTCTGCAAGAGAGACACTTACATGCAAGGA 381
QY 81 PheGluArgAlaSerGluGluIleTyTyTyGluAaArgGlnGlyTyraArgThrAlaSer 100
DB 382 TTGAAAGGGCCAGTGAGAGATTATTATGAAAGCAAGAGGTACAGACAGCCAGC 441
QY 101 ValIleIleAlaLeuThrAapGlyGluLeuHsiGluAapLeuPhePheTySerGluArg 120
DB 442 GTCATCATTCCTTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTGAGAGAG 501
QY 121 GluAlaAaArgSerArgAapLeuGlyAlaIleValTyCyValGlyValIleAapPhe 140
DB 502 GAGGCTTAATAGGCTTCAGAACTTGTGCAATGTTTACTGTGTGTGTAAGATTTC 561
QY 141 AaArgIuThrGluLeuAaArgIleAlaAapSerLyAaPheIleValPheProValAaAap 160
DB 562 AATGAGACACAGCTGCCGAGATTGGGACAGTAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGlnAlaLeuGlnGlyIleIleHsiSerIleLeu 173
DB 622 GGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660
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Search completed: December 19, 2005, 02:10:29
Job time : 561.247 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - nucleic search, using frame_plus.p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 139.602 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_44_216

Perfect score: 899

Sequence: 1 DLYFIDKSGSVLHMNEIY.....HFPVNDGFGALGIHSIL 173

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA_New -QFMT=faeap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=91 -MATRIX=blosum62
-TRANS=human0.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 @CGN_1_1_675 @runcat_14122005_11853_21065
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published_Applications_NA_New.*

1: /cg2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
2: /cg2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cg2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cg2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cg2_6/ptodata/1/pubpna/PCRT_NEW_PUB.seq.*
6: /cg2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cg2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cg2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cg2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cg2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1 | 899 | 100.0 | 5540 | 7 US-11-186-284-198 | Sequence 198, App |
| 2 | 128.5 | 14.3 | 4740 | 7 US-11-080-026-3 | Sequence 3, Appl |
| 3 | 118.5 | 13.2 | 11447 | 7 US-11-186-284-25 | Sequence 25, Appl |
| 4 | 115 | 12.8 | 2834 | 6 US-10-750-185-39040 | Sequence 39040, A |
| 5 | 108 | 12.0 | 3564 | 6 US-10-601-368-20 | Sequence 20, Appl |
| 6 | 108 | 12.0 | 4858 | 6 US-10-601-368-19 | Sequence 19, Appl |
| 7 | 104 | 11.6 | 3564 | 6 US-10-601-368-2 | Sequence 2, Appl |
| 8 | 104 | 11.6 | 3967 | 7 US-11-000-463-574 | Sequence 574, App |

| | | | | | |
|----|-------|------|-------|-----------------------|--------------------|
| 9 | 104 | 11.6 | 3969 | 7 US-11-000-463-102 | Sequence 102, App |
| 10 | 104 | 11.6 | 5042 | 6 US-10-601-368-1 | Sequence 1, Appl |
| 11 | 101.5 | 11.3 | 2501 | 6 US-10-821-234-182 | Sequence 182, App |
| 12 | 100.5 | 11.2 | 3449 | 6 US-10-131-826A-293 | Sequence 293, App |
| 13 | 98.5 | 11.0 | 1325 | 6 US-10-750-185-56394 | Sequence 56394, A |
| 14 | 96.5 | 10.7 | 3175 | 6 US-10-995-561-464 | Sequence 464, App |
| 15 | 96.5 | 10.7 | 3464 | 6 US-10-995-561-465 | Sequence 465, App |
| 16 | 96.5 | 10.7 | 3468 | 6 US-10-995-561-466 | Sequence 466, App |
| 17 | 96.5 | 10.7 | 47572 | 6 US-10-995-561-13356 | Sequence 13356, A |
| 18 | 95 | 10.6 | 3884 | 6 US-10-601-368-17 | Sequence 17, Appl |
| 19 | 91.5 | 10.2 | 3868 | 6 US-10-995-561-404 | Sequence 404, App |
| 20 | 82 | 9.1 | 2773 | 7 US-11-102-240-33 | Sequence 33, Appl |
| 21 | 81.5 | 9.1 | 1062 | 7 US-11-137-465-11 | Sequence 11, Appl |
| 22 | 81.5 | 9.1 | 1347 | 7 US-11-137-465-12 | Sequence 12, Appl |
| 23 | 79.5 | 8.8 | 3366 | 6 US-10-467-657-6111 | Sequence 6111, App |
| 24 | 75 | 8.3 | 3435 | 6 US-10-793-626-3648 | Sequence 3648, App |
| 25 | 74 | 8.2 | 1688 | 6 US-10-510-186-157 | Sequence 157, App |
| 26 | 73.5 | 8.2 | 1530 | 6 US-10-793-626-2879 | Sequence 2879, App |
| 27 | 73.5 | 8.2 | 2996 | 6 US-10-793-626-3563 | Sequence 3563, App |
| 28 | 73.5 | 8.2 | 3092 | 6 US-10-793-626-3559 | Sequence 3559, App |
| 29 | 73.5 | 8.2 | 3900 | 6 US-10-793-626-4177 | Sequence 4177, App |
| 30 | 72 | 8.0 | 795 | 6 US-10-793-626-387 | Sequence 387, App |
| 31 | 72 | 8.0 | 2361 | 6 US-10-467-962B-102 | Sequence 102, App |
| 32 | 72 | 8.0 | 2657 | 6 US-10-793-626-3472 | Sequence 3472, App |
| 33 | 72 | 8.0 | 3281 | 6 US-10-793-626-4324 | Sequence 4324, App |
| 34 | 72 | 8.0 | 3633 | 6 US-10-793-626-4307 | Sequence 4307, App |
| 35 | 70 | 7.8 | 1305 | 6 US-10-793-626-2635 | Sequence 2635, App |
| 36 | 70 | 7.8 | 1305 | 6 US-10-467-657-5693 | Sequence 5693, App |
| 37 | 70 | 7.8 | 1404 | 6 US-10-467-657-5695 | Sequence 5695, App |
| 38 | 70 | 7.8 | 3290 | 6 US-10-793-626-3569 | Sequence 3569, App |
| 39 | 70 | 7.8 | 96988 | 7 US-11-117-187-196 | Sequence 196, App |
| 40 | 69.5 | 7.7 | 730 | 6 US-10-750-185-61019 | Sequence 61019, A |
| 41 | 69.5 | 7.7 | 1457 | 6 US-10-467-657-7845 | Sequence 7845, App |
| 42 | 69 | 7.7 | 726 | 6 US-10-467-657-7305 | Sequence 7305, App |
| 43 | 69 | 7.7 | 766 | 6 US-10-467-657-7299 | Sequence 7299, App |
| 44 | 68.5 | 7.6 | 3144 | 6 US-10-392-234A-17 | Sequence 17, Appl |
| 45 | 68.5 | 7.6 | 5592 | 7 US-11-192-967-5 | Sequence 5, Appl |

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Sequence 198, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA

```
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (144)...(1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 1,71e-108 Length: 5540
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-11-186-284-198 (1-5540)

QY 1 AapLeuTyRPhelIeLeuAapLySeRgLySeRValLeuHshIeRTPaNgLuIleTyR 20
DB 273 GACCTGTACTTCAATTTTGGCAAAATCAGAAAGTGTGTGCACACCTGGAATGAAATCTTAT 332
QY 21 TyRPhVaIgLuGInLeuAlAhIshYsPhelIeSeRProGInLeuArGMeSeRPhelIe 40
DB 333 TACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATGTCTTTATT 392
QY 41 ValPheSeRThArGgLyThRThLeuMeLyLeuThRgLuAsPaRgGInIleArG 60
DB 393 GTTTTTCACCCAGAGAACACCTTAATGAACTGACAGAAACAGAAACAAATCCGT 452
QY 61 GInGlyLeuGInGluLeuGInLyVaIleuProGlyGlyAsPThRThMeThIeGluGly 80
DB 453 CAAGGCTTAAAGAAATCCAGAAAGTTCTGCAGAGAGAACACTTAATCATGTGAAGGA 512
QY 81 PhGgLuArGAlaSeRgInIleTyRThRgLuAsPaRgGInGlyThArGThRAlaSeR 100
DB 513 TTTGAAAGGCCCAAGTGCAGATTTATTATGAAACAGACAGGTRACAGAACCCAGC 572
QY 101 ValIleIleAlaLeuThRAsPglYgLuLeuHshIeGluAsPLeuPhePhyTySeRgLuArG 120
DB 573 GTCATCATTCCTTTGATGATGAGAACTCCATGAACATCTTTTCTATTCAGAGAG 632
QY 121 GInuAlaAsPaRgSeRThArGAsPLeuGlyAlaIleValTyRcYsValGlyValIlyAsPPh 140
DB 633 GAGGCTAAATGAGTCTTCAGATCTTGTGCAATGTTTAACTGTGTGTGAAAGATTC 692
QY 141 AsnGluThRcInLeuAlaRgIleAlaAsPSeRThAsPshIeValPheProValAsnAsP 160
DB 693 AATGAGACACAGCTGCGCCGATTCGCGACAGTRAGATCATGTGTTCCCGATGAC 752
QY 161 GlyPheGInAlaLeuGInGlyIleIleHshIeSerIleLeu 173
DB 753 GGCCTTCAGGCTCTGCAAGGATCATCATCATTTTG 791

RESULT 2
US-11-080-026-3
/ Sequence 3, Application US/11080026
/ Publication No. US20050260192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shimooka, Motomu
/ APPLICANT: Lu, Chafen
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
/ FILE REFERENCE: CBBF-P02-021
/ CURRENT APPLICATION NUMBER: US/11/080,026
/ PRIOR FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: 09/945,265
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 4740
```

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/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-11-080-026-3

Alignment Scores:
Pred. No.: 8,26e-06 Length: 4740
Score: 128.50 Matches: 51
Percent Similarity: 46.60% Conservative: 38
Best Local Similarity: 26.70% Mismatches: 63
Query Match: 14.29% Indels: 39
DB: 7 Gaps: 11

US-09-970-076-2_COPY_44_216 (1-173) x US-11-080-026-3 (1-4740)

QY 1 AapLeuTyRPhelIeLeuAapLySeRgLySeRValLeuHshIeRTPaNgLuIleTyR 19
DB 520 GACATTCCTTTTATTTGATGAGCTCTGTGTACATCATTCACATGACTTGGCGGAG 579
QY 20 TyRTyRPhVaIgLuGInLeuAlAhIshYsPhelIeSeRProGInLeuArGMeSeRPh 39
DB 580 AAGGAGTTGTCTCAACT-----GTGATGAGACCAATTAATAAAGTCCAA 624
QY 40 IleValPheSeRThArGgLyThRThLeuMeLyLeuThRgLuAsP----- 55
DB 625 ACCTGTCTCT-----TGATGCACTACTGTGAAGAAATTCGGATTCAC 669
QY 56 -----ArgGluGInIleArGInGlyLeuGluGluGln 67
DB 670 TTTACTCTAAAGAGTTCAGAAACCAACCTTAACCAAGTCACTGTGAAAGCAATTAAG 729
QY 68 LySValLeuProGlyGlyAsPThRThMeThIeGluGlyPheGluArGAlaSeRgLuGln 87
DB 730 CAGCTGCTT-----GGCGGACACACACGCGCAGCGGATCCGCAAGTGTGACAGAG 783
QY 88 IleTyRThRgLuAsPaRgGInGlyThRArgThRAla-----SeRValIleIleAlaLeuThR 106
DB 784 CTGTTTAACATCACCAACGAGCCGAAAGAAATGCTTTTAAGATCTTCAATGTCATCAG 843
QY 107 AapGlyGluLeuHshIeGluAsPLeuPhePhyTySeRgLu-----ArgGluAlaAsnArG 124
DB 844 GATGAGAAAGATTTGGCGATCCCTTGGGATGAGAGATGATCCCTGAGGACAGACAG 903
QY 125 SeRThAsPLeuGlyAlaIleValTyRcYsValGlyValIlyAsPPhAsnGluThRgIn 144
DB 904 GAG-----GAGTCAATTCGCTACATGATGGGTGGAGATCCCTTCCGACATGAG 954
QY 145 LeuAlaArG-----IleAlaAsPSeR-----LySAsPshIeValPhePro 157
DB 955 AATCCCGCAAGAGCTTAATACATCGCATCCAGCCGCTGTGATCAGTGTTCCAG 1014
QY 158 ValAsnAsPglyPheGInAlaLeuGInGlyIle 168
DB 1015 GTGAATAC---TTTGAGGCTCTGAAGACATT 1044

RESULT 3
US-11-186-284-25
/ Sequence 25, Application US/11186284
/ Publication No. US2005026493A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Thibodeau, Stephen N.
/ APPLICANT: Burgart, Lawrence J.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF COLON CANCER
/ FILE REFERENCE: MP001-029P2RM
/ CURRENT APPLICATION NUMBER: US/11/186,284
/ CURRENT FILING DATE: 2005-07-21
```

```
/ PRIOR APPLICATION NUMBER: US/10/301,832
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 11447
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(9192)
/ US-11-186-284-25
```

```
Alignment Scores:
Pred. No.: 0.00645 Length: 11447
Score: 118.50 Matches: 54
Percent Similarity: 49.44% Conservative: 35
Best Local Similarity: 30.00% Mismatches: 68
Query Match: 13.18% Indels: 23
DB: Gaps: 12
```

US-09-970-076-2_COPY_44_216 (1-173) x US-11-186-284-25 (1-11447)

```
QY 1 AspleuTyRheileuAplySerglyServal--LeuHsih1rPaengluile 19
DB 1318 GATATTGTGTTTGGTGTGATGCTCTATAGCATGGAGATGGCAATCTTTGAAGTT 1377
QY 20 TyTyTyRheValGluGlnLeuAlaHsiLysPhe---lleserPro--GlnLeuArgMet 37
DB 1378 AGAGCCCTTTTGGAGAGTCTTGTAAGAAAGTTTGAAATTTGACCAATAGGGTCCAGATT 1437
QY 38 SerPheileValPheSerThr-----ArgGlyThrLysMetLysLeuThrGlu 54
DB 1438 AGCTTGTGCAATACACCGCGGATCTCTATAGCATGCTTGTGAAATTAATTCACCAAA 1497
QY 55 AspArgGluGlnIleArgGlnGlyLeuGluGlnLysValLeuPro-----Gly 72
DB 1498 GTTGAAGATATTAATTT-----GAAGCATTAACAACCTTCCTTACAGAGGA 1542
QY 73 GlyAspThrTyRheHsiGluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsn 92
DB 1543 GGATCTCAAAATCTGGCAAAAGCAATGATCTATGTCAAGAGAAATATTTGTGCTACG 1602
QY 93 ArgGlnGlyTyTyTyRgThr-----AlaSerValIleIleAlaLeuThrAspGlyGluLeu 110
DB 1603 AAG--GGATCAAGAACCAATGTGCCAAAGGTCTATGTTCTTACAGAGTGGGAA-- 1656
QY 111 HieGluAspLeuPhePheTyRserGluArgGluAlaAsnArgSerArgAspLeuGlyAla 130
DB 1657 TCATTCAGATCTTTC-----AGAGATCCCTGCGTAAACCTGAGGAATTCAGATGT 1707
QY 131 IleValTyCyValGlyValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp 150
DB 1708 GAATCTTTCAGTGGTGTGAAGATGCCGTTGCTGCAAGATTTGAAAGCTATGCTCT 1767
QY 151 -----SerLysAspHsiLeValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 168
DB 1768 CTTCTGCAAGAACCCATGTTGTTTCAACAGTGAAGAT--TTTGAATGCTTTTCAAGAGATA 1824
```

```
RESULT 4
/ US-10-185-39040/c
/ Sequence 39040, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
```

```
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: NM11100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 39040
/ LENGTH: 2834
/ TYPE: DNA
/ ORGANISM: Bovine
/ US-10-750-185-39040
```

```
Alignment Scores:
Pred. No.: 0.00247 Length: 2834
Score: 115.00 Matches: 53
Percent Similarity: 50.00% Conservative: 38
Best Local Similarity: 29.12% Mismatches: 69
Query Match: 12.79% Indels: 24
DB: Gaps: 10
```

US-09-970-076-2_COPY_44_216 (1-173) x US-10-750-185-39040 (1-2834)

```
QY 1 AspleuTyRheileuAplySerglyServalLeuHsih1rPaengluile 18
DB 2115 GACATTACTTCTCTATATGACGGGTCTGGCAGTAC-----CACCAAGACGACTTCTC 2062
QY 19 ---lletyTyRheValGluGlnLeuAlaHsiLysPhe---lleserProGlnLeuArg 36
DB 2061 GCGATAGAGTGTCTTATGATGATGAAGATGAAGATGTTCCACCTTGACCGGAC--AGA 2005
QY 37 MetSerPheileValPheSerThrArgGlyThrLysMetLysLeuThrGluAsp 56
DB 2004 GTCCAGTTTGAATCGTTCACTGATCTGAGATGAAGTCAAGTCCACGTTACCTCAGCCAG 1945
QY 56 gGluGlnIleArgGlnGlyLeuGlu-----GluLeuGlnLysValLeuProG 72
DB 1944 CACTCGAGTGTGCAAGGCTTGGAGGTAGCCGTTGACAGATCCAGAG-----AAGGG 1891
QY 72 yGlyAspThrTyRheHsiGluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAs 92
DB 1890 AGGGGACACCAAGATGAGTGAAGCCCTG--GGCACCATGATCCAGGTCTTTCAGAGCTC 1834
QY 92 nArgGlnGlyTyTyTyRgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHsiG 112
DB 1833 TGCTCGAGCAA-CGAGCCTT-GGTATCTCATTTGTTGTCACTGACGCGCAATCTATGCA 1776
QY 112 uAspLeuPhePheTyRserGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleVa 132
DB 1775 CCGGCG-----GCTGATGCTGAGAGGGCGTGAAGGGCGCATGGAATCCACCAT 1728
QY 132 lTyTyCyValGlyValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLy 152
DB 1727 TTATGAGTTGGAGTGAAGATGCTTAATTTGCTGAGCTTCAAGAGATTTGCTA-- 1673
QY 152 sAspHsiLeValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsiSer 172
DB 1672 -GACAGAAATTTTGTGTCATGAT--TTTGAATGCTTTGAGAACATCCACAAAGAGT 1617
QY 172 eLeu 173
DB 1616 GGTGA 1613
```

```
RESULT 5
/ US-10-601-368-20
/ Sequence 20, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FaastSeq for Windows Version 3.0
/ SEQ ID NO 20
/ LENGTH: 3564
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.00296 Length: 3564
Score: 108.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 12.01% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_44_216 (1-173) x US-10-601-368-20 (1-3564)

QY 1 AapLeuTyrrPheIleuAerlySerGlySerValLeuHisIleTPraEngIuIleTyx 20
DB 490 GACATGCTCATTTGCTTAAGTGGCTCCACAGCATC--TACCCCTGGGGAGGCTCCA 546
QY 21 TyrrPheValGlulInleuAlaHisIlyrPhe---IleSerPro---GlnleuArgMetSer 38
DB 547 CACTTCCTCATCAATATCCTCAAAAAGTTCTACATTGGCCCGGCGAGATCCAGGTCCGA 606
QY 39 PheIleValPheSerThrArgIlyThrIleuMetIlyleuThrgIuAraArgIuIn 58
DB 607 ATAGTCCAGTATGGAGAGATGCCGTCCATGATTCACCTT--AATGACTACAGGCTC 663
QY 59 IleArgInGlyleuGluInleuGlnIyValleuProGlyIyAerThrTyMetHis 78
DB 664 GTAAAGATGTGTGGAGAGCCGCCACCATTCAGACAGAGAGGAGACAGACCCGC 723
QY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrrTyrgIuAraArgInGly 95
DB 724 ACGGCATTGGCATTTGAATTGGACGCTCGGAGGCTTCCAGAAAGGTGGAGAAAGGG 783
QY 96 TyrrArgThrAlaSerValIleIleAlaIleuThraPrgIyGluuHisIsgIuAerP 113
DB 784 GCCAAG-----AAAGTATGATGTTCATCAGGACGGGAAATCCACGACGCCAGAC 837
QY 113 ----- 113
DB 838 CTGAGAAAGTGATCCGGCAGAGGAGACAACTGACCAAGATACGCTGTGGCCGTT 897
QY 114 LeuPhePheTyrrSerGluArgIuAlaAraArgSerArgPheIleuGlyAlaIleValTyx 133
DB 898 TTGGGCTACTACAAACCGGAGGGGATCAATCCAGACTTTCTTAATGAATCAATATAC 957
QY 134 CysValGlyValIyAerP-----PheAengIuThrgInleuAlaArgIleAla 149
DB 958 ATCCGACGACACCTCGACAGACAACTTTCTTCAACGTCAACAGATGAGAGCGGCCCTG 1014
QY 150 AapSerIyAerPHisIyValPheProValAraPrgIyPheGlnAlaIleuGlnIy 167
DB 1015 -----AAGGACATTTGTGATGCCCTTGGGACAGAGATCTTCAGCTTGAAGGC 1062
RESULT 6
US-10-601-368-19
```

```
/ Sequence 19, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FaastSeq for Windows Version 3.0
/ SEQ ID NO 19
/ LENGTH: 4858
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (28)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.00465 Length: 4858
Score: 108.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 12.01% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_44_216 (1-173) x US-10-601-368-19 (1-4858)

QY 1 AapLeuTyrrPheIleuAerlySerGlySerValLeuHisIleTPraEngIuIleTyx 20
DB 517 GACATGCTCATTTGCTTAAGTGGCTCCACAGCATC--TACCCCTGGGGAGGCTCCA 573
QY 21 TyrrPheValGlulInleuAlaHisIlyrPhe---IleSerPro---GlnleuArgMetSer 38
DB 574 CACTTCCTCATCAATATCCTCAAAAAGTTCTACATTGGCCCGGCGAGATCCAGGTCCGA 633
QY 39 PheIleValPheSerThrArgIlyThrIleuMetIlyleuThrgIuAraArgIuIn 58
DB 634 ATAGTCCAGTATGGAGAGATGCCGTCCATGATTCACCTT--AATGACTACAGGCTC 690
QY 59 IleArgInGlyleuGluInleuGlnIyValleuProGlyIyAerThrTyMetHis 78
DB 691 GTAAAGATGTGTGGAGAGCCGCCACCATTCAGACAGAGAGGAGACAGACCCGC 750
QY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrrTyrgIuAraArgInGly 95
DB 751 ACGGCATTGGCATTTGAATTGGACGCTCGGAGGCTTCCAGAAAGGTGGAGAAAGGG 810
QY 96 TyrrArgThrAlaSerValIleIleAlaIleuThraPrgIyGluuHisIsgIuAerP 113
DB 811 GCCAAG-----AAAGTATGATGTTCATCAGGACGGGAAATCCACGACGCCAGAC 864
QY 113 ----- 113
DB 865 CTGAGAAAGTGATCCGGCAGAGGAGACAACTGACCAAGATACGCTGTGGCCGTT 924
QY 114 LeuPhePheTyrrSerGluArgIuAlaAraArgSerArgPheIleuGlyAlaIleValTyx 133
DB 925 TTGGGCTACTACAAACCGGAGGGGATCAATCCAGACTTTCTTAATGAATCAATATAC 984
QY 134 CysValGlyValIyAerP-----PheAengIuThrgInleuAlaArgIleAla 149
DB 985 ATCCGACGACACCTCGACAGACAACTTTCTTCAACGTCAACAGATGAGAGCGGCCCTG 1041
QY 150 AapSerIyAerPHisIyValPheProValAraPrgIyPheGlnAlaIleuGlnIy 167
DB 1042 -----AAGGACATTTGTGATGCCCTTGGGACAGAGATCTTCAGCTTGAAGGC 1089
```

```
RESULT 7
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2
```

```
Alignment Scores:
Pred. NO.: 0.0101 Length: 3564
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.57% Indels: 38
DB: 6 Gaps: 9
```

US-09-970-076-2_COPY_44_216 (1-173) x US-10-601-368-2 (1-3564)

```
QY 1 AspleuTyrrhelleuaplyserserlyserValuethshstpaangluiletyr 20
DB 490 GACATCGTCATGTCCTGATGCGTCCAGACGATC--TACCCCTGGGTGAAGTTGAG 546
QY 21 TyrPheValGluGlnLeuAlaHisIleuPhe--IleSerPro--GlnLeuArgMetSer 38
DB 547 CACTTCCTCATCAACATCCTCGAAGATTTTACATTCGCGGAGGAGATCCAGATTGGA 606
QY 39 PheIleValIlePheSerThrArgGlyThrThleuMetIleuThrGluAspArgGluIn 58
DB 607 GTTGTGAGATGAGCGAAGATGTGTCATGATTCACCTC--AACGACTACAGGTCT 663
QY 59 IleArgGlnIleuGluGlnLeuGlnIleuValIleuProGlyIleuAspThrTyMetHis 78
DB 664 GTAAAGATGTGTGTGAAGCTGCCAGCCACATTCAGCAGAGAGAGAGAGAACAGACCCGG 723
QY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrrTyGluAsnArgGlnGly 95
DB 724 ACGCATTGGCATGTAATTGCAACGCTCAGAGGCTTCCAGAAAGGATGGAAGAAAGGA 783
QY 96 TyrArgThrAlaSerValIleIleAlaLeuThrArgGlyIleuHisGluAsp----- 113
DB 784 GCCAAG-----AAGTGATGATGTTGATCATCAGATGGGAGTCCACAGACGCCAGAC 837
QY 113 ----- 113
DB 838 CTGAGAAAGTGATCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 897
QY 114 LeuPhePheTyrserserlyserGluAlaAsnArgSerArgAspLeuGluAlaIleValTyr 133
DB 898 CTGGGCTACTACACCGGAGGGGATGATCCAGAACTTTCTTAATGAATGAATGAATAC 957
QY 134 CysValGlyValIleuAsp-----PheAsnGluThrGlnIleuAlaArgIleAla 149
DB 958 ATCCGACGATGACCTGATGACAGACATTCCTTCAATGATGATGATGAGTGGCTTG--- 1014
```

```
QY 150 AspSerIysAspHisValIlePheProValAsnAspGlyPheGlnAlaLeuGlnGly 167
DB 1015 -----AAGGACATTCGATGCGCTGGGGGAGCAGAAATCTTCACCTCGAAGGCC 1062
```

```
RESULT 8
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 574
; LENGTH: 3967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-574
```

```
Alignment Scores:
Pred. NO.: 0.0118 Length: 3967
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.57% Indels: 38
DB: 7 Gaps: 9
```

US-09-970-076-2_COPY_44_216 (1-173) x US-11-000-463-574 (1-3967)

```
QY 1 AspleuTyrrhelleuaplyserserlyserValuethshstpaangluiletyr 20
DB 539 GACATCGTCATGTCCTGATGCGTCCAGACGATC--TACCCCTGGGTGAAGTTGAG 595
QY 21 TyrPheValGluGlnLeuAlaHisIleuPhe--IleSerPro--GlnLeuArgMetSer 38
DB 596 CACTTCCTCATCAACATCCTCGAAGATTTTACATTCGCGGAGGAGATCCAGATTGGA 655
QY 39 PheIleValIlePheSerThrArgGlyThrThleuMetIleuThrGluAspArgGluIn 58
DB 656 GTTGTGAGATGAGCGAAGATGTGTCATGATTCACCTC--AACGACTACAGGTCT 712
QY 59 IleArgGlnIleuGluGlnLeuGlnIleuValIleuProGlyIleuAspThrTyMetHis 78
DB 713 GTAAAGATGTGTGTGAAGCTGCCAGCCACATTCGAGCAGAGAGAGAGAGAGAGACCCGG 772
QY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrrTyGluAsnArgGlnGly 95
```

```
Db 773 ACGGCACTTGGCATGTAATTGCAAGCTCAGAGCCTTCCAGAAAGGTGGAAGAAAGGA 832
Qy 96 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 113
Db 833 GCCAAG-----AAGGTGATGATGTTCATCAGATGGGAGTCCACGACGACCCAGAC 886
Qy 113 ----- 113
Db 887 CTGGAGAGGTGATCCAGCAAGCGAAAGACACGTAACAAGATATGCGTGGCCGTC 946
Qy 114 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 133
Db 947 CTGGGCTACTACAAACGCGAGGGGAGTCAATCCAGAAACTTTCTTAATGAATCAAAATAC 1006
Qy 134 CysValGlyValIlyAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 149
Db 1007 ATGCCGAGTACCCCTGATGACAAAGCACTTCTCAATGTCACTGATGAGGCTGCTTG--- 1063
Qy 150 AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 167
Db 1064 -----AAGGACATTTGTGATGCCCTGGGGGACAGAAATCTTCAAGCTCGAAGGC 1111

RESULT 9
US-11-000-463-102
/ Sequence 102, Application US/11000463
/ Publication No. US20050266423A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Aaundi, Vinod
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Qian, Xiaohong B.
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhou, Ping
/ APPLICANT: Cao, Yi-cheng
/ APPLICANT: Dimanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
/ FILE REFERENCE: 785CIP4CN
/ CURRENT APPLICATION NUMBER: US/11/000,463
/ CURRENT FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: 10/291,265
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/922,279
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 09/617,746
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/631,451
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 09/633,870
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 3969
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3618)
US-11-000-463-102

Alignment Scores:
Pred. No.: 0.0118 Length: 3969
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
```

```
Query Match: 11.57% Indels: 38
DB: 7 Gaps: 9
US-09-970-076-2_COPY_44_216 (1-173) x US-11-000-463-102 (1-3969)
Qy 1 AppLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIleTyrAsnGluIleTyr 20
Db 541 GACATCGTCAATGCTCGTGGATGGCTTCCAAACACATC---TACCCTGGTGAAGGTTCA 597
Qy 21 TyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro---GlnLeuArgMetSer 38
Db 598 CACTTCTCTATCAACACTCTGAAAGATTTCATTTGCGCCGAGGCGAGATCCAGGTTGA 657
Qy 39 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGln 58
Db 658 GTTGTGCACTATGGGGAAGATGTGGATGATGATTCACCTC---AAGCATTAAGGTCCT 714
Qy 59 IleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHis 78
Db 715 GTAAAGATGTGTGGAGAGCTGCCAGCCACATTTGAGCAGAGAGGAGGAACAGACCAG 774
Qy 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 95
Db 775 ACGGCACTTGGCATGTAATTGCAAGCTCAGAGGCTTCCAGAAAGGTGGAAGAAAGGA 834
Qy 96 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 113
Db 835 GCCAAG-----AAGGTGATGATGTTCATCAGATGGGAGTCCACGACGACCCAGAC 888
Qy 113 ----- 113
Db 889 CTGGAGAGGTGATCCAGCAAGCGAAAGACACGTAACAAGATATGCGTGGCCGTC 948
Qy 114 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 133
Db 949 CTGGGCTACTACAAACGCGAGGGGAGTCAATCCAGAAACTTTCTTAATGAATCAAAATAC 1008
Qy 134 CysValGlyValIlyAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 149
Db 1009 ATGCCGAGTACCCCTGATGACAAAGCACTTCTCAATGTCACTGATGAGGCTGCTTG--- 1065
Qy 150 AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 167
Db 1066 -----AAGGACATTTGTGATGCCCTGGGGGACAGAAATCTTCAAGCTCGAAGGC 1113

RESULT 10
US-10-601-368-1
/ Sequence 1, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 5042
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (127)...(3690)
US-10-601-368-1

Alignment Scores:
Pred. No.: 0.0168 Length: 5042
```


Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.57% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-2_COPY_44_216 (1-173) x US-10-601-368-1 (1-5042)

```
OY 1 AspleuYrThrHeIleuAerlySerGlySerValLeuHIShSTRaNGIuIleTyR 20
DB 616 GACATGCTCATTTGCTGGATGGCTCCAAACGCAATC--TACCTCGGTGGAGATTGAG 672
OY 21 TyrPheValGluGlnLeuAlaHISLeuPhe--IleSerPro--GlnLeuArgMetSer 38
DB 673 CACTTCCTCATCAACATCCCGAAGATTTTACTTTGCCCCAGGCGAGATCCAGTTGGA 732
OY 39 PheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAerArgGluGln 58
DB 733 GTTGTCAGATGCGCAAGATGTGTCATGATGTTCACTTC--AAGCACTACAGGCT 789
OY 59 IleArgGlnGluLeuGluGlnLeuGlnLysValLeuProGlyAerThrTyRMetHis 78
DB 790 GTAAGAATGTGTGGAGAGCTGCCAGCCATTGAGAGAGAGAGAGAGAGAGAGAGAGAG 849
OY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyRtyrGluAerArgGlnGly 95
DB 850 ACGGCATTTGGCATGTAATTTGCACGCTCAGAGGCTTCCAGAAAGGTGGAGAGAGAG 909
OY 96 TyrArgThrAlaSerValIleIleAlaLeuThrAerGlyGluLeuHISgluAer----- 113
DB 910 GCCAAG-----AAGTGATGATGTGTATCATCAGATGGAGATGCCACAGACGCCAGAC 963
OY 113 ----- 113
DB 964 CTGAGAGAGGTATCCAGCAAGAGCAAGAGCAACATTCAGATGCGGTGGCCGCTC 1023
OY 114 LeuPhePheTyRserGluArgGluAlaAerArgSerAerPheGluAlaIleValTyR 133
DB 1024 CTGGGCTACTTCAACACCGGAGGAGATATCCAGAACTTTTCTTAATGAATCAATAC 1083
OY 134 CysValGlyValLysAer-----PheAerGluThrGlnLeuAlaArgIleAla 149
DB 1084 ATCGCCAGTACCCTGATGACAGCACTTCTCAATGTCACTGATGAGCGTGCCTTG-- 1140
OY 150 AspSerLysAerPheIleValPheProValAerPheGlyPheGlnAlaLeuGlnGly 167
DB 1141 -----AAGGACATTTGTGATGCCCTGGGAGACGAATCTTCAGCCTGAAAGGC 1188
```

RESULT 11

US-10-821-234-182/c
Sequence 182, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Steache-Crain, Birgit
APPLICANT: Andermani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PC_SEQ_genes Version 1.0
SEQ ID NO 182
LENGTH: 2501
TYPE: DNA
ORGANISM: Homo sapiens
US-10-821-234-182
Alignment Scores: 0.013 Length: 2501

Score: 101.50 Matches: 47
Percent Similarity: 43.06% Conservative: 43
Best Local Similarity: 22.49% Mismatches: 74
Query Match: 11.29% Indels: 45
DB: 6 Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-10-821-234-182 (1-2501)

```
OY 1 AspleuYrThrHeIleuAerlySerGlySerVal-----LeuHIShIS 15
DB 1550 AACATTAACCTGGATGGATGAGATGACAGACGATTTGGGCGCCAGCAATTCACAGAGCC 1491
OY 16 TrpAerGluIleTyRtyrPheValGluGlnLeuAlaHISLysPheIleSerProGlnLeu 35
DB 1490 AAAAGTGTATGCAACTTAATTGAGAGGTGGCAAGTATGTTGTAAGGCCA----- 1437
OY 36 ArgMetSerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAer 54
DB 1436 AGATATGCTGATGATGACATATGCAATACCCCAAAATTTGGGTCAAAAGTGTGAAGCA 1377
OY 55 -----AspArgGluGlnIleArgGlnGlyLeuGluGlnLeu-----Gln 67
DB 1376 GACAGCAGTAATGACAGCTGGTCCAGAACACCTCAATGAATCAATTATGAAGACCA 1317
OY 68 LysValLeuProGlyGlyAerThrTyRMetHisGluGlyPheGluArgAlaSerGluGln 87
DB 1316 AAGTTGAAGTACAGGAGCAATACACC-----AAGAAAGCCTCCAGCA 1275
OY 88 IleTyRtyrGluAerArg-----GlnGlyTyR--ArgThrAla 99
DB 1274 GTGTACAGCATGATGATGAGCTGCCAGATGACGCTCCCTGTGAAGCTGAAACCCAGCCG 1215
OY 100 SerValIleIleIleAlaLeuThrAerGly----- 108
DB 1214 CAGTGCATCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1155
OY 109 -----GluLeuHISgluAerPhePheTyRserGlyArgGluAlaAerArgSerArg 126
DB 1154 ATTGATGAGATCCCGGACTTGTATATCATTTGCGAAGATGCAAAAACCAAGGAGAT 1095
OY 127 AspLeuGlyAlaIleValTyRtyrCysValGly-----ValLysAerPheAerGluThrGln 144
DB 1094 TATCTGATGTCTATATGATGTTGGGTGCGGCTTGTGTGAACCAAGTGAATCATATGCT 1035
OY 145 LeuAlaArgIleAlaAerSerLysAerPheIleValPheProValAerPheGlyPheGlnAla 164
DB 1034 TTGGCTTCCAAAGAAAGACATGAGCAACATGTGTCAAGTCAAGAT--ATGGAAGAC 978
OY 165 LeuGlnGlyIleIleHISerIleLeu 173
DB 977 CTGAAAGATGTTTCTTACCAATGATC 951
```

RESULT 12

US-10-131-826A-293
Sequence 293, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William

```

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
PRIOR FILING DATE: 2002-04-24
APPLICATION NUMBER: 60/045911
PRIOR FILING DATE: 1997-06-18
APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 293
LENGTH: 3449
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-293

```

| Alignment Scores: | 0.0282 | Length: | 3449 |
|------------------------|--------|---------------|------|
| Pred. No.: | 100.50 | Matches: | 42 |
| Percent Similarity: | 46.82% | Conservative: | 39 |
| Best Local Similarity: | 24.28% | Mismatches: | 67 |
| Query Match: | 11.18% | Indels: | 25 |
| DB: | 6 | Gaps: | 9 |

| US-09-970-076-2_COPY_4_216 (1-173) x US-10-131-826A-293 (1-3449) |
|---|
| <p>QY 1 AapLeuTyrPheIleuAapLySerGlySerVal---LeuHsiHsrTPaenGluIle 19</p> <p>DB 372 GACCTGGTTTCATCTATTaACAGCTTCGCAAGTGTCAACCCATGACTATGCAAAAGTC 431</p> <p>QY 20 TyrTyrPhe---ValGluInLeuAaHsiLyPheIleSerProGluIn---ArgMet 37</p> <p>DB 432 AAGAGATTATGCTGGACATCTTGCAATCTTGAGACTTGCTGTATGTACCCAGGTG 491</p> <p>QY 38 SerPheIleValPheSerThrArgGlyThrIleu-----MetLybLeu 52</p> <p>DB 492 GGCCTGCTCCAAATAT-----GGCAGACGTGCAAGATAGTTCTCCCTCAAGACC 542</p> <p>QY 53 ThrGluAapArgGluInIleArgGluInGlyLeuGluInGluInLySerValLeuProGly 72</p> <p>DB 543 TTCAGAGAGAAAGTCCAGAGGTGAGCGCTGTCAAGAGGATGGCGGCAATCTGTCCACGGGC 602</p> <p>QY 73 GluAapThrTyrMetHsiGluInPheGluArgAlaSerGluInGlyTyrTrgLuAaIn 92</p> <p>DB 603 ACCATGACTGGGGTGGCCATCCAGTAT-----GCCCTGAACATCGCAATCTCAGAA 653</p> <p>QY 93 ArgGluInGlyTyrArg-----ThrAlaSerValIleIleAlaLeuThrAsp 107</p> <p>DB 654 GCAGAGGGGGGGGGGGGGGGGGGGAGAGAAATGTGCCAGGGTCTAATATGATCTGCACGAT 713</p> <p>QY 108 GlyGluLeuHsiGluAapLeuPhePheTyrSerGluArgGluIlaAenArgSerArgAsp 127</p> <p>DB 714 GGGAGACCTTCAGGACTCCGGT-----GCCGAGGTGGCTGTAAAGCAGCGGAC 761</p> <p>QY 128 LeuGlyAlaIleValTyrCybValGlyVal-----LysAapPheanGluThrGluLeu 145</p> |

```

Db          762  ACGGCGATCCTATCTTTCCATTGTGTGGGCGCAGTAGACTTCAACACCTTGAAAGTCC 821
Oy          146  AAlArYglEalAaSpSerYsAspHsIvAlpHeProVal 158
Db          822  ATTGGAGAGTGAGCCCCCATAGGAGCAGCATGCTTCTCTTG 860

RESULT 13
US-10-750-185-56394
; Sequence 56394, Application US/10750185
; Publication No. US20050260603A1
GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56394
LENGTH: 1325
TYPE: DNA
ORGANISM: Bovine 19866880505724
US-10-750-185-56394

```

| | | | |
|------------------------|--------|---------------|------|
| Alignment Scores: | | | |
| Pred. No.: | 0.0129 | Length: | 1325 |
| Score: | 98.50 | Matches: | 41 |
| Percent Similarity: | 46.82% | Conservative: | 40 |
| Best Local Similarity: | 23.70% | Mismatches: | 67 |
| Query Match: | 10.96% | Indels: | 25 |
| DB: | 6 | Gaps: | 9 |

US-09-970-076-2_COPY_44_216 (1-173) x US-10-750-185-56394 (1-1325)

| | | | | |
|----|-----|---|-----------------------|----|
| QY | 1 | AspLeuTyRPhlelleLeuAapLySserGlySerVal--- | LeuHlshierPnaangluile | 19 |
| | | | | |
| DB | 483 | GACGCGCTTTATATATGACACGCTCCACGACGCTCAACACCCACGACCTAACCGAAGGTC | 542 | |
| QY | 20 | TyTyRPhle---ValGluGlnLeuAlaHisLysPheIleSerProGlnLeu--ArgMet | 37 | |
| | | | | |
| DB | 543 | AAGAGATTCATGTGTGACATCTCTGACAGTTCTTGACATTTGGCCCTGACCTGACCCGCTGAC | 602 | |
| QY | 38 | SerPheIleValPheSerThrArgGlyThyRThrLeu-----MetLysLeu | 52 | |
| | | | | |
| DB | 603 | GCTGCGCTCCAGAT-----GCGACACAGGCTCAAGACAGATTCTCCCTCAAGACC | 653 | |
| QY | 53 | ThirGluAapArgGlnGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGly | 72 | |
| | | | | |
| DB | 654 | TTCAAGAGCAAGACTCCGAGGTGAGGAGGCTCCGTCMAAGAGATGGGATCTGTCCACGGG | 713 | |
| QY | 73 | GlyAapThyRMetHisGlnGlyPheGluArgAlaSerGlnGlnIleTyTyRArgLysAsn | 92 | |
| | | | | |
| DB | 714 | ACCATGACCGGGGCTGGCCATCCAGTAC-----GCCCTGAACATCGGCTTCTGGAA | 764 | |
| QY | 93 | ArgGlnGlyTyArg-----ThrAlaSerValIleLeuAlaLeuThrAsp | 107 | |
| | | | | |
| DB | 765 | GCAAGAGGGGGCCGGCCCTGAGGAGAGATGCGCTCGGTCATATATGATCTGACTGAT | 824 | |
| QY | 108 | GlyGluLeuHisGlnAapLeuPheThyRSerGluArgGluAlaHisnArgSerArgAsp | 127 | |
| | | | | |
| DB | 825 | GGGAGGCCCCACAGACTCGGTG-----GCCAGAGTGGCCGCAAAAGCCCGGAC | 872 | |
| QY | 128 | LeuGlyAlaIleValTyRcysValGlyVal-----LysAapPheAsnGluThrGlnLeu | 145 | |
| | | | | |

Db 873 ACAGCATCTGATCTTTCATCGGTGGCCAGGTGACCTTCAACAGCTGAGGCC 932
Qy 146 AlargilleAlaerSerlyAaphiValPheProVal 158
Db 933 ATTGGAGGACGCCCGCCAGAGACCACTTCTCTGATG 971

RESULT 14
US-10-995-561-464
/ Sequence 464, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: C1001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 464
/ LENGTH: 3175
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.0855 Length: 3175
Score: 96.50 Matches: 45
Percent Similarity: 41.12% Conservative: 36
Best Local Similarity: 22.84% Mismatches: 83
Query Match: 10.73% Indels: 33
Gaps: 8

US-09-970-076-2_COPY_44_216 (1-173) x US-10-995-561-464 (1-3175)

Qy 2 LeuTYRheIleuAphlySerGlySerVal----- 12
Db 243 GTGTACTGTGCTGTGACCTCTGGAGAGGTGACCATGACATGCCCGCCAGCATCTG 302
Qy 13 LeuNIHietrAphnglu---IleTYRtyrPheValGluGlnleuAlaNIshlyPheIle 31
Db 303 CTCTCCACATGACGAGTTCGTGCGCCAGCTTCAAGCACTGCGAGCAAGATCTTAC 362
Qy 32 SerProGlnleuAphMetSerPhe-----IleValPheSerThrArgGlyThr 47
Db 363 CTGACACAGGTGGCGTGAAGCTGCGCTAGGCGCGCTGACTTCTTGCACAGGTGAG 422
Qy 48 ThrLeuMetIlyleuThrGluAraArgGluGlnIleArgGlnIlyleuGluIleuGln 67
Db 423 GTGTTCAGCCACCGGCGAGCGGCGCTCTTCATCAAGAACTGCGAGGCGCATCAG 482
Qy 68 LysValIleuProGlyGlyAerThrTyrmehNIshGluIlyPheGluArgAlaSerGluGln 87
Db 483 TCCTTCGCGCGCGGCG-----ACCTTCACCGAGCTGCGCGCTGCGCAACATGAGGAGCAG 536
Qy 88 IleTYRtyrGluAphnArgGlnIlyTyArgThrAlaSerValIleIleAlaIleuThrAer 107
Db 537 ATCCGGCAGAGACCGGCGAGGAGGCG-----ACGTCACATTCGCGCGGTGATCAGCCGAC 590
Qy 108 GlyGluLeuNIshGluAerIlyleuPhePheTySerGluAraGluAlaAphnArgSerArgAer 127
Db 591 GCGCAGCTACCGGCGAGCGCGCTGCGGGGAGATCAAGCTGACAGCGCGGCGCGCGAG 650
Qy 128 LeuGlyAlaIleValIlyTyCyVal-----GlyValIly 138
Db 651 GAGGGCATCCGCGCTTTCGCGCGTGGCGCCCAACAGAACTGAAGAGAGCGCGCTGCGG 710
Qy 139 AepPheAenGluThr-----GlnleuAlaArgIleAlaAerSerIlyAerPhIValPhe 156
Db 711 GACATGCCAGACGCGCGAGCTTCTTACCG-----AACGACTAGCGGCAC 758
Qy 157 ProValAphAerGlyPheGlnAlaIleuGlnIlyIleIshSerIleIleu 173

Db 759 ATGCTGCYAGATTCACCGAGATTCACAGAGACCATCAACCGCATCATC 809
Qy 759 ATGCTGCYAGATTCACCGAGATTCACAGAGACCATCAACCGCATCATC 809

RESULT 15
US-10-995-561-465
/ Sequence 465, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: C1001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 465
/ LENGTH: 3464
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-465

Alignment Scores:
Pred. No.: 0.0971 Length: 3464
Score: 96.50 Matches: 45
Percent Similarity: 41.12% Conservative: 36
Best Local Similarity: 22.84% Mismatches: 83
Query Match: 10.73% Indels: 33
Gaps: 8

US-09-970-076-2_COPY_44_216 (1-173) x US-10-995-561-465 (1-3464)

Qy 2 LeuTYRheIleuAphlySerGlySerVal----- 12
Db 243 GTGTACTGTGCTGTGACCTCTGGAGAGGTGACCATGACATGCCCGCCAGCATCTG 302
Qy 13 LeuNIHietrAphnglu---IleTYRtyrPheValGluGlnleuAlaNIshlyPheIle 31
Db 303 CTCTCCACATGACGAGTTCGTGCGCGCGAGTTCAGCGCGAGCAAGATCTTAC 362
Qy 32 SerProGlnleuAphMetSerPhe-----IleValPheSerThrArgGlyThr 47
Db 363 CTGACACAGGTGGCGTGAAGCTGCGCTAGGCGCGCTGACTTCTTGCACAGGTGAG 422
Qy 48 ThrLeuMetIlyleuThrGluAraArgGluGlnIleArgGlnIlyleuGluIleuGln 67
Db 423 GTGTTCAGCCACCGGCGAGCGGCGCTCTTCATCAAGAACTGCGAGGCGCATCAG 482
Qy 68 LysValIleuProGlyGlyAerThrTyrmehNIshGluIlyPheGluArgAlaSerGluGln 87
Db 483 TCCTTCGCGCGCGGCG-----ACCTTCACCGAGCTGCGCGCTGCGCAACATGAGGAGCAG 536
Qy 88 IleTYRtyrGluAphnArgGlnIlyTyArgThrAlaSerValIleIleAlaIleuThrAer 107
Db 537 ATCCGGCAGAGACCGGCGAGGAGGCG-----ACGTCACATTCGCGCGGTGATCAGCCGAC 590
Qy 108 GlyGluLeuNIshGluAerIlyleuPhePheTySerGluAraGluAlaAphnArgSerArgAer 127
Db 591 GCGCAGCTACCGGCGAGCGCGCTGCGGGGAGATCAAGCTGACAGCGCGGCGCGCGAG 650
Qy 128 LeuGlyAlaIleValIlyTyCyVal-----GlyValIly 138
Db 651 GAGGGCATCCGCGCTTTCGCGCGTGGCGCCCAACAGAACTGAAGAGAGCGCGCTGCGG 710
Qy 139 AepPheAenGluThr-----GlnleuAlaArgIleAlaAerSerIlyAerPhIValPhe 156
Db 711 GACATGCCAGACGCGCGAGCTTCTTACCG-----AACGACTAGCGGCAC 758
Qy 157 ProValAphAerGlyPheGlnAlaIleuGlnIlyIleIshSerIleIleu 173
Db 759 ATGCTGCYAGATTCACCGAGATTCACAGAGACCATCAACCGCATCATC 809

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Search completed: December 19, 2005, 02:30:41
JOB time : 155.602 secs
